

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application No. : 12/970,052 Confirmation No. : 5362
Applicant : Scott Diehn
Filed : December 16, 2010
TC/A.U. : 1638
Examiner : Jeffery R. Bolland
Docket No. : 3700
Customer No. : 27310
Title : Maize Event DP-004114-3 and Methods of Detecting Thereof

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

AMENDMENT UNDER 37 C.F.R. § 1.111

In response to the Office Action of February 04, 2013, please amend the above-identified application as follows:

Amendments to the Specification begin on page 2 of this paper.

A Complete Listing of the Claims begins on page 3 of this paper.

Remarks/Arguments begin on page 11 of this paper.

Inari Exhibit 1095 Inari v. Corteva IPR2024-01014

AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraphs from page 52, line 7 to page 53, line 20 with the following amended paragraphs:

To characterize the inserted T-DNA in 4114 maize, PCR primers were designed to amplify the T-DNA insert in six separate, overlapping PCR products as outlined in Table 7: fragments A through F (Positions indicated in Figure 5). As expected, the predicted PCR products were generated only from 4114 maize genomic DNA samples, and were not present in the control maize samples. The six PCR products were cloned and sequenced. When comparing the sequence of the inserted T-DNA in 4114 maize to the T-DNA region of plasmid PHP27118 used to create 4114 maize, it was determined that there was a 29 bp deletion on the RB end, and a 24 bp deletion on the LB end. RB and LB termini deletions often occur in *Agrobacterium*-mediated transformation (Kim *et al.* (2007) *Plant J.* 51:779-791). All remaining sequence is intact and identical to that of plasmid PHP27118. The sequence of the insertion is presented in ~~SEQ ID NO: 27~~ **SEQ ID NO: 6**.

To verify the additional 5' genomic border sequence, PCR was performed with a forward primer (SEQ ID NO: 11) in the 5' genomic border region and a reverse primer (SEQ ID NO: 12) within the inserted T-DNA. The resulting 2,511 bp PCR fragment A from 4114 maize genomic DNA samples was cloned and sequenced (Figure 3). The 2,422 bp of the 5' genomic border region sequence is set forth in nucleotides 1-2,422 of ~~SEQ ID NO: 27~~ **SEQ ID NO: 6**.

To verify the additional 3' genomic border sequence, PCR was performed with a forward primer (SEQ ID NO: 21) within the inserted T-DNA and a reverse primer (SEQ ID NO: 22) in the 3' genomic border region. The resulting 2,612 bp PCR fragment F from 4114 maize genomic DNA samples was cloned and sequenced (Figure 3). The 2,405 bp of the 3' genomic border region sequence is set forth in nucleotides 14,348 to 16,752 of ~~SEQ ID NO: 27~~ **SEQ ID NO: 6**.

Amendments to the Claims:

1. (currently amended) A DNA construct comprising: a first, second, third and fourth expression cassette, wherein said first expression cassette in operable linkage comprises:

- (a) a maize ubiquitin promoter;
- (b) a 5' untranslated exon of a maize ubiquitin gene;
- (c) a maize ubiquitin first intron;
- (d) a Cry1F encoding DNA molecule; and
- (e) a poly(A) addition signal from ORF 25 terminator;

said second expression cassette in operable linkage comprises:

- (1) a maize ubiquitin promoter;
- (2) a 5' untranslated exon of a maize ubiquitin gene;
- (3) a maize ubiquitin first intron;
- (4) a Cry34Ab1 encoding DNA molecule; and
- (5) a PinII transcriptional terminator;

said third expression cassette **in operable linkage comprises;** ~~comprising in operable linkage~~

- (i) a wheat peroxidase promoter;
- (ii) a Cry35Ab1 encoding DNA molecule; and
- (iii) a PinII transcriptional terminator; and

said fourth expression cassette **in operable linkage comprises;** ~~comprising in operable linkage~~

- (a) a CaMV 35S promoter;
- (b) a *pat* encoding DNA molecule; and
- (c) a 3' transcriptional terminator from CaMV 35S;

wherein the DNA construct is flanked by the 5' junction sequence of SEQ ID NO: 27 and the 3' junction sequence of SEQ ID NO: 28.

2. (currently amended) A plant comprising the DNA construct of claim 1, **wherein the DNA construct is flanked by the 5' junction sequence of SEQ ID NO: 27 and the 3' junction sequence of SEQ ID NO: 28.**

3. (original) A plant of claim 2, wherein said plant is a corn plant.

4. (original) A plant comprising the sequence set forth in SEQ ID NO: 6.

5. (currently amended) A corn plant comprising the genotype of the corn event DP-004114-3 **deposited with American Type Culture Collection (ATCC) under Accession No. PTA-11506**, wherein said genotype comprises the **DNA construct of claim 1 flanked by the** nucleotide sequence set forth in SEQ ID NO: 27 and SEQ ID NO: 28.

Claims 6. and 7. (cancelled)

8. (original) A corn event DP-004114-3, wherein a representative sample of seed of said corn event has been deposited with American Type Culture Collection (ATCC) with Accession No. PTA-11506.

9. (original) Plant parts of the corn event of claim 8.

10. (currently amended) Seed comprising corn event DP-004114-3, wherein said seed comprises **the DNA construct of claim 1 flanked by the 5' junction sequence of SEQ ID NO: 27 and the 3' junction sequence of SEQ ID NO: 28** ~~a DNA molecule selected from the group consisting of SEQ ID NO: 27 and SEQ ID NO: 28~~, wherein a representative sample of corn event DP-004114-3 seed of has been deposited with American Type Culture Collection (ATCC) with Accession No. PTA-11506.

11. (original) A corn plant, or part thereof, grown from the seed of claim 10.

12. (original) A transgenic seed produced from the corn plant of claim 11 comprising event DP-004114-3.

13. (original) A transgenic corn plant, or part thereof, grown from the seed of claim 12.

14. (original) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 6; SEQ ID NO: 27; SEQ ID NO: 28, and full length complements thereof.

15. (original) An amplicon comprising the nucleic acid sequence selected from the group consisting of SEQ ID NO: 27, SEQ ID NO: 28 and full length complements thereof.

16. (currently amended) A biological sample derived from corn event DP-004114-3 plant, tissue, or seed, wherein said sample comprises a nucleotide sequence ~~which is or is complementary to a sequence~~ selected from the group consisting of SEQ ID NO: 27 and SEQ ID NO: 28 **or the complement thereof**, wherein said nucleotide sequence is detectable in said sample using a nucleic acid amplification or nucleic acid hybridization method, wherein a representative sample of said corn event DP-004114-3 seed of has been deposited with American Type Culture Collection (ATCC) with Accession No. PTA-11506.

17. (original) The biological sample of claim 16, wherein said biological sample comprise plant, tissue, or seed of transgenic corn event DP-004114-3.

18. (original) The biological sample of claim 17, wherein said biological sample is a DNA sample extracted from the transgenic corn plant event DP-004114-3, and wherein said DNA sample comprises one or more of the nucleotide sequences selected from the group consisting of SEQ ID NO: 27, SEQ ID NO: 28, and the complement thereof.

19. (original) The biological sample of claim 18, wherein said biological sample is selected from the group consisting of corn flour, corn meal, corn syrup, corn oil, corn starch, and cereals manufactured in whole or in part to contain corn by-products.

20. (currently amended) An extract derived from corn event DP-004114-3 plant, tissue, or seed and comprising a nucleotide sequence ~~which is or is complementary to a sequence~~ selected from the group consisting of SEQ ID NO: 27 and SEQ ID NO: 28 **or the complement thereof**, wherein a representative sample of said corn event DP-004114-3 seed has been deposited with American Type Culture Collection (ATCC) with Accession No. PTA-11506.

21. (original) The extract of claim 20, wherein said nucleotide sequence is detectable in said extract using a nucleic acid amplification or nucleic acid hybridization method.

22. (original) The extract of claim 21, wherein said extract comprises plant, tissue, or seed of transgenic corn plant event DP-004114-3.

23. (original) The extract of claim 22, further comprising a composition selected from the group consisting of corn flour, corn meal, corn syrup, corn oil, corn starch, and cereals manufactured in whole or in part to contain corn by-products, wherein said composition comprises a detectable amount of said nucleotide sequence.

24. (currently amended) A method of producing hybrid corn seeds comprising:

- (a) planting seeds of a first inbred corn line comprising **the DNA construct of claim 1 flanked by the 5' junction sequence of SEQ ID NO: 27 and the 3' junction sequence of SEQ ID NO: 28** ~~a nucleotide sequence selected from the group consisting of SEQ ID NO: 27, SEQ ID NO: 28~~ and seeds of a second inbred line having a different genotype;
- (b) cultivating corn plants resulting from said planting until time of flowering;
- (c) emasculating said flowers of plants of one of the corn inbred lines;
- (d) sexually crossing the two different inbred lines with each other; and
- (e) harvesting the hybrid seed produced thereby.

25. (original) The method according to claim 24, wherein the plants of the first inbred corn line are the female parents.

26. (original) The method according to claim 24, wherein the plants of first inbred corn line are the male parents.

27. (currently amended) A method for producing a corn plant resistant to lepidopteran pests comprising:

- (a) sexually crossing a first parent corn plant with a second parent corn plant, wherein said first or second parent corn plant comprises event DP-004114-3 DNA, **deposited under Accession No. PTA-11506 with American Type Culture Collection (ATCC)**, thereby producing a plurality of first generation progeny plants;
- (b) selecting a first generation progeny plant that is resistant to lepidopteran insect infestation;
- (c) selfing the first generation progeny plant, thereby producing a plurality of second generation progeny plants; and
- (d) selecting from the second generation progeny plants, a plant that is resistant to lepidopteran pests;

wherein the second generation progeny plants comprise the DNA construct according to claim 1.

28. (currently amended) A method of producing hybrid corn seeds comprising:

- (a) planting seeds of a first inbred corn line comprising the DNA construct of claim 1 **flanked by the 5' junction sequence of SEQ ID NO: 27 and the 3' junction sequence of SEQ ID NO: 28** and seeds of a second inbred line having a genotype different from the first inbred corn line;
- (b) cultivating corn plants resulting from said planting until time of flowering;
- (c) emasculating said flowers of plants of one of the corn inbred lines;
- (d) sexually crossing the two different inbred lines with each other; and
- (e) harvesting the hybrid seed produced thereby.

29. (currently amended) The method of claim 28 further comprising ~~the step of~~ backcrossing the second generation progeny plant of step (d) that comprises corn event DP-004114-3 DNA, **deposited under Accession No. PTA-11506 with American Type Culture Collection (ATCC)**, to the parent plant that lacks the corn event DP-004114-3 DNA, thereby producing a backcross progeny plant that is resistant to at least western corn rootworm.

30. (currently amended) A method for producing a corn plant resistant to at least corn rootworm, said method comprising:

- (a) sexually crossing a first parent corn plant with a second parent corn plant, wherein said first or second parent corn plant is a corn event DP-004114-3, **deposited under Accession No. PTA-11506 with American Type Culture Collection (ATCC)**, plant, thereby producing a plurality of first generation progeny plants;
- (b) selecting a first generation progeny plant that is resistant to at least corn rootworm infestation;
- (c) backcrossing the first generation progeny plant of step (b) with the parent plant that lacks corn event DP-004114-3 DNA, thereby producing a plurality of backcross progeny plants; and
- (d) selecting from the backcross progeny plants, a plant that is resistant to at least corn rootworm infestation;

wherein the selected backcross progeny plant of step (d) comprises SEQ ID NO: 6.

31. (original) The method according to claim 28, wherein the plants of the first inbred corn line are the female parents or male parents.

32. (original) Hybrid seed produced by the method of claim 28.

33. (withdrawn) A method of determining zygosity of DNA of a corn plant comprising corn event DP-004114-3 in a biological sample comprising:

(a) contacting said sample with a first primer selected from the group consisting of SEQ ID NOs: 11, 13, 23 or 24, and a second primer selected from the group consisting of SEQ ID NOs: 20, 22, 25 or 26, such that

(1) when used in a nucleic acid amplification reaction comprising corn event DP-004114-3 DNA, produces a first amplicon that is diagnostic for corn event DP-004114-3, and

(2) when used in a nucleic acid amplification reaction comprising corn genomic DNA other than DP-004114-3 DNA, produces a second amplicon that is diagnostic for corn genomic DNA other than DP-004114-3 DNA;

(b) performing a nucleic acid amplification reaction; and

(c) detecting the amplicons so produced, wherein detection of presence of both amplicons indicates that said sample is heterozygous for corn event DP-004114-3 DNA, wherein detection of only the first amplicon indicates that said sample is homozygous for corn event DP-004114-3 DNA.

34. (withdrawn) A method of detecting the presence of a nucleic acid molecule that is unique to event DP-004114-3 in a sample comprising corn nucleic acids, the method comprising:

(a) contacting the sample with a pair of primers that, when used in a nucleic-acid amplification reaction with genomic DNA from event DP-004114-3 produces an amplicon that is diagnostic for event DP-004114-3;

(b) performing a nucleic acid amplification reaction, thereby producing the amplicon; and

(c) detecting the amplicon.

35. (withdrawn) A pair of polynucleotide primers comprising a first polynucleotide primer and a second polynucleotide primer which function together in the presence of an event DP-004114-3 DNA template in a sample to produce an amplicon diagnostic for event DP-004114-3.

36. (withdrawn) The pair of polynucleotide primers according to claim 35, wherein the sequence of the first polynucleotide primer is or is complementary to a corn plant genome sequence flanking the point of insertion of a heterologous DNA sequence inserted into the corn plant genome of event DP-004114-3, and the sequence of the second polynucleotide primer is or is complementary to the heterologous DNA sequence inserted into the genome of event DP-004114-3.

37. (withdrawn) The pair of polynucleotide primers according to claim 36, wherein

- (a) the first polynucleotide primer comprises at least 10 contiguous nucleotides of a nucleotide sequence selected from the group consisting of nucleotides 1-2422 of SEQ ID NO: 6, nucleotides 14348-16752 of SEQ ID NO: 6, and the complements thereof; and
- (b) the second polynucleotide primer comprises at least 10 contiguous nucleotides from nucleotides 2423-14347 of SEQ ID NO: 6, or the complements thereof.

38. (withdrawn) The pair of polynucleotide primers according to claim 37, wherein

- (a) the first polynucleotide primer comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 20, SEQ ID NOs: 22-26 and the complements thereof; and
- (b) the second polynucleotide primer comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 12, SEQ ID NOs: 14-19, SEQ ID NO: 21, and the complements thereof.

39. (withdrawn) The primer pair of claim 37, wherein said first primer and said second primer are at least 18 nucleotides.

40. (withdrawn) The primer pair of claim 37, wherein said first primer and said second primer are at least 24 nucleotides.

41. (withdrawn) A method of detecting the presence of DNA corresponding to the DP-004114-3 event in a sample, the method comprising:

- (a) contacting the sample comprising maize DNA with a polynucleotide probe that hybridizes under stringent hybridization conditions with DNA from maize event DP-004114-3 and does not hybridize under said stringent hybridization conditions with a non- DP-004114-3 maize plant DNA;
- (b) subjecting the sample and probe to stringent hybridization conditions; and

(c) detecting hybridization of the probe to the DNA;

wherein detection of hybridization indicates the presence of the DP-004114-3 event.

42. (withdrawn) A kit for detecting nucleic acids that are unique to event DP-004114-3 comprising at least one nucleic acid molecule of sufficient length of contiguous polynucleotides to function as a primer or probe in a nucleic acid detection method, and which upon amplification of or hybridization to a target nucleic acid sequence in a sample followed by detection of the amplicon or hybridization to the target sequence, are diagnostic for the presence of nucleic acid sequences unique to event DP-004114-3 in the sample.

43. (withdrawn) The kit according to claim 42, wherein the nucleic acid molecule comprises a nucleotide sequence from SEQ ID NO: 6.

44. (withdrawn) The kit according to claim 43, wherein the nucleic acid molecule is a primer selected from the group consisting of SEQ ID NOs: 11-26, and the complements thereof.

REMARKS

Status of the Claims

Claims 1-5 and 8-44 are pending are pending. Claims 6 and 7 are presently cancelled. Claims 33-44 have been withdrawn from consideration.

Claim 1 has been amended to insert a “semicolon” at the end of the lines beginning “said third expression” and “said forth expression” as suggested by the Examiner. For further clarity Applicant has also amended these lines beginning “said third expression” and “said forth expression” of Claim 1 to recite the “expression cassette in operable linkage comprises” to make said lines consistent with the preceding similar lines. These amendments to claim 1 are formal in nature and thus, do not introduce new matter.

Claims 1, 2, 5, 10, 24, 28 have been amended to recite that the “... DNA construct is flanked by the 5' junction sequence of SEQ ID NO: 27 and the 3' junction sequence of SEQ ID NO: 28.” Support for this amendment can found throughout the specification, at least on p. 13, lines 6-9; SEQ ID NO: 6; and Figure 5.

Claims 16 and 20 have been amended to clarify that the sequence of SEQ ID NO: 27 and SEQ ID NO: 28 are distinct from the complement as suggested by the Examiner. This amendment to claims 16 and 20 is formal in nature and thus, does not introduce new matter.

Claims 5, 27, 29, and 30 have been amended to reference the DP-004114-3 event by the ATCC deposit accession number as required by the Examiner. This amendment to claim 5, 27, 29, and 30 is formal in nature and thus, does not introduce new matter.

Amendments to the Specification

Applicant has amended the specification to correct the typographical error in the SEQ ID NO: identifier occurring on page 3, line 8, line 14, and line 20. Applicant has amended said to SEQ ID NO: 6. From the specification (p. 13 lines 6-9) and the sequence listing SEQ ID NO: 27 is the junction sequence point between the maize genomic DNA and the 5' end of the insert and is 20 nucleotides in length. SEQ ID NO: 6 is the total (16,752 bp) genomic 5', 3' genomic border sequences flanking the insert that was sequenced (p. 47, lines 18-28). The amended paragraphs as filed refer to this 16,752 bp sequence, which is SEQ ID NO: 6 and not SEQ ID NO: 27. Applicant request that amended paragraphs be substituted into specification. No new matter has been added.

Claim Objections

As suggested by the Examiner the lines beginning "said third expression cassette" "said fourth expression cassette" of claim 1 have been amended to clarify the claim to recite " ... expression cassette in operable linkage comprises: ... ".

Claim Rejections – 35 USC § 112 second paragraph

Claims 5-7, 16-23, 27, and 29-30 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which the inventor or a joint inventor. Claims 5, 16, 20, 27, 29, and 30 have been amended. Claims 6 and 7 have been cancelled. This rejection is respectfully traversed.

The Action alleges **Claim 5** is indefinite as the event name is an arbitrary designation in the absence of a deposit organization and accession number such as American Type Culture Collection (ATCC) with Accession No. PTA-004114-3.

Applicant has amended claim 5 to refer to the ATCC deposit as suggested by the Examiner and to recite the "genotype comprises the DNA construct of claim 1 flanked by the nucleotide sequence set forth in SEQ ID NO: 27 and SEQ ID NO: 28. Claims 6 and 7 are presently cancelled.

The Action alleges **Claims 16 and 20** are indefinite in the recitation of "...a nucleotide sequence which is or is complementary to a sequence selected from the group consisting of...".

Applicant has amended claims 16 and 20 to recite " ... nucleotide sequence selected from the group consisting of SEQ ID NO: 27 and SEQ ID NO: 28 or the complement thereof ...".

The Action alleges **Claims 27 and 29-30** are indefinite in the recitation of "...event DP-004114-3...".

Applicant has amended claims 27, 29 and 30 to refer to the ATCC deposit as required by the Examiner.

The Action alleges **Claim 29** there is insufficient antecedent basis for the limitation "the step" in line 1 in the claim.

To overcome the rejection Applicant has amended claim 29 to delete the phrase “the step of”.

In view of the amendment to the claims and the above remarks, it is submitted that the rejections of the claims under 35 USC § 112 second paragraph, are obviated and should be withdrawn.

Claim Rejections – 35 USC § 112 first paragraph

Claims 5-13 and 16-32 are rejected under 35 U.S.C. 112, first paragraph, as allegedly failing to comply with the enablement requirement. The claim(s) allegedly contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. Claim 24 has been amended. This rejection is respectfully traversed.

The Action states the specification discloses the deposit of corn seed with the American Type Culture Collection, ATCC Deposit Number PTA- 11506, however no statement has been provided stating that the instant invention will be irrevocably and without restriction released to the public upon the issuance of a patent.

Applicant respectfully disagrees with this position of the Examiner and submits that requirements of 37 CFR § 1.801 -1.809 are fully met by the information that is provided in the paragraph from line 2 of page 10 to line 5 of page 11. Specifically, the specification states: *“Upon allowance of any claims in the application, the Applicant(s) will make available to the public, pursuant to 37 C.F.R. § 1.808, sample(s) of the deposit of at least 2500 seeds of hybrid maize ...”* (p. 10, lines 15-17). 37 CFR § 1.808 (a)(2) states: *“all restrictions imposed by the depositor on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent”*.

Accordingly, the Applicant respectfully submits that said statement is fully compliant of the requirements of 37 CFR § 1.801-1.809 and Applicant requests that the rejection under 35 USC § 112 first paragraph be withdrawn.

The Action asserts **Claims 24-26** drawn to a method of producing hybrid corn seed comprising sequences of SEQ ID NO: 27 and 28 do not encode any of the Cry proteins or the

phosphinothricin resistance gene and asserts the Applicant has failed to provide any guidance on a plant that comprises SEQ ID NO: 27 and 28 but not the DNA construct comprising the four expression cassettes.

Applicant has amended claim 24 to recite a “... first inbred corn line comprising a DNA construct of claim 1, wherein the DNA construct is flanked by the 5' junction sequence of SEQ ID NO: 27 and the 3' junction sequence of SEQ ID NO: 28”.

The Action also states the specification allegedly fails to provide enablement for the genotype of the corn even DP-004114-3 wherein the genotype comprises the four expression cassettes flanked by SEQ ID NO: 27 and 28.

Applicant respectfully disagrees with this position of the Examiner on the enablement of the specification for the genotype of the corn even DP-004114-3 wherein the genotype comprises the four expression cassettes flanked by SEQ ID NO:27 and 28. Example 4 discloses the sequence characterization of the insert and genomic border regions of event DP-004114-3. In total, 16,752 bp of 4114 maize genomic sequence (SEQ ID NO: 6) was confirmed, comprising 2,422 bp of the 5' genomic border sequence, 2,405 bp of the 3' genomic border sequence, and 11,925 bp of inserted T-DNA from PHP27118. The 5' and 3' genomic border regions of 4114 maize were verified to be of maize origin by PCR amplification and sequencing of the genomic border regions from both 4114 maize and control maize plants. All 4114 maize plants were positive for the event-specific PCR and the PAT, Cry1F, and Cry34Ab1 proteins, whereas all the control maize plants were negative (Table 6). The T-DNA sequence information of plasmid PHP27118 was used to design primers to verify the inserted sequence in 4114 maize (Tables 7 and 8).

Therefore, Applicant submits that the specification is enabling for the genotype of corn comprising the DP-004114-3 event and in light of the amendments and the teaching of the specification.

In view of the amendments and above remarks, it is respectfully submitted that rejection of claims claims 5-13 and 16-32 under 35 USC § 112 first paragraph should be withdrawn.

Claim Rejections - 35 USC § 103

Claims 1-4 and 14 are rejected under 35 U.S.C. 103(a) as allegedly being unpatentable over Bing et al (U.S. PG PUB 2008/0178357 A1) in view of Barbour et al (WO2004099447 A2), further in view of each of Castle et al (2006. Curr Opin Biotechno. 17:105-112), Hua et al (2001.

Appl Environ Microbiol. 67(2):872-879), and Kaiser-Alexnat et al (2009. Insect Path Insect Parasit Nematodes. 45:235-238). Claims 1 and 2 have been amended. This rejection is respectfully traversed.

Without acquiescing as to the merits of the rejection and solely to facilitate prosecution Applicant has amended claims 1 and 2 to recite that the DNA construct is flanked by the 5' junction sequence of SEQ ID NO: 27 and the 3' junction sequence of SEQ ID NO: 28.

Claim 14 is directed to an isolated nucleic acid molecule of SEQ ID NO: 6; SEQ ID NO: 27 or SEQ ID NO: 28 and Claim 4 is directed to a plant comprising the sequence of SEQ ID NO: 6 that comprises the DNA construct comprising the four operably linked cassettes comprising three Cry toxins and a phosphinothricin resistance gene and 2,422 bp of the 5' genomic border region sequence set forth in nucleotides 1-2,422 of SEQ ID NO: 6 and the 2,405 bp of the 3' genomic border region sequence is set forth in nucleotides 14,348 to 16,752 of SEQ ID NO: 6, which respectively are the junction points into the genome as represented by SEQ ID NO: 27 and SEQ ID NO: 28. Therefore, Bing et al in view of Barbour et al, further in view of each of Castle et al and Kaiser-Alexnat et al do not teach all of the claim elements since they don't teach the insertion point of the instant DP-004114-3 event.

The Action states that Claim 15 is allowable and acknowledges the corn event DP-004114-3 is not known in the prior art where the event is described as a DNA construct comprising four operably linked cassettes comprising three Cry toxins and a phosphinothricin resistance gene, wherein the construct is flanked by SEQ ID NO: 27 and 28. The Action also states that Claims 5-13 and 15-27, and 29-30 are free of the prior art.

In view of the amendments to the claims, the arguments set forth above, and the Actions acknowledgement that the corn event DP-004114-3 is not known in the prior art, Applicant respectfully submits that the presently claimed subject matter is non-obvious over Bing et al in view of Barbour et al, further in view of each of Castle et al and Kaiser-Alexnat et al. and the rejection under 35 USC § 103 be withdrawn.

CONCLUSIONS

In view of the foregoing remarks and amendments, the Examiner is respectfully requested to withdraw the rejections made to the pending claims. Applicants respectfully submit that this application is now ready for allowance. Early notice to this effect is solicited.

Should the Examiner have further questions or comments with respect to examination of this case, it is respectfully requested that the Examiner telephone the undersigned so that further examination of this application can be expedited.

It is not believed that extensions of time or fees for net addition of claims are required, beyond those that may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR § 1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-1852.

Respectfully submitted,

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Electronic Acknowledgement Receipt

EFS ID:	15673137
Application Number:	12970052
International Application Number:	
Confirmation Number:	5362
Title of Invention:	Maize event DP-004114-3 and methods for detection thereof
First Named Inventor/Applicant Name:	Scott Diehn
Customer Number:	27310
Filer:	S. Christopher Bauer/Jessica Moyer
Filer Authorized By:	S. Christopher Bauer
Attorney Docket Number:	3700
Receipt Date:	02-MAY-2013
Filing Date:	16-DEC-2010
Time Stamp:	12:53:02
Application Type:	Utility under 35 USC 111(a)

Payment information:

Submitted with Payment	no
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File Listing:

Document Number	Document Description	File Name	File Size(Bytes)/ Message Digest	Multi Part /.zip	Pages (if appl.)
1	Amendment/Req. Reconsideration-After Non-Final Reject	3700_US_Non_Final_Rejection_Response_20130502.PDF	166513 5d13e1b326ef95e0c6b2f3a0cb5b01d8ed630417	no	16

Warnings:

Information:

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New Applications Under 35 U.S.C. 111

If a new application is being filed and the application includes the necessary components for a filing date (see 37 CFR 1.53(b)-(d) and MPEP 506), a Filing Receipt (37 CFR 1.54) will be issued in due course and the date shown on this Acknowledgement Receipt will establish the filing date of the application.

National Stage of an International Application under 35 U.S.C. 371

If a timely submission to enter the national stage of an international application is compliant with the conditions of 35 U.S.C. 371 and other applicable requirements a Form PCT/DO/EO/903 indicating acceptance of the application as a national stage submission under 35 U.S.C. 371 will be issued in addition to the Filing Receipt, in due course.

New International Application Filed with the USPTO as a Receiving Office

If a new international application is being filed and the international application includes the necessary components for an international filing date (see PCT Article 11 and MPEP 1810), a Notification of the International Application Number and of the International Filing Date (Form PCT/RO/105) will be issued in due course, subject to prescriptions concerning national security, and the date shown on this Acknowledgement Receipt will establish the international filing date of the application.

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PATENT APPLICATION FEE DETERMINATION RECORD Substitute for Form PTO-875	Application or Docket Number 12/970,052	Filing Date 12/16/2010	☐ To be Mailed
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ENTITY: ☒ LARGE ☐ SMALL ☐ MICRO

APPLICATION AS FILED – PART I

FOR	NUMBER FILED	NUMBER EXTRA	RATE (\$)	FEE (\$)
☐ BASIC FEE (37 CFR 1.16(a), (b), or (c))	N/A	N/A	N/A	
☐ SEARCH FEE (37 CFR 1.16(k), (i), or (m))	N/A	N/A	N/A	
☐ EXAMINATION FEE (37 CFR 1.16(o), (p), or (q))	N/A	N/A	N/A	
TOTAL CLAIMS (37 CFR 1.16(i))	minus 20 =	*	X \$ =	
INDEPENDENT CLAIMS (37 CFR 1.16(h))	minus 3 =	*	X \$ =	
☐ APPLICATION SIZE FEE (37 CFR 1.16(s))	If the specification and drawings exceed 100 sheets of paper, the application size fee due is \$310 (\$155 for small entity) for each additional 50 sheets or fraction thereof. See 35 U.S.C. 41(a)(1)(G) and 37 CFR 1.16(s).			
☐ MULTIPLE DEPENDENT CLAIM PRESENT (37 CFR 1.16(j))				
* If the difference in column 1 is less than zero, enter "0" in column 2.			TOTAL	

APPLICATION AS AMENDED – PART II

AMENDMENT	(Column 1)	(Column 2)	(Column 3)	HIGHEST NUMBER PREVIOUSLY PAID FOR	PRESENT EXTRA	RATE (\$)	ADDITIONAL FEE (\$)
	05/02/2013	CLAIMS REMAINING AFTER AMENDMENT					
	Total (37 CFR 1.16(i))	* 42	Minus	** 44	= 0	X \$80 =	0
	Independent (37 CFR 1.16(h))	* 13	Minus	*** 16	= 0	X \$420 =	0
	☐ Application Size Fee (37 CFR 1.16(s))						
	☐ FIRST PRESENTATION OF MULTIPLE DEPENDENT CLAIM (37 CFR 1.16(j))						
TOTAL ADD'L FEE						0	

AMENDMENT	(Column 1)	(Column 2)	(Column 3)	HIGHEST NUMBER PREVIOUSLY PAID FOR	PRESENT EXTRA	RATE (\$)	ADDITIONAL FEE (\$)
		CLAIMS REMAINING AFTER AMENDMENT					
	Total (37 CFR 1.16(i))	*	Minus	**	=	X \$ =	
	Independent (37 CFR 1.16(h))	*	Minus	***	=	X \$ =	
	☐ Application Size Fee (37 CFR 1.16(s))						
	☐ FIRST PRESENTATION OF MULTIPLE DEPENDENT CLAIM (37 CFR 1.16(j))						
TOTAL ADD'L FEE							

* If the entry in column 1 is less than the entry in column 2, write "0" in column 3.
 ** If the "Highest Number Previously Paid For" IN THIS SPACE is less than 20, enter "20".
 *** If the "Highest Number Previously Paid For" IN THIS SPACE is less than 3, enter "3".

The "Highest Number Previously Paid For" (Total or Independent) is the highest number found in the appropriate box in column 1.

LIE
/NICOLE LAWRENCE/

This collection of information is required by 37 CFR 1.16. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 12 minutes to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. **SEND TO: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.**

If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.