



**Event 5307 Maize:  
Insert Sequence Analysis**

**AMENDED REPORT NO.1**

<b>Data Requirement:</b>	Not applicable
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<b>Study Completion Date:</b>	November 3, 2010
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<b>Syngenta Study No.:</b>	Not applicable
<b>Report No.:</b>	SSB-159-10 A1

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*The following statement applies to submissions to the United States Environmental Protection Agency (US EPA).*

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**Company:** *Syngenta Seeds, Inc.*

**Company Representative:**



Demetra Vlachos  
*Regulatory Affairs Manager*



Date

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**STATEMENT CONCERNING GOOD LABORATORY PRACTICES STANDARDS**

This study was not conducted in compliance with the relevant provisions of Good Laboratory Practices Standards (GLPS) (40 CFR Part 160, US EPA 1989) pursuant to the Federal Insecticide, Fungicide, and Rodenticide Act. However, all components of the study were performed according to accepted scientific practices, and relevant study records (including raw data) have been retained.

**Study Director:**




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Stephen New  
*Technical Expert I*  
 Product Safety  
 Syngenta Biotechnology, Inc.

*November 3, 2010*

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Date

**Submitted by:**




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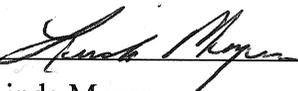
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## LIST OF ACRONYMS AND ABBREVIATIONS

3'	three prime
5'	five prime
<i>aadA</i>	streptomycin adenylyltransferase gene from <i>Escherichia coli</i> that confers resistance to streptomycin and spectinomycin
BC	backcross
bp	base pair
CMP	cestrum yellow leaf curling virus promoter
ColE1 ori	<i>Escherichia coli</i> origin of replication 1
Cry	crystal protein
<i>cryIAb</i>	Cry1Ab gene
Cry1Ab	Cry1Ab protein
<i>cry3A</i>	Cry3A gene
Cry3A	Cry3A protein
CTAB	cetyltrimethyl ammonium bromide
DNA	deoxyribonucleic acid
dsDNA	double-stranded DNA
<i>ecry3.1Ab</i>	eCry3.1Ab gene
eCry3.1Ab	eCry3.1Ab protein
EDTA	ethylenediaminetetraacetic acid
FIFRA	Federal Insecticide, Fungicide, and Rodenticide Act
g	gram
GLPS	Good Laboratory Practices Standards
LB	left border
M	molar
<i>manA</i>	phosphomannose isomerase gene
<i>mcry3A</i>	modified Cry3A gene
mCry3A	modified Cry3A protein
ml	milliliter
mM	millimolar
NaCl	sodium chloride
NOS	nopaline synthase
NTI	New Technologies Informax
PCR	polymerase chain reaction
<i>pmi</i>	phosphomannose isomerase gene
PMI	phosphomannose isomerase protein
RB	right border
<i>repA</i>	pVS1 replication gene from <i>Pseudomonas aeruginosa</i>
<i>spec</i>	streptomycin adenylyltransferase gene from <i>Escherichia coli</i>
T <sub>0</sub>	original transformant
T-DNA	transferred deoxyribonucleic acid
TE	tris-EDTA
Tris	2-amino-2-(hydroxymethyl)-1,3-propanediol
US EPA	United States Environmental Protection Agency
v/v	volume to volume
<i>vir</i>	virulence regulon in <i>Agrobacterium tumefaciens</i>

LIST OF ACRONYMS AND ABBREVIATIONS (*Continued*)

<i>virG</i>	part of the two-component regulatory system for the virulence regulon in <i>Agrobacterium tumefaciens</i>
VirGN54D	VirG protein with a N54D substitution
VS1 ori	plasmid pVS1 origin of replication and partitioning region
w/v	weight to volume
ZmUbiInt	<i>Zea mays</i> ubiquitin promoter with intron
°C	degrees Celsius
®	registered trademark
™	trademark
µg	microgram
×	cross
× <i>g</i>	times gravity
⊗	self-pollination

**REPORT AMENDMENTS****Amendment No. 1: November 3, 2010**

This amended report has the following corrections:

On page 1, the department title has been changed to Product Safety.

On page 2, the Regulatory Affairs Manager name has been updated.

On page 3, the Regulatory Affairs Manager and Sponsor names have been updated, and position and department titles for the Study Director and the Sponsor have been updated.

On page 4, the Table of Contents has been updated.

On page 8, a new section has been added listing the Report Amendments.

On page 10, a reference citation was added.

On page 10, the Accession number for the gene *ecry3.IAb* has been updated.

On page 11, typographical errors in the description of *ecry3.IAb* have been corrected.

On page 21, the Sponsor name has been updated, and position and department titles for the Study Director and the Sponsor have been updated.

On page 24, an additional reference was added.

The corrected pages in this amended report SSB-159-10 A1 are indicated as “REVISED”.

## SUMMARY

Using the techniques of modern molecular biology, Syngenta has transformed maize (*Zea mays*) to produce Event 5307 maize, a new cultivar that has insecticidal activity against certain corn rootworm (*Diabrotica*) species. Maize plants derived from transformation Event 5307 ("5307 maize") contain the gene *ecry3.1Ab* encoding an eCry3.1Ab protein and the gene *pmi* (also known as *manA*) encoding the enzyme phosphomannose isomerase (PMI).

The purpose of this study is to determine the deoxyribonucleic acid (DNA) sequence of the 5307 maize insert and to assess the intactness of the insert, the organization of the functional elements, and the presence of any rearrangements, deletions, and/or base pair changes within the 5307 maize insert.

Two overlapping fragments that span the 5307 maize insert were amplified from genomic DNA extracted from 5307 maize using polymerase chain reaction. These fragments were cloned, and sequences of the clones were aligned to create a consensus of the transferred-DNA (T-DNA) sequence. This sequence was compared to plasmid pSYN12274, the transformation plasmid used to create 5307 maize.

The DNA sequence analysis demonstrated that the 5307 maize insert was intact and that the organization of the functional elements within the insert, as present in plasmid pSYN12274, was maintained.

**INTRODUCTION**

Using the techniques of modern molecular biology, Syngenta has transformed maize (*Zea mays*) to produce Event 5307 maize, a new cultivar that has insecticidal activity against certain corn rootworm (*Diabrotica*) species. Maize plants derived from transformation Event 5307 ("5307 maize") contain the gene *ecry3.1Ab* encoding an eCry3.1Ab protein and the gene *pmi* (also known as *manA*) encoding the enzyme phosphomannose isomerase (PMI). The eCry3.1Ab protein is an engineered chimera of modified Cry3A (mCry3A) and Cry1Ab proteins (Walters *et al.* 2010). The gene *pmi* was obtained from *Escherichia coli* strain K-12 and the protein it encodes was utilized as a plant selectable marker during development of 5307 maize.

The purpose of this study is to determine the deoxyribonucleic acid (DNA) sequence of the 5307 maize insert and to assess the intactness of the insert, the organization of the functional elements, and the presence of any rearrangements, deletions, and/or base pair changes within the 5307 maize insert. The insert sequence was compared to plasmid pSYN12274, the transformation plasmid used to create 5307 maize.

The DNA sequence analysis comparing the 5307 maize insert sequence and the plasmid pSYN12274 sequence demonstrated that the insert was intact and that the organization of the functional elements within the insert, as present in plasmid pSYN12274, was maintained.

**MATERIALS AND METHODS**

**Genetic Elements for 5307 maize in Plasmid pSYN12274**

The genetic elements in plasmid pSYN12274, the 5307 maize transformation plasmid, are listed in Table 1 and mapped in Figure 1. The table also contains a description of each of the constituents of the plasmid pSYN12274, including the size in base pairs (bp) and the position within the plasmid.

**Table 1. Genetic elements in plasmid pSYN12274**

<b>Active ingredient cassette</b>			
<b>Genetic element</b>	<b>Size (bp)</b>	<b>Position</b>	<b>Description</b>
Intervening sequence	203	26 to 228	Intervening sequence with restriction sites used for cloning
CMP promoter	346	229 to 574	Cestrum Yellow Leaf Curling Virus promoter region (Hohn <i>et al.</i> 2007). Provides constitutive expression in maize.
Intervening sequence	9	575 to 583	Intervening sequence with restriction sites used for cloning
<i>ecry3.1Ab</i>	1962	584 to 2545	An engineered Cry gene active against certain corn rootworm ( <i>Diabrotica</i> ) species (Entrez® Accession No. GU327680 [NCBI 2010]). As an engineered chimeric protein, eCry3.1Ab has similarities to other well characterized Cry proteins. Because Cry proteins share structural similarities, chimeric Cry genes can be

**Table 1. Genetic elements in plasmid pSYN12274 (Continued)**

Genetic element	Size (bp)	Position	Description
			<p>engineered <i>via</i> the exchange of domains that are homologous between different Cry genes. The gene <i>ecry3.1Ab</i> consists of a fusion between the 5' end (Domain I, Domain II and 15 AA of Domain III) of a modified Cry3A gene (<i>mcry3A</i>) and the 3' end (Domain III and Variable Region 6 [Hofte and Whiteley 1989]) of a synthetic Cry1Ab gene (see descriptions of <i>mcry3A</i> and <i>cry1Ab</i> below). Upstream of the <i>mcry3A</i> domain, the gene <i>ecry3.1Ab</i> carries a 67 bp long oligomer extension at its 5' end, which was introduced during the engineering of the variable regions and is translated into the following 22 amino acid residues: MTSNGRQCAGIRPYDGRQQHRG. The next 459 amino acid residues are identical to those of mCry3A, followed by 172 residues of Cry1Ab.</p> <p>Description of <i>mcry3A</i>: a maize-optimized <i>cry3A</i> was synthesized to accommodate the preferred codon usage for maize (Murray <i>et al.</i> 1989). The synthetic sequence was based on the native Cry3A protein sequence from <i>Bacillus thuringiensis</i> subsp. <i>tenebrionis</i> (Sekar <i>et al.</i> 1987). The maize-optimized gene was then modified to incorporate a consensus cathepsin-G protease recognition site within the expressed protein. The amino acid sequence of the encoded mCry3A corresponds to that of the native Cry3A, except that (1) its N-terminus corresponds to methionine-48 of the native protein and (2) a cathepsin G protease recognition site has been introduced, beginning at amino acid residue 155 of the native protein. This cathepsin-G recognition site has the sequence alanine-alanine-proline-phenylalanine, and has replaced the amino acids valine-155, serine-156, and serine-157 in the native protein (Chen and Stacy 2007).</p> <p>Description of <i>cry1Ab</i>: the gene <i>cry1Ab</i> was originally cloned from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> strain HD-1 (Geiser <i>et al.</i> 1986). Its amino acid sequence has been codon-optimized (Koziel <i>et al.</i> 1997) to accommodate the preferred codon usage for maize (Murray <i>et al.</i> 1989)</p>
Intervening sequence	30	2546 to 2575	Intervening sequence with restriction sites used for cloning

**Table 1. Genetic elements in plasmid pSYN12274 (Continued)**

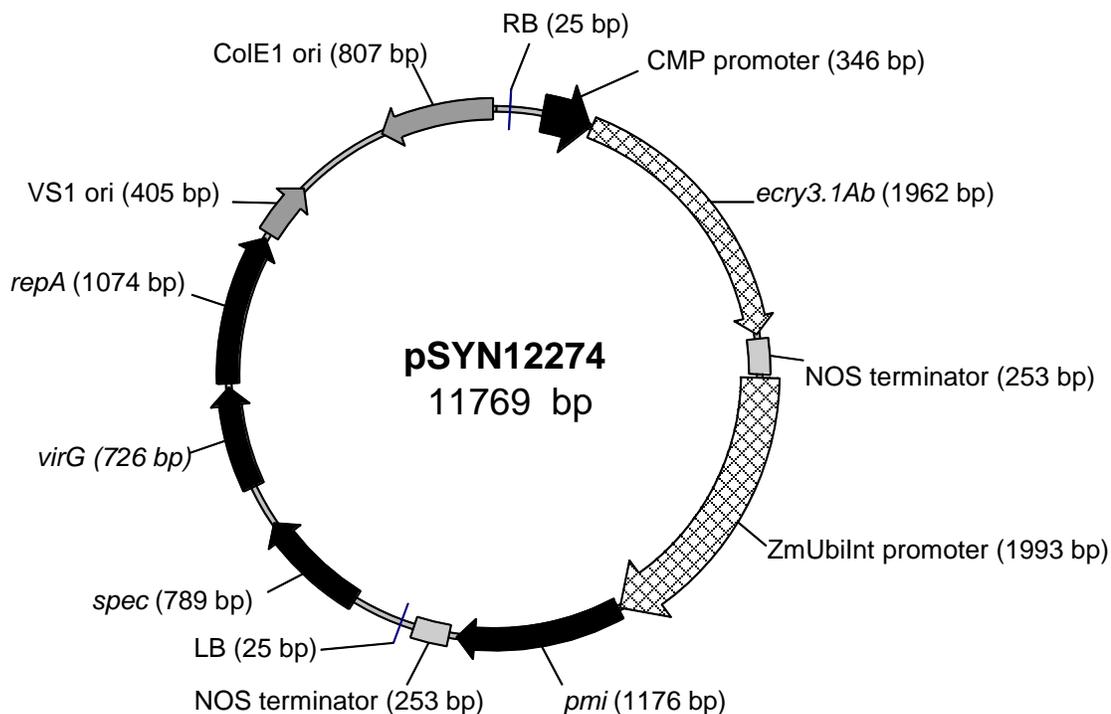
Genetic element	Size (bp)	Position	Description
NOS terminator	253	2576 to 2828	Terminator sequence from the nopaline synthase gene of <i>Agrobacterium tumefaciens</i> (Entrez® Accession No. V00087 [NCBI 2010]). Provides a polyadenylation site (Depicker <i>et al.</i> 1982)
<b>Selectable marker cassette</b>			
Genetic element	Size (bp)	Position	Description
Intervening sequence	25	2829 to 2853	Intervening sequence with restriction sites used for cloning
ZmUbilnt promoter	1993	2854 to 4846	Promoter region from the maize polyubiquitin gene which contains the first intron (Entrez® Accession Number S94464 [NCBI 2010]). Provides constitutive expression in monocots (Christensen <i>et al.</i> 1992)
Intervening sequence	12	4847 to 4858	Intervening sequence with restriction sites used for cloning
<i>pmi</i>	1176	4859 to 6034	<i>Escherichia coli</i> gene <i>pmi</i> encoding the enzyme phosphomannose isomerase (PMI) (Entrez® Accession Number M15380 [NCBI 2010]); this gene is also known as <i>manA</i> . Catalyzes the isomerization of mannose-6-phosphate to fructose-6-phosphate (Negrotto <i>et al.</i> 2000)
Intervening sequence	60	6035 to 6094	Intervening sequence with restriction sites used for cloning
NOS terminator	253	6095 to 6347	Terminator sequence from the nopaline synthase gene of <i>Agrobacterium tumefaciens</i> (Entrez® Accession No. V00087 [NCBI 2010]). Provides a polyadenylation site (Depicker <i>et al.</i> 1982)
Intervening sequence	88	6348 to 6435	Intervening sequence with restriction sites used for cloning
<b>Plasmid backbone</b>			
Genetic element	Size (bp)	Position	Description
Left border (LB)	25	6436 to 6460	Left border region of T-DNA from <i>Agrobacterium tumefaciens</i> nopaline Ti-plasmid (Entrez® Accession Number J01825 [NCBI 2010]). Short direct repeat that flanks the T-DNA and is required for the transfer of the T-DNA into the plant cell (Zambryski <i>et al.</i> 1982)
Intervening sequence	349	6461 to 6809	Intervening sequence with restriction sites used for cloning

**Table 1. Genetic elements in plasmid pSYN12274 (Continued)**

Genetic element	Size (bp)	Position	Description
<i>spec</i>	789	6810 to 7598	Streptomycin adenylyltransferase, <i>aadA</i> gene from <i>Escherichia coli</i> transposon Tn7 (similar to Entrez® Accession Number X03043 [NCBI 2010]). Confers resistance to streptomycin and spectinomycin and is used as a bacterial selectable marker (Fling <i>et al.</i> 1985)
Intervening sequence	299	7599 to 7897	Intervening sequence with restriction sites used for cloning
<i>virG</i>	726	7898 to 8623	The VirGN54D gene ( <i>virG</i> ) from pAD1289 (similar to Entrez® Accession Number AF242881 [NCBI 2010]). The N54D substitution results in a constitutive <i>virG</i> phenotype. VirG is part of the two-component regulatory system for the virulence ( <i>vir</i> ) regulon in <i>Agrobacterium tumefaciens</i> (Hansen <i>et al.</i> 1994)
Intervening sequence	29	8624 to 8652	Intervening sequence with restriction sites used for cloning
<i>repA</i>	1074	8653 to 9726	Gene encoding the pVS1 replication protein from <i>Pseudomonas aeruginosa</i> (similar to Entrez® Accession Number AF133831 [NCBI 2010]), which is a part of the minimal pVS1 replicon that is functional in Gram-negative, plant-associated bacteria (Heeb <i>et al.</i> 2000)
Intervening sequence	42	9727 to 9768	Intervening sequence with restriction sites used for cloning
VS1 ori	405	9769 to 10173	Consensus sequence for the origin of replication and partitioning region from plasmid pVS1 of <i>Pseudomonas aeruginosa</i> (Entrez® Accession Number U10487 [NCBI 2010]). Serves as origin of replication in <i>Agrobacterium tumefaciens</i> host (Itoh <i>et al.</i> 1984)
Intervening sequence	677	10174 to 10850	Intervening sequence with restriction sites used for cloning
ColE1 ori	807	10851 to 11657	Origin of replication (similar to Entrez® Accession Number V00268 [NCBI 2010]) that permits replication of plasmids in <i>Escherichia coli</i> (Itoh and Tomizawa 1979)
Intervening sequence	112	11658 to 11769	Intervening sequence with restriction sites used for cloning
Right border (RB)	25	1 to 25	Right border region of T-DNA from <i>Agrobacterium tumefaciens</i> nopaline Ti-plasmid (Entrez® Accession Number J01826 [NCBI 2010]). Short direct repeat that flanks the T-DNA and is required for the transfer of the T-DNA into the plant cell (Wang <i>et al.</i> 1984)

T-DNA = transferred DNA

**Figure 1. Plasmid map of plasmid pSYN12274**



**Test Substance**

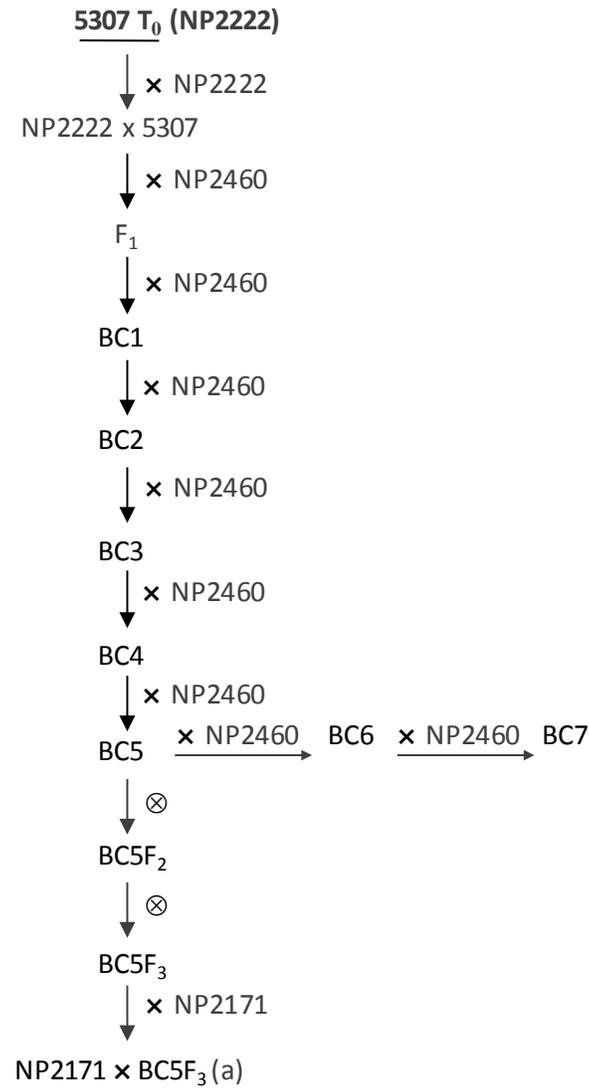
The test substance for this study was 5307 maize seed from generation NP2171 x BC5F<sub>3</sub>. Table 2 shows the description and pedigree code for the test substance. Figure 2 illustrates a pedigree chart demonstrating the production of the test substance.

**Table 2. Test substance**

Seed identification	Pedigree
NP2171 x BC5F <sub>3</sub>	NP2171 /(NP2460*/NP2222/(5307)1) B>B>B>B<2>B-B(T++)-

The test substance was characterized by real-time polymerase chain reaction (PCR) (Ingham *et al.* 2001) analysis to confirm the identity and purity.

**Figure 2. Pedigree history for 5307 maize indicating the generation used in the study presented in this report**



(a) = insert sequence analysis  
 T<sub>0</sub> = original transformant  
 x = cross  
 BC = backcross  
 ⊗ = self-pollination

## Plant Tissue for Genomic DNA Extraction

Test substance seed was grown in a Syngenta Biotechnology, Inc. greenhouse in Research Triangle Park, North Carolina, USA. Following verification of the plants' identity by real-time PCR analysis, leaf tissue from plants grown from the test substance was pooled into a sampling bag and stored at  $-80^{\circ}\text{C} \pm 10^{\circ}\text{C}$ .

## Genomic DNA Extraction

Genomic DNA used for insert sequence determination was isolated from the pooled leaf tissue using a modification of the method described in Saghai-Marooif *et al.* (1984).

Pooled leaf tissue was ground into a fine powder using a pre-chilled mortar and pestle, with liquid nitrogen, and then placed into a bottle for storage. For each DNA extraction, approximately 40 g of this tissue and 200 ml of prewarmed CTAB buffer (100 mM Tris pH 8.0, 20 mM EDTA pH 8.0, 1.4 M NaCl, 2% CTAB [w/v], 0.2% [v/v]  $\beta$ -mercaptoethanol) were combined in a bottle; the sample was then mixed gently and incubated for 90 minutes at  $65^{\circ}\text{C} \pm 5^{\circ}\text{C}$ . An equal volume of chloroform:isoamyl alcohol (24:1) was then added, followed by gentle mixing and centrifugation for 10 minutes at  $7277 \times g$  at room temperature.

The resulting aqueous phase was transferred to a clean container, and 10  $\mu\text{g}$  of ribonuclease per ml of aqueous phase was added. The sample was mixed and incubated for 30 minutes at  $37^{\circ}\text{C} \pm 2^{\circ}\text{C}$ . An equal volume of chloroform:isoamyl alcohol (24:1) was then added, followed by gentle mixing and centrifugation for 10 minutes at  $7277 \times g$  at room temperature. The aqueous phase was collected in a clean bottle, and the DNA was precipitated with a 0.8 volume of isopropanol. The DNA was then pelleted by centrifugation at  $291 \times g$  and washed once with 70% ethanol. The DNA pellet was air-dried and dissolved in 2.5 ml of prewarmed 0.1X TE.

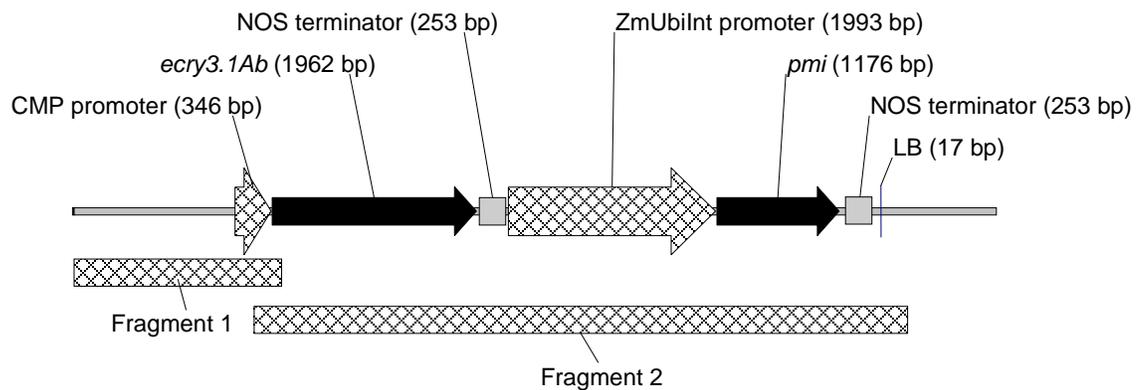
## DNA Quantitation

The concentration of DNA was measured using a Quant-iT™ PicoGreen® dsDNA kit. A two-point standard curve was generated using a Lambda DNA standard. The linear attribute of the standard curve was verified with samples generated from a serial dilution of Lambda DNA standard in 1X TE. Genomic DNA was quantified by interpolation from the two point standard curve, and each genomic DNA was assayed in triplicate using the TBS-380 Mini-Fluorometer.

## PCR Amplification

Two overlapping fragments that span the 5307 maize insert were amplified from genomic DNA extracted from 5307 maize using PCR analysis (Figure 3). PCR amplification was carried out using the Expand™ Long Template PCR System. Table 3 lists the primers used to amplify the insert fragments; Tables 4 and 5 contain the thermalcycling parameters.

**Figure 3. Map of the 5307 maize insert and location of PCR-amplified fragments from 5307 maize to determine insert sequence**



**Table 3. Primers used to amplify the insert of 5307 maize**

Fragment	Forward primer sequence (5' to 3')	Reverse primer sequence (5' to 3')
1	GTGTAAGCCCAAGCCATTTACTT CCTC	CGTCCTTGGTGGTGCTGCTGTCC AGGC
2	ATTCGTGGCCGACAGGTGG	AGCCGTACTATAAAGAGGGGTTG TCG

**Table 4. Cycling parameters for Fragment 1**

Cycle	Step	Temperature (°C)	Time	Number of cycles
A	1	94	2 min	1
B	1	94	15 sec	30
B	2	65	30 sec	30
B	3	72	90 sec	30
C	1	72	5 min	1
D	1	4	Hold	1

**Table 5. Cycling parameters for Fragment 2**

Cycle	Step	Temperature (°C)	Time	Number of cycles
A	1	94	2 min	1
B	1	94	10 sec	1
B	2	60	30 sec	1
B	3	68	5 min	1
C	1	94	15 sec	25
C	2	60	30 sec	25
C	3	68	5 min (+20 sec each cycle)	25
D	1	68	7 min	1
E	1	4	Hold	1

The PCR fragments were cloned into pCR®4-TOPO® vector, and three colonies for each PCR product were randomly selected and grown. The plasmid DNA was then

independently extracted, and the resulting plasmid preparations, which contained the PCR amplification products, were subsequently sequenced.

### Sequencing

Dye-terminator sequencing, a modification of the dideoxynucleotide chain-terminator sequencing method, was carried out using the ABI3730XL analyzer with ABI BigDye® 3.1 terminator chemistry. The sequence analysis was done using the Phred, Phrap, and Consed package (from the University of Washington), and was carried out to an error rate of less than 1 in 10,000 bases (Ewing and Green 1998).

Three individual clones for each PCR product were sequenced individually, and a consensus sequence was generated for each clone. These sequences were aligned using AlignX™, a component of Vector NTI Advance™, version 10.3.0, to obtain the final consensus sequence for each segment of the insert sequence.

### Statistical Analysis

No statistical analysis was used during this study.

## RESULTS AND DISCUSSION

### Insert Sequencing

The consensus sequence data for the 5307 maize insert was compared to sequence of the transformation plasmid pSYN12274 (Figure 4). The data demonstrated that the insert was intact and that the organization of the functional elements within the insert, as present in plasmid pSYN12274, was maintained. One nucleotide change was determined in the 5307 maize insert 48 bp upstream of the CMP promoter in a non-coding region of the T-DNA (Figure 4). This nucleotide change has no effect on the genes encoded by 5307 maize.

The functional elements *ecry3.1Ab*, *pmi*, the CMP promoter, the ZmUbiInt promoter, and the NOS terminators in 5307 maize were identical to those in the transformation plasmid pSYN12274.

Sequence analysis revealed that some truncation occurred at the right border (RB) and left border (LB) ends of the transferred DNA (T-DNA) during the transformation process. The entire RB, three bp of non-coding sequence at the 5' end of the insert, and eight bp of the LB were truncated. These deletions had no effect on the functionality of the insert as this phenomenon was previously observed in transformations with *Agrobacterium tumefaciens* (Tinland and Hohn 1995, Brunaud *et al.* 2002, Chilton and Que 2003).

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274**  
{ CBI Cross Reference Number 1 }

**Data Quality and Integrity**

No circumstances occurred during the conduct of this study that would have adversely affected the quality or integrity of the data generated.

**CONCLUSIONS**

Sequence analysis of the entire T-DNA present in 5307 maize confirmed that the insert remained intact and that the organization of the functional elements within the insert, as present in the transformation plasmid pSYN12274, was maintained. One nucleotide change was determined in the 5307 maize insert 48 bp upstream of the CMP promoter in a non-coding region of the T-DNA; however, this nucleotide change had no effect on the functionality of the T-DNA.

Sequence analysis revealed that some truncation occurred at the 5' and 3' ends of the T-DNA during the transformation process (resulting in 5307 maize). The entire RB, three bp of the non-coding sequence at the 5' end of the insert, and eight bp of the LB were truncated; however, these deletions had no effect on the functionality of the T-DNA.

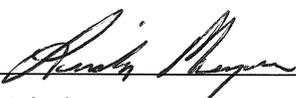
**RECORDS RETENTION**

Raw data, the original copy of this report, and other relevant records are archived at Syngenta Biotechnology, Inc., 3054 East Cornwallis Road, Research Triangle Park, NC 27709-2257, USA.

**CONTRIBUTING SCIENTISTS**

The analytical work reported herein was conducted by Stephen New, B.S., and Annick de Framond, PhD. This work was conducted at Syngenta Biotechnology, Inc.

**Reported by:**  November 3, 2010  
 Stephen New  
*Technical Expert I*  
 Product Safety  
 Syngenta Biotechnology, Inc.  
 Date

**Approved by:**  November 3, 2010  
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*Technical Leader III*  
 Product Safety  
 Syngenta Biotechnology, Inc.  
 Date

## REFERENCES

- Brunaud V, Balzergue S, Dubreucq B, Aubourg S, Samson F, Chauvin S, Bechtold N, Cruaud C, DeRose R, Pelletier G, Lepiniec L, Caboche M, Lecharny A. 2002. T-DNA integration into the *Arabidopsis* genome depends on sequences of pre-insertion sites. *EMBO Rep* 3:1152–1157.
- Chen E, Stacy C. 2007. Modified Cry3A toxins and nucleic acid sequences coding therefor. Syngenta Participations AG, assignee. U.S. Patent No. 7,276,583. Washington, DC: U.S. Patent Office.
- Chilton M-D, Que Q. 2003. Targeted Integration of T-DNA into the Tobacco Genome at Double-Stranded Breaks: New Insights on the Mechanism of T-DNA Integration. *Plant Physiol* 133:956–965.
- Christensen AH, Sharrock RA, Quail PH. 1992. Maize polyubiquitin genes: structure, thermal perturbation of expression and transcript splicing, and promoter activity following transfer to protoplasts by electroporation. *Plant Mol Biol* 18:675–689.
- Depicker A, Stachel S, Dhaese P, Zambryski P, Goodman HM. 1982. Nopaline synthase: transcript mapping and DNA sequence. *J Mol Appl Genet* 1:561–573.
- Ewing B, Green P. 1998. Base-calling of automated sequencer traces using Phred. II. Error probabilities. *Genome Res* 8:186–194.
- Fling ME, Kopf J, Richards C. 1985. Nucleotide sequence of the transposon Tn7 gene encoding an aminoglycoside-modifying enzyme, 3''(9)-O-nucleotidyltransferase. *Nucleic Acids Res* 13:7095–7106.
- Geiser M., Schweizer S, Grimm C. 1986. The hypervariable region in the genes coding for entomopathogenic crystal proteins of *Bacillus thuringiensis*: nucleotide sequence of the *kurhd1* gene of subsp. *kurstaki* HD-1 *Gene* 48:109-118.
- Hansen G, Das A, Chilton M-D. 1994. Constitutive expression of the virulence genes improves the efficiency of plant transformation by *Agrobacterium*. *P Natl Acad Sci USA* 91:7603–7607.
- Heeb S, Itoh Y, Nishijyo T, Schnider U, Keel C, Wade J, Walsh U, O'gara F, Haas D. 2000. Small, stable shuttle vectors based on the minimal pVS1 replicon for use in gram-negative, plant-associated bacteria. *Mol Plant Microbe In* 13:232–237.
- Hohn T, Stavolone L, De Haan P, Ligon H, Kononova M. 2007. Cestrum yellow leaf curling virus promoters. Syngenta Participations AG, assignee. U.S. Patent No.7,166,770. Washington DC: U.S. patent Office.
- Hofte H, Whiteley H. 1989. Insecticidal Crystal Proteins of *Bacillus thuringiensis*. *Microbiol. Rev.* 53:242-255.

- Ingham DJ, Beer S, Money S, Hansen G. 2001. Quantitative real-time PCR assay for determining transgene copy number in transformed plants. *BioTechniques* 31:132–140.
- Itoh T, Tomizawa J. 1979. Initiation of Replication of Plasmid ColE1 DNA by RNA Polymerase, Ribonuclease H and DNA Polymerase I. *Cold Spring Harb Sym. Pt1*:409–417.
- Itoh Y, Watson JM, Dieter H, Leisinger T. 1984. Genetic and Molecular Characterization of the *Pseudomonas* plasmid pVS1. *Plasmid* 11:206–220.
- Koziel MG, Desai NM, Lewis KS, Kramer VC, Warren GW, Evola SV, Crossland LD, Wright MS, Merlin EJ, Launis KL, Rothstein SJ, Bowman CG, Dawson JL, Dunder EM, Pace GM, Suttie JL. 1997. Synthetic DNA sequence having enhanced insecticidal activity in maize. Ciba-Geigy, assignee. U.S. Patent No. 5,625,136. Washington, DC: U.S. Patent Office.
- Murray EE, Lotzer J, Eberle M. 1989. Codon usage in plant genes. *Nucleic Acids Res* 17:477–498.
- NCBI. 2010. Entrez® Nucleotide Database. Bethesda, MD: National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health. <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Nucleotide>.
- Negrotto D, Jolley M, Beer S, Wenck AR, Hansen G. 2000. The use of phosphomannose-isomerase as a selectable marker to recover transgenic maize plants (*Zea mays L.*) via *Agrobacterium* transformation. *Plant Cell Rep* 19:798–803.
- Saghai-Marroof MA, Soliman KM, Jorgensen RA, Allard RW. 1984. Ribosomal DNA spacer-length polymorphisms in barley: Mendelian inheritance, chromosomal location, and population dynamics. *P Natl Acad Sci USA* 81:8014–8018.
- Sekar V, Thompson DV, Maroney MJ, Bookland RG, Adang MJ. 1987. Molecular cloning and characterization of the insecticidal crystal protein gene of *Bacillus thuringiensis* var. *tenebrionis*. *Proc Natl Acad Sci USA* 84:7036–7040.
- Tinland B, Hohn B. 1995. Recombination between prokaryotic and eukaryotic DNA: Integration of *Agrobacterium tumefaciens* T-DNA into the plant genome. *Genetic Engineering* Setlow JK, ed. New York, NY: Plenum Press. pp. 209–229.
- US EPA. 1989. Good Laboratory Practices Standards. 40 CFR Part 160.

Walters FS, deFontes CM, Hart H, Warren GW, Chen JS. 2010. Lepidopteran-active variable-region sequence imparts coleopteran activity in eCry3.1Ab, an engineered *Bacillus thuringiensis* hybrid insecticidal protein. *Appl Environ Microb* 76:3082-3088.

Wang K, Herrera-Estrella L, Van Montagu M, Zambryski P. 1984. Right 25 bp terminus sequence of the nopaline T-DNA is essential for and determines direction of DNA transfer from *Agrobacterium* to the plant genome. *Cell* 38:455-462.

Zambryski P, Depicker A, Kruger K, Goodman HM. 1982. Tumor induction by *Agrobacterium tumefaciens*: analysis of the boundaries of T-DNA. *J Mol Appl Genet* 1:361-370.



**Event 5307 maize:  
Insert Sequence Analysis**

***CONTAINS CONFIDENTIAL BUSINESS INFORMATION***

<b>Data Requirement(s):</b>	Not applicable
<b>Author:</b>	Stephen New
<b>Study Completion Date:</b>	November 3, 2010
<b>Performing Laboratory:</b>	Syngenta Biotechnology, Inc. Product Safety 3054 East Cornwallis Road PO Box 12257 Research Triangle Park, NC 27709-2257, USA
<b>Syngenta Study No.:</b>	Not applicable
<b>Report No.:</b>	SSB-159-10 A1

CBI Cross-Reference Number 1

This cross-reference number noted on a place holder page is used in place of the following whole page at the indicated volume and page references.

Deleted pages are attached immediately behind this page.

<u>Pages</u>	<u>Reason for Deletion</u>	<u>FIFRA Reference</u>
18	Discloses information concerning the composition of the product	§10(d)(1)(A)

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274**

The base pair discrepancy is indicated by the following text format: **G**  
**T**

		RB	
pSYN12274	(1)	<u>GTTTACCCGCCAATATATATCTGTCAAACACTGATAGTTTAAACTGAAGGC</u>	
5307 insert	(1)	-----ACTGATAGTTTAAACTGAAGGC	
pSYN12274	(51)	GGGAAACGACAATCTGATCATGAGCGGAGAATTAAGGGAGTCACGTTATG	
5307 insert	(23)	GGGAAACGACAATCTGATCATGAGCGGAGAATTAAGGGAGTCACGTTATG	
pSYN12274	(101)	ACCCCCGCCGATGACGCGGGACAAGCCGTTTTACGTTTGGAACTGACAGA	
5307 insert	(73)	ACCCCCGCCGATGACGCGGGACAAGCCGTTTTACGTTTGGAACTGACAGA	
pSYN12274	(151)	ACCGCAACGCTGCAGGAATTGGCCGAGCGGCCCATTTAAATCAATTGGGC	▼
5307 insert	(123)	ACCGCAACGCTGCAGGAATTGGCCGAGCTGCCCATTTAAATCAATTGGGC	
pSYN12274	(201)	GCGCCGAATTCGAGCTCGGTACAAGCTTCTGGCAGACAAAGTGGCAGACA	CMP promoter
5307 insert	(173)	GCGCCGAATTCGAGCTCGGTACAAGCTTCTGGCAGACAAAGTGGCAGACA	
pSYN12274	(251)	TACTGTCCCACAAATGAAGATGGAATCTGTAAAAGAAAACGCGTGAAATA	CMP promoter
5307 insert	(223)	TACTGTCCCACAAATGAAGATGGAATCTGTAAAAGAAAACGCGTGAAATA	
pSYN12274	(301)	ATGCGTCTGACAAAGGTTAGGTCGGCTGCCTTTAATCAATACCAAAGTGG	CMP promoter
5307 insert	(273)	ATGCGTCTGACAAAGGTTAGGTCGGCTGCCTTTAATCAATACCAAAGTGG	
pSYN12274	(351)	TCCCTACCACGATGGAAAACTGTGCAGTCGGTTTGGCTTTTTCTGACGA	CMP promoter
5307 insert	(323)	TCCCTACCACGATGGAAAACTGTGCAGTCGGTTTGGCTTTTTCTGACGA	
pSYN12274	(401)	ACAAATAAGATTCGTGGCCGACAGGTGGGGTCCACCATGTGAAGGCATC	CMP promoter
5307 insert	(373)	ACAAATAAGATTCGTGGCCGACAGGTGGGGTCCACCATGTGAAGGCATC	
pSYN12274	(451)	TTCAGACTCCAATAATGGAGCAATGACGTAAGGGCTTACGAAATAAGTAA	CMP promoter
5307 insert	(423)	TTCAGACTCCAATAATGGAGCAATGACGTAAGGGCTTACGAAATAAGTAA	
pSYN12274	(501)	GGGTAGTTTGGGAAATGTCCACTCACCCGTCAGTCTATAAATACTTAGCC	CMP promoter
5307 insert	(473)	GGGTAGTTTGGGAAATGTCCACTCACCCGTCAGTCTATAAATACTTAGCC	
pSYN12274	(551)	CCTCCCTCATTGTTAAGGGAGCAAGGATCCACCATGACTAGTAACGGCCG	CMP promoter <i>ecry3.1Ab</i>
5307 insert	(523)	CCTCCCTCATTGTTAAGGGAGCAAGGATCCACCATGACTAGTAACGGCCG	

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

			<i>ecry3.1Ab</i>
pSYN12274	(601)	CCAGTGTGCTGGTATTCGCCCTTATGACGGCCGACAACAACACCGAGGCC	
5307 insert	(573)	CCAGTGTGCTGGTATTCGCCCTTATGACGGCCGACAACAACACCGAGGCC	
			<i>ecry3.1Ab</i>
pSYN12274	(651)	TGGACAGCAGCACCACCAAGGACGTGATCCAGAAGGGCATCAGCGTGGTG	
5307 insert	(623)	TGGACAGCAGCACCACCAAGGACGTGATCCAGAAGGGCATCAGCGTGGTG	
			<i>ecry3.1Ab</i>
pSYN12274	(701)	GGCGACCTGCTGGGCGTGGTGGGCTTCCCCTTCGGCGGGCGCCCTGGTGAG	
5307 insert	(673)	GGCGACCTGCTGGGCGTGGTGGGCTTCCCCTTCGGCGGGCGCCCTGGTGAG	
			<i>ecry3.1Ab</i>
pSYN12274	(751)	CTTCTACACCAACTTCCTGAACACCATCTGGCCCAGCGAGGACCCCTGGA	
5307 insert	(723)	CTTCTACACCAACTTCCTGAACACCATCTGGCCCAGCGAGGACCCCTGGA	
			<i>ecry3.1Ab</i>
pSYN12274	(801)	AGGCCTTCATGGAGCAGGTGGAGGCCCTGATGGACCAGAAGATCGCCGAC	
5307 insert	(773)	AGGCCTTCATGGAGCAGGTGGAGGCCCTGATGGACCAGAAGATCGCCGAC	
			<i>ecry3.1Ab</i>
pSYN12274	(851)	TACGCCAAGAACAAGGCACTGGCCGAGCTACAGGGCCTCCAGAACAACGT	
5307 insert	(823)	TACGCCAAGAACAAGGCACTGGCCGAGCTACAGGGCCTCCAGAACAACGT	
			<i>ecry3.1Ab</i>
pSYN12274	(901)	GGAGGACTATGTGAGCGCCCTGAGCAGCTGGCAGAAGAACCCCGCTGCAC	
5307 insert	(873)	GGAGGACTATGTGAGCGCCCTGAGCAGCTGGCAGAAGAACCCCGCTGCAC	
			<i>ecry3.1Ab</i>
pSYN12274	(951)	CGTTCCGCAACCCCCACAGCCAGGGCCGCATCCGCGAGCTGTTTCAGCCAG	
5307 insert	(923)	CGTTCCGCAACCCCCACAGCCAGGGCCGCATCCGCGAGCTGTTTCAGCCAG	
			<i>ecry3.1Ab</i>
pSYN12274	(1001)	GCCGAGAGCCACTTCCGCAACAGCATGCCAGCTTCGCCATCAGCGGCTA	
5307 insert	(973)	GCCGAGAGCCACTTCCGCAACAGCATGCCAGCTTCGCCATCAGCGGCTA	
			<i>ecry3.1Ab</i>
pSYN12274	(1051)	CGAGGTGCTGTTCTTGACCACCTACGCCAGGCCGCAACACCCACCTGT	
5307 insert	(1023)	CGAGGTGCTGTTCTTGACCACCTACGCCAGGCCGCAACACCCACCTGT	
			<i>ecry3.1Ab</i>
pSYN12274	(1101)	TCCTGCTGAAGGACGCCCAAATCTACGGAGAGGAGTGGGGCTACGAGAAG	
5307 insert	(1073)	TCCTGCTGAAGGACGCCCAAATCTACGGAGAGGAGTGGGGCTACGAGAAG	
			<i>ecry3.1Ab</i>
pSYN12274	(1151)	GAGGACATCGCCGAGTTCTACAAGCGCCAGCTGAAGCTGACCCAGGAGTA	
5307 insert	(1123)	GAGGACATCGCCGAGTTCTACAAGCGCCAGCTGAAGCTGACCCAGGAGTA	
			<i>ecry3.1Ab</i>
pSYN12274	(1201)	CACCGACCACTGCGTGAAGTGGTACAACGTGGGTCTAGACAAGCTCCGCG	
5307 insert	(1173)	CACCGACCACTGCGTGAAGTGGTACAACGTGGGTCTAGACAAGCTCCGCG	

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

		<i>ecry3.1Ab</i>
pSYN12274	(1251)	GCAGCAGCTACGAGAGCTGGGTGAACTTCAACCGCTACCGCCGCGAGATG
5307 insert	(1223)	GCAGCAGCTACGAGAGCTGGGTGAACTTCAACCGCTACCGCCGCGAGATG
		<i>ecry3.1Ab</i>
pSYN12274	(1301)	ACCCTGACCGTGCTGGACCTGATCGCCCTGTTCCCCCTGTACGACGTGCG
5307 insert	(1273)	ACCCTGACCGTGCTGGACCTGATCGCCCTGTTCCCCCTGTACGACGTGCG
		<i>ecry3.1Ab</i>
pSYN12274	(1351)	CCTGTACCCCAAGGAGGTGAAGACCGAGCTGACCCGCGACGTGCTGACCG
5307 insert	(1323)	CCTGTACCCCAAGGAGGTGAAGACCGAGCTGACCCGCGACGTGCTGACCG
		<i>ecry3.1Ab</i>
pSYN12274	(1401)	ACCCCATCGTGGGCGTGAACAACCTGCGCGGCTACGGCACCACCTTCAGC
5307 insert	(1373)	ACCCCATCGTGGGCGTGAACAACCTGCGCGGCTACGGCACCACCTTCAGC
		<i>ecry3.1Ab</i>
pSYN12274	(1451)	AACATCGAGAACTACATCCGCAAGCCCCACCTGTTTCGACTACCTGCACCG
5307 insert	(1423)	AACATCGAGAACTACATCCGCAAGCCCCACCTGTTTCGACTACCTGCACCG
		<i>ecry3.1Ab</i>
pSYN12274	(1501)	CATCCAGTTCCACACGCGTTTCCAGCCCGGCTACTACGGCAACGACAGCT
5307 insert	(1473)	CATCCAGTTCCACACGCGTTTCCAGCCCGGCTACTACGGCAACGACAGCT
		<i>ecry3.1Ab</i>
pSYN12274	(1551)	TCAACTACTGGAGCGGCAACTACGTGAGCACCCGCCAGCATCGGCAGC
5307 insert	(1523)	TCAACTACTGGAGCGGCAACTACGTGAGCACCCGCCAGCATCGGCAGC
		<i>ecry3.1Ab</i>
pSYN12274	(1601)	AACGACATCATCACCAGCCCCCTTCTACGGCAACAAGAGCAGCGAGCCCCGT
5307 insert	(1573)	AACGACATCATCACCAGCCCCCTTCTACGGCAACAAGAGCAGCGAGCCCCGT
		<i>ecry3.1Ab</i>
pSYN12274	(1651)	GCAGAACCTTGAGTTCAACGGCGAGAAGGTGTACCGCGCCGTGGCTAACA
5307 insert	(1623)	GCAGAACCTTGAGTTCAACGGCGAGAAGGTGTACCGCGCCGTGGCTAACA
		<i>ecry3.1Ab</i>
pSYN12274	(1701)	CCAACCTGGCCGTGTGGCCCTCTGCAGTGTACAGCGGCGTGACCAAGGTG
5307 insert	(1673)	CCAACCTGGCCGTGTGGCCCTCTGCAGTGTACAGCGGCGTGACCAAGGTG
		<i>ecry3.1Ab</i>
pSYN12274	(1751)	GAGTTCAGCCAGTACAACGACCAGACCGAGGCCAGCACCCAGACCTA
5307 insert	(1723)	GAGTTCAGCCAGTACAACGACCAGACCGAGGCCAGCACCCAGACCTA
		<i>ecry3.1Ab</i>
pSYN12274	(1801)	CGACAGCAAGCGCAACGTGGGCGCCGTGAGCTGGGACAGCATCGACCAGC
5307 insert	(1773)	CGACAGCAAGCGCAACGTGGGCGCCGTGAGCTGGGACAGCATCGACCAGC
		<i>ecry3.1Ab</i>
pSYN12274	(1851)	TGCCCCCCGAGACCACCGACGAGCCCCTGGAGAAGGGCTACAGCCACCAG
5307 insert	(1823)	TGCCCCCCGAGACCACCGACGAGCCCCTGGAGAAGGGCTACAGCCACCAG

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

		<u><i>ecry3.1Ab</i></u>
pSYN12274	(1901)	CTGAACTACGTGATGTGCTTCCTGATGCAGGGCAGCCGCGGCACCATCCC
5307 insert	(1873)	CTGAACTACGTGATGTGCTTCCTGATGCAGGGCAGCCGCGGCACCATCCC
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(1951)	CGTGCTGACCTGGACCCACAAGAGCGTCGACTTCTTCAACATGATCGACA
5307 insert	(1923)	CGTGCTGACCTGGACCCACAAGAGCGTCGACTTCTTCAACATGATCGACA
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2001)	GCAAGAAGATCACCCAGCTGCCCCTGACCAAGAGCACCAACCTGGGCAGC
5307 insert	(1973)	GCAAGAAGATCACCCAGCTGCCCCTGACCAAGAGCACCAACCTGGGCAGC
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2051)	GGCACCAGCGTGGTGAAGGGCCCCGGCTTCACCGCGGGCGACATCCTGCG
5307 insert	(2023)	GGCACCAGCGTGGTGAAGGGCCCCGGCTTCACCGCGGGCGACATCCTGCG
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2101)	CCGCACCAGCCCCGGCCAGATCAGCACCTGCGCGTGAACATCACCGCCC
5307 insert	(2073)	CCGCACCAGCCCCGGCCAGATCAGCACCTGCGCGTGAACATCACCGCCC
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2151)	CCCTGAGCCAGCGCTACCGCGTCCGCATCCGCTACGCCAGCACCACCAAC
5307 insert	(2123)	CCCTGAGCCAGCGCTACCGCGTCCGCATCCGCTACGCCAGCACCACCAAC
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2201)	CTGCAGTTCCACACCAGCATCGACGGCCGCCCATCAACCAGGGCAACTT
5307 insert	(2173)	CTGCAGTTCCACACCAGCATCGACGGCCGCCCATCAACCAGGGCAACTT
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2251)	CAGCGCCACCATGAGCAGCGGCAGCAACCTGCAGAGCGGCAGCTTCCGCA
5307 insert	(2223)	CAGCGCCACCATGAGCAGCGGCAGCAACCTGCAGAGCGGCAGCTTCCGCA
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2301)	CCGTGGGCTTCACCACCCCTTCAACTTCAGCAACGGCAGCAGCGTGTTC
5307 insert	(2273)	CCGTGGGCTTCACCACCCCTTCAACTTCAGCAACGGCAGCAGCGTGTTC
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2351)	ACCCTGAGCGCCACGTGTTCAACAGCGGCAACGAGGTGTACATCGACCG
5307 insert	(2323)	ACCCTGAGCGCCACGTGTTCAACAGCGGCAACGAGGTGTACATCGACCG
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2401)	CATCGAGTTCGTGCCCGCCGAGGTGACCTTCGAGGCCGAGTACGACCTGG
5307 insert	(2373)	CATCGAGTTCGTGCCCGCCGAGGTGACCTTCGAGGCCGAGTACGACCTGG
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2451)	AGAGGGCTCAGAAGGCCGTGAACGAGCTGTTTACCAGCAGCAACCAGATC
5307 insert	(2423)	AGAGGGCTCAGAAGGCCGTGAACGAGCTGTTTACCAGCAGCAACCAGATC
		<u><i>ecry3.1Ab</i></u>
pSYN12274	(2501)	GGCCTGAAGACCGACGTGACCGACTACCACATCGATCAGGTGTAGGAGCT
5307 insert	(2473)	GGCCTGAAGACCGACGTGACCGACTACCACATCGATCAGGTGTAGGAGCT

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

			<u>NOS terminator</u>
pSYN12274	(2551)	GAGCTCTAGATCCCCGAATTTCCCCGATCGTTCAAACATTTGGCAATAAA	
5307 insert	(2523)	GAGCTCTAGATCCCCGAATTTCCCCGATCGTTCAAACATTTGGCAATAAA	
			<u>NOS terminator</u>
pSYN12274	(2601)	GTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAA	
5307 insert	(2573)	GTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAA	
			<u>NOS terminator</u>
pSYN12274	(2651)	TTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGAC	
5307 insert	(2623)	TTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGAC	
			<u>NOS terminator</u>
pSYN12274	(2701)	GTTATTTATGAGATGGGTTTTTATGATTAGAGTCCC GCAATTATACATTT	
5307 insert	(2673)	GTTATTTATGAGATGGGTTTTTATGATTAGAGTCCC GCAATTATACATTT	
			<u>NOS terminator</u>
pSYN12274	(2751)	AATACGCGATAGAAAACAAAATATAGCGCGCAA AACTAGGATAAAATTATCG	
5307 insert	(2723)	AATACGCGATAGAAAACAAAATATAGCGCGCAA AACTAGGATAAAATTATCG	
			<u>NOS terminator</u>
pSYN12274	(2801)	CGCGCGGTGTCATCTATGTTACTAGATCGGGAATTGGGTACCAGCTTGCA	
5307 insert	(2773)	CGCGCGGTGTCATCTATGTTACTAGATCGGGAATTGGGTACCAGCTTGCA	
			<u>ZmUbiInt promoter</u>
pSYN12274	(2851)	TGCCTGCAGTGCAGCGTGACCCGGTTCGTGCC CCTCTCTAGAGATAATGAG	
5307 insert	(2823)	TGCCTGCAGTGCAGCGTGACCCGGTTCGTGCC CCTCTCTAGAGATAATGAG	
			<u>ZmUbiInt promoter</u>
pSYN12274	(2901)	CATTGCATGTCTAAGTTATAAAAAATTACCACATATTTTTTTTGT CACAC	
5307 insert	(2873)	CATTGCATGTCTAAGTTATAAAAAATTACCACATATTTTTTTTGT CACAC	
			<u>ZmUbiInt promoter</u>
pSYN12274	(2951)	TTGTTTGAAGTGCAGTTTATCTATCTTTATA CATATATTTAACTTTACT	
5307 insert	(2923)	TTGTTTGAAGTGCAGTTTATCTATCTTTATA CATATATTTAACTTTACT	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3001)	CTACGAATAATATAATCTATAGTACTACAATA ATATCAGTGTTTTAGAGA	
5307 insert	(2973)	CTACGAATAATATAATCTATAGTACTACAATA ATATCAGTGTTTTAGAGA	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3051)	ATCATATAAATGAACAGTTAGACATGGTCTAA AGGACAATTGAGTATTTT	
5307 insert	(3023)	ATCATATAAATGAACAGTTAGACATGGTCTAA AGGACAATTGAGTATTTT	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3101)	GACAACAGGACTCTACAGTTTTATCTTTTTT AGTGTGCATGTGTTCTCCTT	
5307 insert	(3073)	GACAACAGGACTCTACAGTTTTATCTTTTTT AGTGTGCATGTGTTCTCCTT	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3151)	TTTTTTTGCAAATAGCTTACCTATATAAATA CTTCATCCATTTTATTAGT	
5307 insert	(3123)	TTTTTTTGCAAATAGCTTACCTATATAAATA CTTCATCCATTTTATTAGT	

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

			<u>ZmUbiInt promoter</u>
pSYN12274	(3201)	ACATCCATTTAGGGTTTAGGGTTAATGGTTTTTATAGACTAATTTTTTTTA	
5307 insert	(3173)	ACATCCATTTAGGGTTTAGGGTTAATGGTTTTTATAGACTAATTTTTTTTA	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3251)	GTACATCTATTTTATTCTATTTTAGCCTCTAAATTAAGAAAACATAAACT	
5307 insert	(3223)	GTACATCTATTTTATTCTATTTTAGCCTCTAAATTAAGAAAACATAAACT	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3301)	CTATTTTAGTTTTTTTATTTAATAATTTAGATATAAAATAGAATAAAATA	
5307 insert	(3273)	CTATTTTAGTTTTTTTATTTAATAATTTAGATATAAAATAGAATAAAATA	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3351)	AAGTGACTAAAAATTAACAAATACCCTTTAAGAAATTAAAAAAACTAAG	
5307 insert	(3323)	AAGTGACTAAAAATTAACAAATACCCTTTAAGAAATTAAAAAAACTAAG	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3401)	GAAACATTTTTCTTGTTTTCGAGTAGATAATGCCAGCCTGTTAAACGCCGT	
5307 insert	(3373)	GAAACATTTTTCTTGTTTTCGAGTAGATAATGCCAGCCTGTTAAACGCCGT	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3451)	CGACGAGTCTAACGGACACCAACCAGCGAACCCAGCAGCGTCGCGTCGGGC	
5307 insert	(3423)	CGACGAGTCTAACGGACACCAACCAGCGAACCCAGCAGCGTCGCGTCGGGC	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3501)	CAAGCGAAGCAGACGGCACGGCATCTCTGTGCTGCCTCTGGACCCCTCT	
5307 insert	(3473)	CAAGCGAAGCAGACGGCACGGCATCTCTGTGCTGCCTCTGGACCCCTCT	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3551)	CGAGAGTTCCGCTCCACCGTTGGACTTGCTCCGCTGTCCGCATCCAGAAA	
5307 insert	(3523)	CGAGAGTTCCGCTCCACCGTTGGACTTGCTCCGCTGTCCGCATCCAGAAA	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3601)	TTGCGTGGCGGAGCGGCAGACGTGAGCCGGCACGGCAGCGCGCCTCCTCC	
5307 insert	(3573)	TTGCGTGGCGGAGCGGCAGACGTGAGCCGGCACGGCAGCGCGCCTCCTCC	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3651)	TCCTCTCACGGCACCGGCAGCTACGGGGGATTCCCTTTCCCACCGCTCCTT	
5307 insert	(3623)	TCCTCTCACGGCACCGGCAGCTACGGGGGATTCCCTTTCCCACCGCTCCTT	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3701)	CGCTTTCCCTTCCCTCGCCCGCCGTAATAAATAGACACCCCTCCACACCC	
5307 insert	(3673)	CGCTTTCCCTTCCCTCGCCCGCCGTAATAAATAGACACCCCTCCACACCC	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3751)	TCTTTCCCAACCTCGTGTTGTTTCGGAGCGCACACACACAACAGATC	
5307 insert	(3723)	TCTTTCCCAACCTCGTGTTGTTTCGGAGCGCACACACACAACAGATC	
			<u>ZmUbiInt promoter</u>
pSYN12274	(3801)	TCCCCAAATCCACCGTCGGCACCTCCGCTTCAAGGTACGCCGCTCGTC	
5307 insert	(3773)	TCCCCAAATCCACCGTCGGCACCTCCGCTTCAAGGTACGCCGCTCGTC	

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

		<u>ZmUbiInt promoter</u>
pSYN12274	(3851)	CTCCCCCCCCCCCCCTCTCTACCTTCTCTAGATCGGCGTTCCGGTCCATG
5307 insert	(3823)	CTCCCCCCCCCCCCCTCTCTACCTTCTCTAGATCGGCGTTCCGGTCCATG
		<u>ZmUbiInt promoter</u>
pSYN12274	(3901)	GTTAGGGCCCCGGTAGTTCTACTTCTGTTCATGTTTGTGTTAGATCCGTGT
5307 insert	(3873)	GTTAGGGCCCCGGTAGTTCTACTTCTGTTCATGTTTGTGTTAGATCCGTGT
		<u>ZmUbiInt promoter</u>
pSYN12274	(3951)	TTGTGTTAGATCCGTGCTGCTAGCGTTCGTACACGGATGCGACCTGTACG
5307 insert	(3923)	TTGTGTTAGATCCGTGCTGCTAGCGTTCGTACACGGATGCGACCTGTACG
		<u>ZmUbiInt promoter</u>
pSYN12274	(4001)	TCAGACACGTTCTGATTGCTAACTTGCCAGTGTCTCTTTGGGGAATCC
5307 insert	(3973)	TCAGACACGTTCTGATTGCTAACTTGCCAGTGTCTCTTTGGGGAATCC
		<u>ZmUbiInt promoter</u>
pSYN12274	(4051)	TGGGATGGCTCTAGCCGTTCCGCAGACGGGATCGATTTTCATGATTTTTTTT
5307 insert	(4023)	TGGGATGGCTCTAGCCGTTCCGCAGACGGGATCGATTTTCATGATTTTTTTT
		<u>ZmUbiInt promoter</u>
pSYN12274	(4101)	TGTTTCGTTGCATAGGGTTTGGTTTGCCCTTTTCCTTTATTTCAATATAT
5307 insert	(4073)	TGTTTCGTTGCATAGGGTTTGGTTTGCCCTTTTCCTTTATTTCAATATAT
		<u>ZmUbiInt promoter</u>
pSYN12274	(4151)	GCCGTGCACTTGTTTGTTCGGGTCATCTTTTCATGCTTTTTTTTTGTCTTGG
5307 insert	(4123)	GCCGTGCACTTGTTTGTTCGGGTCATCTTTTCATGCTTTTTTTTTGTCTTGG
		<u>ZmUbiInt promoter</u>
pSYN12274	(4201)	TTGTGATGATGTGGTCTGGTTGGGCGGTCGTTCTAGATCGGAGTAGAATT
5307 insert	(4173)	TTGTGATGATGTGGTCTGGTTGGGCGGTCGTTCTAGATCGGAGTAGAATT
		<u>ZmUbiInt promoter</u>
pSYN12274	(4251)	CTGTTTCAAACCTACCTGGTGGATTTATTAATTTTGGATCTGTATGTGTGT
5307 insert	(4223)	CTGTTTCAAACCTACCTGGTGGATTTATTAATTTTGGATCTGTATGTGTGT
		<u>ZmUbiInt promoter</u>
pSYN12274	(4301)	GCCATACATATTCATAGTTACGAATTGAAGATGATGGATGGAAATATCGA
5307 insert	(4273)	GCCATACATATTCATAGTTACGAATTGAAGATGATGGATGGAAATATCGA
		<u>ZmUbiInt promoter</u>
pSYN12274	(4351)	TCTAGGATAGGTATAACATGTTGATGCGGGTTTTACTGATGCATATACAGA
5307 insert	(4323)	TCTAGGATAGGTATAACATGTTGATGCGGGTTTTACTGATGCATATACAGA
		<u>ZmUbiInt promoter</u>
pSYN12274	(4401)	GATGCTTTTTTGTTCGCTTGGTTGTGATGATGTGGTGTGGTTGGGCGGTTCG
5307 insert	(4373)	GATGCTTTTTTGTTCGCTTGGTTGTGATGATGTGGTGTGGTTGGGCGGTTCG
		<u>ZmUbiInt promoter</u>
pSYN12274	(4451)	TTCATTTCGTTCTAGATCGGAGTAGAATACTGTTTCAAACCTACCTGGTGTA
5307 insert	(4423)	TTCATTTCGTTCTAGATCGGAGTAGAATACTGTTTCAAACCTACCTGGTGTA

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

		<u>ZmUbiInt promoter</u>
pSYN12274	(4501)	TTTATTAATTTTGGAACTGTATGTGTGTGCATACATCTTCATAGTTACG
5307 insert	(4473)	TTTATTAATTTTGGAACTGTATGTGTGTGCATACATCTTCATAGTTACG
		<u>ZmUbiInt promoter</u>
pSYN12274	(4551)	AGTTTAAGATGGATGGAAATATCGATCTAGGATAGGTATACATGTTGATG
5307 insert	(4523)	AGTTTAAGATGGATGGAAATATCGATCTAGGATAGGTATACATGTTGATG
		<u>ZmUbiInt promoter</u>
pSYN12274	(4601)	TGGGTTTTACTGATGCATATACATGATGGCATATGCAGCATCTATTCATA
5307 insert	(4573)	TGGGTTTTACTGATGCATATACATGATGGCATATGCAGCATCTATTCATA
		<u>ZmUbiInt promoter</u>
pSYN12274	(4651)	TGCTCTAACCTTGAGTACCTATCTATTATAATAAAACAAGTATGTTTTATA
5307 insert	(4623)	TGCTCTAACCTTGAGTACCTATCTATTATAATAAAACAAGTATGTTTTATA
		<u>ZmUbiInt promoter</u>
pSYN12274	(4701)	ATTATTTTGATCTTGATATACTTGGATGATGGCATATGCAGCAGCTATAT
5307 insert	(4673)	ATTATTTTGATCTTGATATACTTGGATGATGGCATATGCAGCAGCTATAT
		<u>ZmUbiInt promoter</u>
pSYN12274	(4751)	GTGGATTTTTTTAGCCCTGCCTTCATACGCTATTTATTTGCTTGGTACTG
5307 insert	(4723)	GTGGATTTTTTTAGCCCTGCCTTCATACGCTATTTATTTGCTTGGTACTG
		<u>ZmUbiInt promoter</u>
pSYN12274	(4801)	TTTCTTTTGTCGATGCTCACCTGTTGTTTGGTGTACTTCTGCAGGGAT
5307 insert	(4773)	TTTCTTTTGTCGATGCTCACCTGTTGTTTGGTGTACTTCTGCAGGGAT
		<u>pmi</u>
pSYN12274	(4851)	CCCCGATCATGCAAAAACCTCATTAACCTCAGTGCAAAAACCTATGCCTGGGGC
5307 insert	(4823)	CCCCGATCATGCAAAAACCTCATTAACCTCAGTGCAAAAACCTATGCCTGGGGC
		<u>pmi</u>
pSYN12274	(4901)	AGCAAAACGGCGTTGACTGAACTTTATGGTATGGAAAATCCGTCCAGCCA
5307 insert	(4873)	AGCAAAACGGCGTTGACTGAACTTTATGGTATGGAAAATCCGTCCAGCCA
		<u>pmi</u>
pSYN12274	(4951)	GCCGATGGCCGAGCTGTGGATGGGCGCACATCCGAAAAGCAGTTCACGAG
5307 insert	(4923)	GCCGATGGCCGAGCTGTGGATGGGCGCACATCCGAAAAGCAGTTCACGAG
		<u>pmi</u>
pSYN12274	(5001)	TGCAGAATGCCGCCGAGATATCGTTTCACTGCGTGATGTGATTGAGAGT
5307 insert	(4973)	TGCAGAATGCCGCCGAGATATCGTTTCACTGCGTGATGTGATTGAGAGT
		<u>pmi</u>
pSYN12274	(5051)	GATAAATCGACTCTGCTCGGAGAGGCCGTTGCCAAAACGCTTTGGCGAACT
5307 insert	(5023)	GATAAATCGACTCTGCTCGGAGAGGCCGTTGCCAAAACGCTTTGGCGAACT
		<u>pmi</u>
pSYN12274	(5101)	GCCTTTCCTGTTCAAAGTATTATGCGCAGCACAGCCACTCTCCATTCAGG
5307 insert	(5073)	GCCTTTCCTGTTCAAAGTATTATGCGCAGCACAGCCACTCTCCATTCAGG

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

		<i>pmi</i>
pSYN12274	(5151)	TTCATCCAAACAAACACAATTCTGAAATCGGTTTTGCCAAAGAAAATGCC
5307 insert	(5123)	TTCATCCAAACAAACACAATTCTGAAATCGGTTTTGCCAAAGAAAATGCC
		<i>pmi</i>
pSYN12274	(5201)	GCAGGTATCCCGATGGATGCCGCCGAGCGTAACTATAAAGATCCTAACCA
5307 insert	(5173)	GCAGGTATCCCGATGGATGCCGCCGAGCGTAACTATAAAGATCCTAACCA
		<i>pmi</i>
pSYN12274	(5251)	CAAGCCGGAGCTGGTTTTTTGCGCTGACGCCTTTCCTTGCGATGAACGCGT
5307 insert	(5223)	CAAGCCGGAGCTGGTTTTTTGCGCTGACGCCTTTCCTTGCGATGAACGCGT
		<i>pmi</i>
pSYN12274	(5301)	TTCGTGAATTTTCCGAGATTGTCTCCCTACTCCAGCCGGTCCGAGGTGCA
5307 insert	(5273)	TTCGTGAATTTTCCGAGATTGTCTCCCTACTCCAGCCGGTCCGAGGTGCA
		<i>pmi</i>
pSYN12274	(5351)	CATCCGGCGATTGCTCACTTTTTTACAACAGCCTGATGCCGAACGTTTAAG
5307 insert	(5323)	CATCCGGCGATTGCTCACTTTTTTACAACAGCCTGATGCCGAACGTTTAAG
		<i>pmi</i>
pSYN12274	(5401)	CGAACTGTTCCGCCAGCCTGTTGAATATGCAGGGTGAAGAAAAATCCCGCG
5307 insert	(5373)	CGAACTGTTCCGCCAGCCTGTTGAATATGCAGGGTGAAGAAAAATCCCGCG
		<i>pmi</i>
pSYN12274	(5451)	CGCTGGCGATTTTAAAATCGGCCCTCGATAGCCAGCAGGGTGAACCGTGG
5307 insert	(5423)	CGCTGGCGATTTTAAAATCGGCCCTCGATAGCCAGCAGGGTGAACCGTGG
		<i>pmi</i>
pSYN12274	(5501)	CAAACGATTTCGTTTAATTTCTGAATTTTACCCGGAAGACAGCGGTCTGTT
5307 insert	(5473)	CAAACGATTTCGTTTAATTTCTGAATTTTACCCGGAAGACAGCGGTCTGTT
		<i>pmi</i>
pSYN12274	(5551)	CTCCCCGCTATTGCTGAATGTGGTGAAATTGAACCCTGGCGAAGCGATGT
5307 insert	(5523)	CTCCCCGCTATTGCTGAATGTGGTGAAATTGAACCCTGGCGAAGCGATGT
		<i>pmi</i>
pSYN12274	(5601)	TCCTGTTTCGCTGAAACACCGCACGCTTACCTGCAAGGCGTGGCGCTGGAA
5307 insert	(5573)	TCCTGTTTCGCTGAAACACCGCACGCTTACCTGCAAGGCGTGGCGCTGGAA
		<i>pmi</i>
pSYN12274	(5651)	GTGATGGCAAACCTCCGATAACGTGCTGCGTGCGGGTCTGACGCCTAAATA
5307 insert	(5623)	GTGATGGCAAACCTCCGATAACGTGCTGCGTGCGGGTCTGACGCCTAAATA
		<i>pmi</i>
pSYN12274	(5701)	CATTGATATTCCGGAACCTGGTTGCCAATGTGAAATTGAAAGCCAAACCGG
5307 insert	(5673)	CATTGATATTCCGGAACCTGGTTGCCAATGTGAAATTGAAAGCCAAACCGG
		<i>pmi</i>
pSYN12274	(5751)	CTAACCAGTTGTTGACCCAGCCGGTGAAACAAGGTGCAGAAGTGGACTTC
5307 insert	(5723)	CTAACCAGTTGTTGACCCAGCCGGTGAAACAAGGTGCAGAAGTGGACTTC

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

			<u>pmi</u>
pSYN12274	(5801)	CCGATTCCAGTGGATGATTTTGCCTTCTCGCTGCATGACCTTAGTGATAA	
5307 insert	(5773)	CCGATTCCAGTGGATGATTTTGCCTTCTCGCTGCATGACCTTAGTGATAA	
			<u>pmi</u>
pSYN12274	(5851)	AGAAACCACCATTAGCCAGCAGAGTGCCGCCATTTTGTCTGCGTCGAAG	
5307 insert	(5823)	AGAAACCACCATTAGCCAGCAGAGTGCCGCCATTTTGTCTGCGTCGAAG	
			<u>pmi</u>
pSYN12274	(5901)	GCGATGCAACGTTGTGGAAAGGTTCTCAGCAGTTACAGCTTAAACCGGGT	
5307 insert	(5873)	GCGATGCAACGTTGTGGAAAGGTTCTCAGCAGTTACAGCTTAAACCGGGT	
			<u>pmi</u>
pSYN12274	(5951)	GAATCAGCGTTTATTGCCGCCAACGAATCACCGGTGACTGTCAAAGGCCA	
5307 insert	(5923)	GAATCAGCGTTTATTGCCGCCAACGAATCACCGGTGACTGTCAAAGGCCA	
			<u>pmi</u>
pSYN12274	(6001)	CGGCCGTTTAGCGCGTGTTTACAACAAGCTGTAAGAGCTTACTGAAAAAA	
5307 insert	(5973)	CGGCCGTTTAGCGCGTGTTTACAACAAGCTGTAAGAGCTTACTGAAAAAA	
			NOS terminator
pSYN12274	(6051)	TTAACATCTCTTGCTAAGCTGGGAGCTCGATCCGTCGACCTGCAGATCGT	
5307 insert	(6023)	TTAACATCTCTTGCTAAGCTGGGAGCTCGATCCGTCGACCTGCAGATCGT	
			NOS terminator
pSYN12274	(6101)	TCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCT	
5307 insert	(6073)	TCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCT	
			NOS terminator
pSYN12274	(6151)	TGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAA	
5307 insert	(6123)	TGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAA	
			NOS terminator
pSYN12274	(6201)	TTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGA	
5307 insert	(6173)	TTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGA	
			NOS terminator
pSYN12274	(6251)	GTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGC	
5307 insert	(6223)	GTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGC	
			NOS terminator
pSYN12274	(6301)	AAACTAGGATAAATTATCGCGCGGGTGTCTATCTATGTTACTAGATCTGC	
5307 insert	(6273)	AAACTAGGATAAATTATCGCGCGGGTGTCTATCTATGTTACTAGATCTGC	
			NOS terminator
pSYN12274	(6351)	TAGCCCTGCAGGAAATTTACCGGTGCCCGGGCGGCCAGCATGGCCGTATC	
5307 insert	(6323)	TAGCCCTGCAGGAAATTTACCGGTGCCCGGGCGGCCAGCATGGCCGTATC	
			LB
pSYN12274	(6401)	CGCAATGTGTTATTAAGTTGTCTAAGCGTCAATTTGTTTACACCACAATA	
5307 insert	(6373)	CGCAATGTGTTATTAAGTTGTCTAAGCGTCAATTTGTTTACACCACAATA	

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

		<u>LB</u>
pSYN12274	(6451)	TATCCTGCCACCAGCCAGCCAACAGCTCCCCGACCGGCAGCTCGGCACAA
5307 insert	(6423)	TA-----
pSYN12274	(6501)	AATCACCACCTCGATACAGGCAGCCCATCAGAATTAATTCTCATGTTTGAC
5307 insert		-----
pSYN12274	(6551)	AGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCGTCAGGCAGCC
5307 insert		-----
pSYN12274	(6601)	ATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTTCG
5307 insert		-----
pSYN12274	(6651)	TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACAT
5307 insert		-----
pSYN12274	(6701)	CATAACGGTTCTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCAT
5307 insert		-----
pSYN12274	(6751)	CCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAATTTACACAGG
5307 insert		-----
pSYN12274	(6801)	<u>spec</u>
5307 insert		AAACAGACCATGAGGGAAGCGTTGATCGCCGAAGTATCGACTCAACTATC
pSYN12274	(6851)	<u>spec</u>
5307 insert		AGAGGTAGTTGGCGTCATCGAGCGCCATCTCGAACCGACGTTGCTGGCCG
pSYN12274	(6901)	<u>spec</u>
5307 insert		TACATTTGTACGGCTCCGCAGTGGATGGCGGCCTGAAGCCACACAGTGAT
pSYN12274	(6951)	<u>spec</u>
5307 insert		ATTGATTTGCTGGTTACGGTGACCGTAAGGCTTGATGAAACAACGCGGCG
pSYN12274	(7001)	<u>spec</u>
5307 insert		AGCTTTGATCAACGACCTTTTGGAAACTTCGGCTTCCCCTGGAGAGAGCG
pSYN12274	(7051)	<u>spec</u>
5307 insert		AGATTCTCCGCGCTGTAGAAGTCACCATTGTTGTGCACGACGACATCATT



**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

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pSYN12274 (7751) AATACTTGGTTTCGCATTTTTGTGCATCCGCGGTCAGCCGCAATTCTGACGA
5307 insert -----

pSYN12274 (7801) ACTGCCCATTTAGCTGGAGATGATTGTACATCCTTCACGTGAAAATTTCT
5307 insert -----

pSYN12274 (7851) CAAGCGCTGTGAACAAGGGTTCAGATTTTAGATTGAAAGGTGAGCCGTTG
5307 insert -----
                                                                virG

pSYN12274 (7901) AAACACGTTCTTCTTGTTCGATGACGACGTCGCTATGCGGCATCTTATTAT
5307 insert -----
                                                                virG

pSYN12274 (7951) TGAATACCTTACGATCCACGCCTTCAAAGTGACCGCGGTAGCCGACAGCA
5307 insert -----
                                                                virG

pSYN12274 (8001) CCCAGTTCACAAGAGTACTCTCTTCCGCGACGGTCGATGTCGTGGTTGTT
5307 insert -----
                                                                virG

pSYN12274 (8051) GATCTAGATTTAGGTTCGTGAAGATGGGCTCGAGATCGTTTCGTAATCTGGC
5307 insert -----
                                                                virG

pSYN12274 (8101) GGCAAAGTCTGATATTCCAATCATAATTATCAGTGGCGACCGCCTTGAGG
5307 insert -----
                                                                virG

pSYN12274 (8151) AGACGGATAAAGTTGTTGCACTCGAGCTAGGAGCAAGTGATTTTATCGCT
5307 insert -----
                                                                virG

pSYN12274 (8201) AAGCCGTTTCAGTATCAGAGAGTTTCTAGCACGCATTTCGGGTTGCCTTGCG
5307 insert -----
                                                                virG

pSYN12274 (8251) CGTGCGCCCAACGTTGTCCGCTCCAAAGACCGACGGTCTTTTTGTTTTA
5307 insert -----
                                                                virG

pSYN12274 (8301) CTGACTGGACACTTAATCTCAGGCAACGTCGCTTGATGTCCGAAGCTGGC
5307 insert -----
                                                                virG

pSYN12274 (8351) GGTGAGGTGAAACTTACGGCAGGTGAGTTCAATCTTCTCCTCGCGTTTTT
5307 insert -----
                                                                virG

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**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

			<i>virG</i>
pSYN12274	(8401)	AGAGAAACCCCGCGACGTTCTATCGCGCGAGCAACTTCTCATTGCCAGTC	-----
5307 insert		-----	
			<i>virG</i>
pSYN12274	(8451)	GAGTACGCGACGAGGAGGTTTATGACAGGAGTATAGATGTTCTCATTTTG	-----
5307 insert		-----	
			<i>virG</i>
pSYN12274	(8501)	AGGCTGCGCCGCAAACCTTGAGGCAGATCCGTCAAGCCCTCAACTGATAAA	-----
5307 insert		-----	
			<i>virG</i>
pSYN12274	(8551)	AACAGCAAGAGGTGCCGGTTATTTCTTTGACGCGGACGTGCAGGTTTCGC	-----
5307 insert		-----	
			<i>virG</i>
pSYN12274	(8601)	ACGGGGGGACGATGGCAGCCTGAGCCAATTCCCAGATCCCCGAGGAATCG	-----
5307 insert		-----	
			<i>repA</i>
pSYN12274	(8651)	GCGTGAGCGGTGCGAAACCATCCGGCCCCGTACAAATCGGCGCGGCGCTG	-----
5307 insert		-----	
			<i>repA</i>
pSYN12274	(8701)	GGTGATGACCTGGTGGAGAAGTTGAAGGCCGCGCAGGCCGCCAGCGGCA	-----
5307 insert		-----	
			<i>repA</i>
pSYN12274	(8751)	ACGCATCGAGGCAGAAGCACGCCCCGGTGAATCGTGGCAAGCGGCCGCTG	-----
5307 insert		-----	
			<i>repA</i>
pSYN12274	(8801)	ATCGAATCCGCAAAGAATCCCGGCAACCGCCGGCAGCCGGTGCGCCGTCG	-----
5307 insert		-----	
			<i>repA</i>
pSYN12274	(8851)	ATTAGGAAGCCGCCCAAGGGCGACGAGCAACCAGATTTTTTCGTTCCGAT	-----
5307 insert		-----	
			<i>repA</i>
pSYN12274	(8901)	GCTCTATGACGTGGGCACCCGCGATAGTCGCAGCATCATGGACGTGGCCG	-----
5307 insert		-----	
			<i>repA</i>
pSYN12274	(8951)	TTTTCCGTCTGTCTGAAGCGTGACCGACGAGCTGGCGAGGTGATCCGCTAC	-----
5307 insert		-----	
			<i>repA</i>
pSYN12274	(9001)	GAGCTTCCAGACGGGCACGTAGAGGTTTCCGACGGGCCGGCCGGCATGGC	-----
5307 insert		-----	

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

		<i>repA</i>
pSYN12274	(9051)	CAGTGTGTGGGATTACGACCTGGTACTGATGGCGGTTTCCCATCTAACCG
5307 insert		-----
		<i>repA</i>
pSYN12274	(9101)	AATCCATGAACCGATACCGGGAAGGGAAGGGAGACAAGCCCGGCCGCGTG
5307 insert		-----
		<i>repA</i>
pSYN12274	(9151)	TTCCGTCCACACGTTGCGGACGTACTCAAGTTCTGCCGGCGAGCCGATGG
5307 insert		-----
		<i>repA</i>
pSYN12274	(9201)	CGGAAAGCAGAAAGACGACCTGGTAGAAACCTGCATTTCGGTTAAACACCA
5307 insert		-----
		<i>repA</i>
pSYN12274	(9251)	CGCACGTTGCCATGCAGCGTACGAAGAAGGCCAAGAACGGCCCGCCTGGTG
5307 insert		-----
		<i>repA</i>
pSYN12274	(9301)	ACGGTATCCGAGGGTGAAGCCTTGATTAGCCGCTACAAGATCGTAAAGAG
5307 insert		-----
		<i>repA</i>
pSYN12274	(9351)	CGAAACCGGGCGGCCGGAGTACATCGAGATCGAGCTAGCTGATTGGATGT
5307 insert		-----
		<i>repA</i>
pSYN12274	(9401)	ACCGCGAGATCACAGAAGGCAAGAACCCGGACGTGCTGACGGTTCACCCC
5307 insert		-----
		<i>repA</i>
pSYN12274	(9451)	GATTACTTTTTGATCGATCCCGGCATCGGCCGTTTTCTCTACCGCCTGGC
5307 insert		-----
		<i>repA</i>
pSYN12274	(9501)	ACGCCGCGCCGACAGGCAAGGCAGAACCCAGATGGTTGTTCAAGACGATCT
5307 insert		-----
		<i>repA</i>
pSYN12274	(9551)	ACGAACGCAGTGGCAGCGCCGGAGAGTTCAAGAAGTTCTGTTTCACCGTG
5307 insert		-----
		<i>repA</i>
pSYN12274	(9601)	CGCAAGCTGATCGGGTCAAATGACCTGCCGGAGTACGATTTGAAGGAGGA
5307 insert		-----
		<i>repA</i>
pSYN12274	(9651)	GGCGGGGCAGGCTGGCCCCGATCCTAGTCATGCGCTACCGCAACCTGATCG
5307 insert		-----

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

		<u>repA</u>
pSYN12274	(9701)	AGGGCGAAGCATCCGCCGGTTCTAATGTACGGAGCAGATGCTAGGGCAA
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(9751)	ATTGCCCTAGCAGGGGAAAAAGGTCGAAAAGGTCTCTTTCTGTGGATAG
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(9801)	CACGTACATTGGGAACCCAAAGCCGTACATTGGGAACCCGGAACCCGTACA
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(9851)	TTGGGAACCCAAAGCCGTACATTGGGAACCCGGTCACACATGTAAGTGA
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(9901)	GATATAAAAGAGAAAAAAGGCGATTTTTCCGCCTAAAACCTTTTAAAAC
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(9951)	TATTAACCTCTTAAAACCCGCCTGGCCTGTGCATAACTGTCTGGCCAGC
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(10001)	GCACAGCCGAAGAGCTGCAAAAAGCGCCTACCCTTCGGTCGCTGCGCTCC
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(10051)	CTACGCCCCGCCGCTTCGCGTCGGCCTATCGCGGCCGCTGGCCGCTCAAA
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(10101)	AATGGCTGGCCTACGGCCAGGCAATCTACCAGGGCGCGGACAAGCCGCGC
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(10151)	CGTCGCCACTCGACCGCCGGCGCTGAGGTCTGCCTCGTGAAGAAGGTGTT
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(10201)	GCTGACTCATAACAGGCCTGAATCGCCCCATCATCCAGCCAGAAAGTGAG
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(10251)	GGAGCCACGGTTGATGAGAGCTTTGTTGTAGGTGGACCAGTTGGTGATTT
5307 insert		-----
		<u>VS1 ori</u>
pSYN12274	(10301)	TGAACTTTTGCTTTGCCACGGAACGGTCTGCGTTGTGCGGAAGATGCGTG
5307 insert		-----



**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

		ColeE1 ori
pSYN12274 (10951)	CTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCG	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11001)	ACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAACCAGG	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11051)	CGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCCTGCCG	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11101)	CTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTC	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11151)	TCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGCTCCA	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11201)	AGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCGACCGCTGCGCCTTA	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11251)	TCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCC	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11301)	ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCG	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11351)	GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11401)	ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11451)	AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11501)	TTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAA	-----
5307 insert	-----	-----
		ColeE1 ori
pSYN12274 (11551)	GATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTC	-----
5307 insert	-----	-----

**Figure 4. Alignment of the 5307 maize insert with the transformation plasmid, pSYN12274 (Continued)**

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                                     ColeE1 ori
pSYN12274 (11601) ACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGA
5307 insert      -----

                                     ColeE1 ori
pSYN12274 (11651) TCCTTTTGATCCGGAATTAATTCCTGTGGTTGGCATGCACATACAAATGG
5307 insert      -----

pSYN12274 (11701) ACGAACGGATAAACCTTTTCACGCCCTTTTAAATATCCGATTATTCTAAT
5307 insert      -----

pSYN12274 (11751) AAACGCTCTTTTCTCTTAG
5307 insert      -----

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