

**CONFIDENTIAL  
ATTACHMENT**

**Title**

**Amended Report for MSL0022130: Molecular Analysis of Soybean MON 87705**

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**Completed On  
Amendment 2**

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**Sponsor/ Testing Facility**

**Monsanto Company  
Regulatory Product Characterization Center  
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**Laboratory Project ID**

**Study # REG-08-060  
MSL0022384**

## **CONFIDENTIAL ATTACHMENT**

### **CBI CROSS REFERENCE 1**

Deleted Pages: Figure 12. DNA Sequence of the Insert and Adjacent Genomic DNA in MON 87705

<u>Pages</u>	<u>Reason for Deletion</u>	<u>FIFRA Reference</u>
51-55	Discloses Manufacturing or Quality Control Processes	10(d)

### **CBI CROSS REFERENCE 2**

Deleted Pages: Figure 14. DNA Sequence of the PCR Product from Conventional Soybean DNA

<u>Pages</u>	<u>Reason for Deletion</u>	<u>FIFRA Reference</u>
57-58	Discloses Manufacturing or Quality Control Processes	10(d)

**Figure 12. DNA Sequence of the Insert and Adjacent Genomic DNA in MON 87705**

The following DNA sequence (13243 bp) represents the consensus sequence of the overlapping PCR products spanning the insert in MON 87705. Base pairs 1-3279 (underlined) represent soybean genomic DNA flanking the 5' end of the insert. Base pairs 3280-10530 represent the inserted DNA, which corresponds to bases 7840 to 6652 in the plasmid PV-GMPQ/HT4404. The arrangement of the elements in MON 87705 is such that the gene suppression elements of T-DNA I and T-DNA II are inverted repeats. However, T-DNA I and T-DNA II are spatially separate in the plasmid. The inserted genetic elements and their specific base pair designations within the DNA sequence are summarized in Table 2 and Figure 11. Base pairs 10531-13243 (double underlined) represents soybean genomic DNA flanking the 3' end of the insert. Base pairs 906-3279 (bold) and 10535-12908 (bold) represent the 2374 bases that were most likely duplicated from the 3' end of the insert during transformation. Base 2402 (larger font; bold) represents the single nucleotide change ('T') in the 5' duplicated 2374 base pair region compared to the corresponding base 12031('A') from the 3' end of the insert.

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1  ATTAGTACAA GTGTATGTGG ATGATATCAT TTTTGGTGCT ACTAATGAAA TGCTCTATGA
61 AGATTTTTTCT AAGTTAATGC AAAGTGAAGT TGAAATGAGC ATGATGGGAG AGCTAAAATT
121 CTTCTTTGGA CTGCAAATAA AGCAAACACC CCAAGGCATT TACATTCATC AGACCAAGTA
181 TGTGAAAAAT TAGTTGAAGA AGTTCAACAT AAGTGATGAA AAAGAGATGA AGACTTTTAT
241 GCATCCCACT ACACATCTTG GACTGGATGA GGAATCAATG AAGGTGGACG TGACTCAATA
301 CAAAGCAATG ATTGGATCAC TGCTCTATCT TAATGCTTCT AGGCCTTATA TAATTTTTAG
361 TGTTTTATTA TGTGCAAGAT TCCAAAAGGA ACCAAGGGAA GTTCATTTAA CTGCAGTTAA
421 ACCTATATTG TAATATTTAA TTAGAAGTCA TAACCTTGGT CTTATGCTTA AGAGAAGAGA
481 TAGTTTCAGA CTCATGAGCT ATTGAGATGT GGACTATGTT GGTGATAAAG TCGAAAGAAA
541 AAGTACAAGT GGAAGTTGTC ACTTTATAGG TGGCAACTTA GTCAGTTGGA TATGGAAGAA
601 GTAGGGATCA ACTACATTGT TCACTGCTGA AGTAGAATGC GTGTCAGTAG CCATGGAGGT
661 TACCCTCGAC ATTGAAGACC CCAAGAAATA GGTTCAAAGT TTTGGAAATC CACAGGGTCA
721 GAGCACAAGT GCAAGTTTCA AGTATCAAGG CAGCAACGAA GCTATATCGT AGGTAGGGGA
781 GTTTAGTGGT ACCAATAATG CCCAAACACC CACTGGTGGG ACTCAAAATC TACAAGGGGA
841 GAGCAGAATG TCTTCTACAT CATCAATATC CAAACCAAGA TTCTCAAGAC CGTGAAACAA
901 AGGATCTCAG GGTGTTGTTA TCACTGCGGT TTGGCCTTTG GGCCAAGGCA CCGTTGTCCT
961 GAAAAAATA TGAGAGTTGT AATACTCGCT AAGGATGAGT AGATTAATGA AGACGGGGAG
1021 ATCATAGGAT TAAAAAATGA GAATGAGGAA GAATGTGAGG AAGTTTTGGA GATGGTTTGC
1081 TAGCGGATGG ATTTGTCAGT TTGTTCCGCA GGTGGGCTAA CCCAGCCTCA AGCATGAAGC
1141 TTAGGTGAGA ATTATAGGGG CAAGAGGTGA TAATCTTGAT TGACAATAGG GCAAGCCACA
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1261 ATTATATGAG ATTGGGGGAT AGTAACCGCA AATCCACTCA AGGATGTTGT AAGAACTTAA
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1801 TGGTTGAGAT GTTATGATTG GGGATTATTA GACTAAGCAA TAGCTCCTAT TCTAGCCAG
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2221 CCCATTGGA TCATTGAGT TAGGTGTTGG CCAGGTTATT AGAACATTAT TTCTTCACAA  
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2341 TCTCTAAAGA AGGAGTTTTG ATGAGGCCAT TTTGTAGTGG CCAATGCCTA AAACCTCTAA  
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2581 GCTTGATTTT TCAAAACAAT TCTCCATAGA ATGTGATGCC TCGGGGAAGG GAATTGGAGT  
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5101	GCTCGCTTAG	CTCAGATGAT	AGAGACCAC	AATTTTTGTG	GTAGAAATCG	GTTTGACTCC
5161	GATAGCGGCT	TTTTACTATG	ATTGTTTTGT	GTTAAAGATG	ATTTTCATAA	TGGTTATATA
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5341	TCTCCAATCT	CTCGAAATCC	AGTCAACGCA	AATCTCCCTT	ATCGGTTTCT	CTGAAGACGC
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5821	CTGGTTGCCG	TTTGACTATG	GGTCTTGTTG	GTGTTTACGA	TTTCGATAGC	ACTTTTCATTG
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12001 TTGTAGTGGC CAATGCCTAA AACTCCTAAG ACTTTGAGAG GGTTTTTGA ACTTACAGGT  
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12601 TTCTAGACCT TTCTGGAAAG ACATAACAAA AATTAATGAA GAAGTTCAGA AGGATCCCGC  
12661 GTTGGCTAAA ATCCGAGAAG AATTGAAGGA TAATCTAGAT TCACACCCTC AGTACACCCT  
12721 GGAGTGTGAC ATATTATACT TCAGAGGGAG GTTGGTCCTA TTAGCTTCTT CATTGTGGAT  
12781 TCCAAAGTTA CTACAAGAAT TCCAGACTTC TCTTATGGGA GGGCACTCGG GTATTTACAT  
12841 AACTTATAGA AGAATCACTC AATCGCTTTA TTGGATACCA ATAAAGGGAG AAATCACTAA  
12901 GTTTGTGGTT GCGTGTCTATG TGGGCCAAAG AAGTAAATAT CAAGCATCCT CTCCAGCAGG  
12961 TTTACTACAA CCTTTGCCAA TTCCAAATGC TATTTGGGAA GAAATTAGTA TGAATTTTAT  
13021 TGTAGGTATG CTAAAATCAA AAGGGTTTGA TGTTATACTA GTAGAGGTCG ACAAGTTAAG  
13081 CAAATATAGA TATTTTATTG TGATTAAGCA CCCATACTTT GCTAGGTCTA TTGTTGATGT  
13141 TAAAGAAATA ATTTGGTTGC TTGAGGTGCC TATATCTATT GTTAGCGACA GTGACCTTAT  
13201 TTTTATGAGT CATTTTTTGC AAGAATTATT CAAATTGCAA AGG



**Figure 14. DNA Sequence of the PCR Product from Conventional Soybean DNA**  
 Bases 1-895 (underlined) represent sequences that match the unique 5' flanking sequences of the MON 87705 insert (11-905 bp, Figure 12). Bases 896-931 represent 36 bp that were not found in the insert nor in the flanking sequences reported in Figure 12. These sequences were likely deleted in MON 87705 upon insertion of the T-DNA. Bases 932- 3309 (double underlined) represent sequence that is identical to the 3' genomic DNA sequence flanking the MON 87705 insert. Of the 2378 bases of 3' flanking sequence, there are 2374 bases (936-3309 bp, Figure 14) that were most likely duplicated in the 5' flanking sequence and match genomic DNA sequence in both the 5' and 3' flanking sequence of MON 87705 (bases 906-3279 and 10535-12908, Figure 12). Bases 3310-3635 represent sequences that match the unique 3' flanking sequence (bases 12909-13234) reported in Figure 12.

The DNA nucleotide sequences of the oligonucleotide primers, Primer A and B, used to generate the PCR products are not included in the DNA sequence listed below since the primers used to amplify the product were also used to sequence the product. Therefore, double stranded sequence data adjacent to the primer sites were not obtained. The primer sequences were as follows:

Primer A: 5' ATGGAATGGTCGACACAACACTCTT 3'

Primer B: 5' CTTATGTCTGCCCATTGATTTTGG 3'

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1  GTGTATGTGG ATGATATCAT TTTTGGTGCT ACTAATGAAA TGCTCTATGA AGATTTTTCT
61  AAGTTAATGC AAAGTGAAGT TGAAATGAGC ATGATGGGAG AGCTAAAATT CTTCCTTGGA
121 CTGCAAATAA AGCAAACACC CCAAGGCATT TACATTCATC AGACCAAGTA TGTGAAAAAT
181 TAGTTGAAGA AGTTCAACAT AAGTGATGAA AAAGAGATGA AGACTTTTAT GCATCCCACT
241 ACACATCTTG GACTGGATGA GGAATCAATG AAGGTGGACG TGAATCAATA CAAAGCAATG
301 ATTGGATCAC TGCTCTATCT TAATGCTTCT AGGCCTTATA TAATTTTTAG TGTTTTATTA
361 TGTGCAAGAT TCCAAAAGGA ACCAAGGGAA GTTCATTTAA CTGCAGTTAA ACCTATATTC
421 TAATATTTAA TTAGAACTCA TAACCTTGGT CTTATGCTTA AGAGAAGAGA TAGTTTCAGA
481 CTCATGAGCT ATTGAGATGT GGACTATGTT GGTGATAAAG TCGAAAGAAA AAGTACAAGT
541 GGAAGTTGTC ACTTTATAGG TGGCAACTTA GTCACCTGGA TATGGAAGAA GTAGGGATCA
601 ACTACATTGT TCACTGCTGA AGTAGAATGC GTGTCAGTAG CCATGGAGGT TACCCTCGAC
661 ATTGAAGACC CCAAGAAATA GGTTCAAAGT TTTGGAAATC CACAGGGTCA GAGCACAAGT
721 GCAAGTTTCA AGTATCAAGG CAGCAACGAA GCTATATCGT AGGTAGGGGA GTTTAGTGGT
781 ACCAATAATG CCCAAACACC CACTGGTGGG ACTCAAATC TACAAGGGGA GAGCAGAATG
841 TCTTCTACAT CATCAATATC CAAACCAAGA TTCTCAAGAC CGTGAAACAA AGGATCTCAA
901 ACCATTCTTT ATGTTGAGTA TGTCAAATGA AGAGACTCAG GGTGTTGTGA TCACTGCGGT
961 TTGGCCTTTG GGCCAAGGCA CCGTTGTCCT GAAAAAATA TGAGAGTTGT AATACTCGCT
1021 AAGGATGAGT AGATTAATGA AGACGGGGAG ATCATAGGAT TAAAAAATGA GAATGAGGAA
1081 GAATGTGAGG AAGTTTTGGA GATGGTTTGC TAGCGGATGG ATTTGTCAGT TTGTTCCGCA
1141 GGTGGGCTAA CCCAGCCTCA AGCATGAAGC TTAGGTGAGA ATTATAGGGG CAAGAGGTGA
1201 TAATCTTGAT TGACAATAGG GCAAGCCACA ACTTTATATC CAACAAATTG GTACATAAAT
1261 TGGGACTCAG CATAGATCCC ACAAAGCCCT ATTATATGAG ATTGGGGGAT AGTAACCGCA
1321 AATCCACTCA AGGATGTTGT AAGAAGTTAA AAAATAGTTG GGAGCTTATA CCATGGTAGG
1381 ATATTTCTAT CTATTTAAGT TGGGAGGAGT GGACCTAATT ATTGGAGTTG CTTAGTTGGA

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1441 AACATTGGGA GAAATTAAGG TGAATTGGAG GACCCTAAGT ATGTCTTTTG TCCACCAAGA  
1501 TCAGAATATG GTGATCAAGG AGATCTTGGT TTATTGAAGA CAATGATCAT TTTGAGAACA  
1561 TTGCAAAAAA TAGTTAGCAA GGAAGTTGAG ATGATGTTCA TGTGTGGGT AATTGAAAGC  
1621 AACTATGTGG AACAAATTGA TTTAACAAAG AACCAAGAAA ATTAGTTGTA GCAAGTACTG  
1681 ATAGAGTTTG CTACAGTTTT TCAGGACCTA AGGGTTTACC ACCATCTAGA GAGGTTGATC  
1741 ACAAGATTGC AATTAAGTCC GGGGCATATC CAGATAATGT TAGGCCTTAT CGTTACCCCC  
1801 ACTTACAGAA GAATGAGATA AAAACTCTAG TGGTTGAGAT GTTATGATTG GGGATTATTA  
1861 GACTAAGCAA TAGCTCCTAT TCTAGCCCAG TAATTTTGGT AAAAAGGAAA GATGGAAGTT  
1921 GACGATTATG TATGGATTAT CAGGCTTTAA GTAAGGCTAC AGTCCCAGAC AAGTTCTCTGA  
1981 TTCCTGTCAT GAAAGAGTTG TTGGATGAGT TAAATGGACC CATCCACTTC TCTAAAATAG  
2041 ATCTAAAGGC AAGGTATCAC CAAATCAGAA TGCACAAACC TACCTTCAGA ACTCACCAGG  
2101 GACATTATGA ATCTCCAGTG ATGCCATTG GATTAACAAA CACCCCGACC ACGTTCCAAT  
2161 GAGCTATGAA TGCCACACTG AAACCGTTCC TTCGTAGGTA TGTGGTAGTG TTCTTTGATG  
2221 ACATTTTGGT CTATAGTAAG TCTTGGGAAG CCCATTTGGA TCATTTGAGT TAGGTGTTGG  
2281 CCAGGTTATT AGAACATTAT TTCTTCACAA ATGTTTTTAA AAAAAAATGT AGTTTTGGTC  
2341 AAATTAAGGC GGGTTGCTTA GGGCACGTTA TCTCTAAAGA AGGAGTTTTG ATGAGGCCAT  
2401 TTTGTAGTGG CCAATGCCTA AAACCTCTAA GACTTTGAGA GGGTTTTTGG AACTTACAGG  
2461 TTATTATAAA AGGTCCATTT GCAATTATGG GAAGATAGCT CGCCCATGGA TTGATCTATT  
2521 AAAGTAAGGA AATTTTAAGT GGAATGAGGA TAGTATTAAG GCTTCCATAC AATTACAACA  
2581 AGCTATTACC ACAATACCAA CACTATCCAT GCTTGATTTT TCAAAACAAT TCTCCATAGA  
2641 ATGTGATGCC TCGGGGAAGG GAATTGGAGT TGTTCTAACA CAAGATAGAA AGCAAATTGC  
2701 TTATTTCAAC AAGGCATTAA AAGATTTGAC TCTTTCTAAA TCTATGTATG AAAAGGAATC  
2761 AATGGCTCTT GTCTTAGCCA TACAACATTG GAGGCCTTAT CTTCCGGATT AGAAATTTAC  
2821 TATATACATT GACCAAAAAA GTTTGAGATA TCTACTAGAT CAGCGAATTA CAACTCAACC  
2881 AACAATATTG GGTAGCCAAG TTGCTGGGGT ATGAGTTTGA CATTGTGTAT AAGGTGGGGG  
2941 CTTCAAACAA GGTGTTGAT GCTCTATCTA GAAGAGATGA AGACAAAGAA TTGCAGGGCA  
3001 TTTCTAGACC TTTCTGAAA GACATAACAA AAATTAATGA AGAAGTTCAG AAGGATCCCCG  
3061 CGTTGGCTAA AATCCGAGAA GAATTGAAGG ATAATCTAGA TTCACACCCT CAGTACACCC  
3121 TGGAGTGTGA CATATTATAC TTCAGAGGGA GGTTGGTCCT ATTAGCTTCT TCATTGTGGA  
3181 TTCCAAAGTT ACTACAAGAA TTCCAGACTT CTCTTATGGG AGGGCACTCG GGTATTTACA  
3241 TAACTTATAG AAGAATCACT CAATCGCTTT ATTGGATACC AATAAAGGGA GAAATCACTA  
3301 AGTTTGTGGT TGCGTGTCAT GTGGGCCAAA GAAGTAAATA TCAAGCATCC TCTCCAGCAG  
3361 GTTTACTACA ACCTTTGCCA ATTCCAAATG CTATTTGGGA AGAAATTAGT ATGAATTTTA  
3421 TTGTAGGTAT GCTAAAATCA AAAGGGTTTG ATGTTATACT AGTAGAGGTC GACAAGTTAA  
3481 GCAAATATAG ATATTTTATT GTGATTAAGC ACCCATACTT TGCTAGGTCT ATTGTTGATG  
3541 TTAAAGAAAT AATTTGGTTG CTTGAGGTGC CTATATCTAT TGTTAGCGAC AGTGACCTTA  
3601 TTTTATGAG TCATTTTTTG CAAGAATTAT TCAAA

