

Supplementary Table S1. Details of reference *Foc* isolates (and their VCGs status) used in this study.

S. No.	<i>Foc</i> isolate number	VCG status of the isolate
1	24662	01213
2	Thai-7-24192	0125
3	W93/395 Aus	0124
4	W93/404	0125
5.	Mal 58	01217
6.	Thai-6-1	0124
7	Aus 23997	0128
8	Thai 6-1	0124
9	Taiwan 194	01213/16
10	W92/276	0129
11	Mal 42	01216
12	Mal 33	01218
13	Phil 8	0123
14	23746	0120
15	India 6	0124/5
16	India 1	0125
17	Phil 6	0126
18	RPSTNP	01212
19	24219	01220
20	Indo 20	0120
21	23631	01211
22	F9130	0121
23	23630	01210

Supplementary Table S2. List of primers designed specific to *Foc* races and their Gene ID.

S. No.	Gene ID	Forward primer	Reverse primer
<i>Foc</i> R1			
1	XM_018396005.1	CTTACCAATTGGGGGCGTCT	GGTAGGTTGCGAACACCAGA
2	XM_018396005.1	TTGGGGCAAGGCATACAAGT	AGACGCCCCCAATTGGTAAG
3	XM_018396005.1	TTCCAATCAGCTTGGGGCAA	GAGACGCCCCCAATTGGTAA
4	XM_018394505.1	CTGAGCAGGAGGAAGCTCGAC	AAAGGCGGCTTCGGACATAA
5	XM_018394505.1	CCTCCGATACGGCTGATGAC	CCAACGTCTCGGTAACCAGT
6	XM_018394505.1	TACCTCCTTGGTCGACAGGT	CAGACTTCCAACGTCTCGGT
7	XM_018394754.1	GAATCTCTGCGCCTCGATGA	CGACAACATTAGAGCGCACG
8	XM_018394754.1	TGCGCCTCGATGACATTGTT	ACCGACAACATTAGAGCGCA
9	XM_018394754.1	ACTTCTGAATCTCTGCGCCTC	GGTGGGCCTTGGTCATAGAG
<i>Foc</i> R4			
10	XM_031217723.1	GCCATGCTATTCCAACGATT	CATCCATTCTGCTGGGTTTT
11	XM_031217723.1	CAAAGCAGCTCTGACCATCA	GGCAAGGATACCGCAGAATA
12	XM_031217723.1	GCTATCCTGTGCACGATCCA	TGGTCAGAGCTGCTTTGGAG
13	XM_031196942.1	GAAGTCGACACCCACGAAGT	AATTGTTGAACTGCAGCGGC
14	XM_031201004.1	GACTTCGTCACCCGCTACAA	CCGAGAACTGCCGGTAGATC
15	XM_031214609.1	AGAAGATCCTTACTGCCGCG	GTCACCGAACCAGTCTTCGT
16	XM_031214609.1	GACCGTCTGACCAATGATGC	TTTTCGAAGGTGGTCTGCAG
17	XM_031212605.1	TATCGGCATCTTCCAGTCGC	CGAGATCACCGTGGAGATGG
18	XM_031212605.1	AGGCCTGATCACGATTCCAA	CGCAGGTACAGAGTGTCGTA
19	XM_031212517.1	GTCGAAGGCCAGGAAGTGAA	GAGTGCGGATAGCCCTCTTC
20	XM_031216888.1	GATTTCTCGACAACCAGGTG	TTCTGCACACCGTCGATGAT
21	XM_031212870.1	GAAATTCCGGAAAAGCGCGT	TTGAGCTCTTCCACCAGCTG
22	XM_031210754.1	AACATCCTGTGCGCGAAGTA	CGATGGTGTACTCGTGCTTG
23	XM_031209143.1	GGGTGAAGGGAGTGAAGCTC	AGCTGCATCAAACAAGCGTG
24	XM_031209143.1	GAAGTCGGCGTTTCATGGATC	TCAAACAAGCGTGCCAATGA
25	XM_031203181.1	AACAACAACACCCCGTCTCTC	TGTAGACGCTGCGCAGATAG
26	XM_031207491.1	ATCTCGAACAACAACACCCC	TCCTGCTCGCTGATGTAACC
27	XM_031214567.1	CGCGGCATCAACAAAGTCAT	CGGAATATCGTCGTCAGCGA
28	XM_031204365.1	AAGTCATCCTGGTCGGCAAT	CCGTAGTTGCCACCACCG
29	XM_031217424.1	CCAGGATGAGAAGACCCTGC	GGGAATTCACCGGTCTCGTT
30	XM_031198305.1	GGCATGTCTTCGCACTACAG	TGGAATCATGCGCATCACTG
31	XM_031213605.1	CAGGAGAGTCTTGCTTGCCA	AAACCCCTTGACACTGGTG
32	XM_031213605.1	CGATCCATCTACCACTGCCT	CGGGCCGTAAAGTTTCGTAG
33	XM_031209245.1	GCGGATCTTCGTCGGGTAAT	CCAATGACTTCCTCGGCTGT
34	XM_031209245.1	CATCCAGGCTGCCAAGAATC	CTAAAGTGCCATATCCGCCG
35	XM_031209245.1	AGCCAATCAGAAGCTCTGCA	ATGCGAGAGATGTTGAGCCG
36	XM_031209245.1	TCTGCATTGCTATCTTCGGC	AATGCGAGAGATGTTGAGCC
37	XM_031197279.1	CCATCATTACCCGTCCCTCG	TCCAGCATGATCTTCTCCGC
38	XM_031216382.1	CTGTCACCCCATGTGCTACT	AGCATGATCTTCTCCGCCAG
39	XM_031211465.1	CCTGTTCAATGCCTTCGAGC	CTCACAACGCAGGATGGACT
40	KX434998.1 (SIX1)	TGATTTGCCGTGGAATGACA	TGGTCTTGACACGACCCA
<i>Foc</i> TR4			
41	KF548063.1 (SIX8a)	CGCACTCTTACGTTGAGGAT	TCCACGCAACACTAGCTACT
<i>Foc</i> STR4			
42	XM_031212766.1	CTTCGAGCTGACCATTTCGG	CAGCGAATCGAAGTACAGCG
43	XM_031208009.1	CCAAGAACAACCGAAGCCG	GTTGGCAGTCATCCAGGTGA
44	XM_031197922.1	TCGCCAAGAACAACCGAAG	TTTTGAAGCCCCACCAATCG
45	KX434398.1 (SIX7)	GCGCAAGTAGTCTTGCTTCC	ATTAAGCGGTTGGCGTATTG

Supplementary Figure S1. Forward and reverse primers binding site (A) and DNA sequence alignment of hypothetical protein (B) for *Foc* R1 of *Foc*R1F/*Foc*R1R.

A.

Results for linear 323 residue sequence "XM_018394505.1 Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein partial mRNA" starting "TACCTCCTTG"

>>>F>>> 1 to 20

1 TACCTCCTTGSTCGACAGGTAGCCGGTCACTCCAGCGTTGAGGGCTACATCTCGGCTCTTATTGAGGCTACCGCTGTGTGAGATTGAC

1 10 20 30 40 50 60 70 80

1 ATGGAGGAACCACTGTCCATCGGCCAGTCAGGTGCAACTCCCGATGTAGAGCCGAGAATAAGCTCCGATGGGACACAGCTCTAACTG

91 TGTGGGATGGCAACTCTGGGCAAGCCGAGGTCAACCAAGGTCAAGGCTTACGACCTCGATTAGTTTCCGTGAGGTATAGCCACGATC

91 100 110 120 130 140 150 160 170

91 ACGACCCCTACCGTTGAGACCGCTCGGGCTCCAGTTGGTGGCAGTGTGGAATGCTGGAGCTAATCAAAGGCACTCCAGTATCGGTGCTAG

181 AATAAGTATGCCTTTGTTAAGTCGAGGTTCCCTCTCTGGATCCCCCTCGAAGTTCATTGCAACCTAATCAGCAAGCCATCATGGTCAAC

181 190 200 210 220 230 240 250 260

181 TTATTATACGGAACAATTTCAGCTCCAAGGGAGAGACCTAGGGGAGCTTCAAGTAACGTTGGGATTAGTCGTTCCGTAGTACCAAGTTG

<<<R<<< 304 to 323

271 ATTATGAGGAGGTCCTTCGGCTCTCGACTGGTTACCGAGACGTTGGAAGTCTG

271 280 290 300 310 320

271 TAATACTTCTCCAGAAGCCGAGAGCTGACCAATGGCTCTGCAACCTTCAGAC

B.

1. VCG0125 CM028857.1 Chr-15	T A C C T C C T T G G T C G A C A G G T A G C C G G T C A G T C C A G C G T C G A G G G C T A C A T C T C G G T T C T T A T T C G A G G C T G C C G C T G T G T C G A G
2. VCG0124 CM027183.2 Chr-15	T A C C T C C T T G G T C G A C A G G T A G C C G G T C A G T C C A G C G T C G A G G G C T A C A T C T C G G T T C T T A T T C G A G G C T G C C G C T G T G T C G A G
3. VCG0120 CM028827.1 Chr-15	T A C C T C C T T G G T C G A C A G G T A G C C G G T C A G T C C A G C G T C G A G G G C T A C A T C T C G G T T C T T A T T C G A G G C T G C C G C T G T G T C G A G
4. VCGVCG01213/16 CM026318.2 Chr-15	T A C C T C C T T G G T C G A C A G G T A G C C G G T C A G T C C A G C G T C G A G G G C T A C A T C T C G G T T C T T A T T C G A G G C T G C C G C T G T G T C G A G
5. VCG01220 CM028842.1 Chr-15	T A C C T C C T T G G T C G A C A G G T A G C C G G T C A G T C C A G C G T C G A G G G C T A C A T C T C G G T T C T T A T T C G A G G C T G C C G C T G T G T C G A G
6. XM 018394505.1 F04287	T A C C T C C T T G G T C G A C A G G T A G C C G G T C A G T C C A G C G T C G A G G G C T A C A T C T C G G T T C T T A T T C G A G G C T G C C G C T G T G T C G A G
1. VCG0125 CM028857.1 Chr-15	A A C C C T A A T C A G C A A G C C A T C A T G G T C A A C A T T A T A A A G G A G G C C T T C G G C T C T C G A C T G G T C A C T G A G A C G T T G G A A G C T G
2. VCG0124 CM027183.2 Chr-15	A A C C C T A A T C A G C A A G C C A T C A T G G T C A A C A T T A T A A A G G A G G C C T T C G G C T C T C G A C T G G T C A C T G A G A C G T T G G A A G A C T G
3. VCG0120 CM028827.1 Chr-15	A A C C C T A A T C A G C A A G C C A T C A T G G T C A A C A T T A T A A A G G A G G C C T T C G G C T C T C G A C T G G T C A C T G A G A C G T T G G A A G A C T G
4. VCGVCG01213/16 CM026318.2 Chr-15	A A C C C T A A T C A G C A A G C C A T C A T G G T C A A C A T T A T A A A G G A G G C C T T C G G C T C T C G A C T G G T C A C T G A G A C G T T G G A A G A C T G
5. VCG01220 CM028842.1 Chr-15	A A C C C T A A T C A G C A A G C C A T C A T G G T C A A C A T T A T A A A G G A G G C C T T C G G C T C T C G A C T G G T C A C T G A G A C G T T G G A A G A C T G
6. XM 018394505.1 F04287	A A C C C T A A T C A G C A A G C C A T C A T G G T C A A C A T T A T A A A G G A G G C C T T C G G C T C T C G A C T G G T C A C T G A G A C G T T G G A A G A C T G

Supplementary Figure S2. Forward and reverse primers binding site (A) and DNA sequence alignment of SIX8a (B) for *Foc* R4 of *Foc*R4F/*Foc*R4R.

A.

Results for linear 198 residue sequence "KF548063.1_Six8a_INDO 155" starting "CGCACTCTTA"

>>>F>>> 1 to 20

1	CGCACTCTTACGTTGAGGATGGACAGAACTAGGGGCGGAGGGACATCGAACGTGCTTGTCCCTTTTGAGCGGGGAGCGCTATCACATGCGGTACGGGAAGTAGTC
1	10 20 30 40 50 60 70 80 90 100
1	CGGTGAGAATGCAACTCCTACCTGTCTTGATCCCGCCTCCCTGTAGCTTGACAGAACAGGAAAACTCGCCCCCTCGGATAGTGTACGCCATGCCCTTCATCAG

>>>R>>> 179 to 198

106	CAGATCATGCCGGGTGAGGTGAAGAGCTTAGCTACTTTAGGTGCATCGACTGTCCAGTTTATAAACAATTGGTAGTAGCTAGTGTGGTGGGA
106	110 120 130 140 150 160 170 180 190
106	GTCTAGTACGGCCCACTCCACTTCTCGAATCGATGAAATCCAGTAGCTGACAGGTCAAATATTTGTTAACCATCATCGATCACAAACGCACCT

B.

1. CM026317.2 VCG01213/16 SIX8a	CGCACTCTTACGTTGAGGA	TGGACAGAACTAGGGGCGGAGGGACATCGAACGTGCTTGTCTTTTGA	CGGGGGAGCGCTATCACA
2. CM028626.1 VCG0120 SIX8b	CGCACTCTTACGTTGAGGA	TGGACAAAACTAGGGGTGAACGGATATCGAACGTGCTTGTATTTTGA	CGGGGGAGCGCTATCACA
3. KF548063.1 Six8a INDO 155	CGCACTCTTACGTTGAGGA	TGGACAGAACTAGGGGCGGAGGGACATCGAACGTGCTTGTCTTTTGA	CGGGGGAGCGCTATCACA
4. MN417222.1 Foc4 SIX8	CGCACTCTTACGTTGAGGA	TGGACAGAACTAGGGGCGGAGGGACATCGAACGTGCTTGTCTTTTGA	CGGGGGAGCGCTATCACA
5. KF548064.1 Six8b Foc22615	CGCACTCTTACGTTGAGGA	TRGACAGAACTAGGGGCGGAGGGATATCGAACGTGCTTGTATTTTGA	CGGGGGAGCGCTMTACA

1. CM026317.2 VCG01213/16 SIX8a	CGGGTGAAGTGAGAGCTTAACTATTTAGGTGCATCGACTGTCCAGTTTATAAACAATTGGT	AGTAGCTAGTATTGCGTGG
2. CM028626.1 VCG0120 SIX8b	CGGGTGCGGTGAGGAACCTTAGCTACTTTAGGTGCATCGACTGTCCAGTTTCTACACAATTGGT	AGTAGCTAGTATTGCGTGG
3. KF548063.1 Six8a INDO 155	CGGGTGAAGTGAGAGCTTAACTATTTAGGTGCATCGACTGTCCAGTTTATAAACAATTGGT	AGTAGCTAGTATTGCGTGG
4. MN417222.1 Foc4 SIX8	CGGGTGAAGTGAGAGCTTAACTATTTAGGTGCATCGACTGTCCAGTTTATAAACAATTGGT	AGTAGCTAGTATTGCGTGG
5. KF548064.1 Six8b Foc22615	CGGGTGAAGTGAGAACTTGGCTACTTTAGGTGCATCGACTATCCAGTTTCTTACCAATTCT	CTAGATAGTATTGCGTGG

Supplementary Figure S3. Sequence comparison of SIX1a (A) and forward and reverse primers binding site (B).

A.

Fusarium oxysporum f. sp. cubense strain BC2-4 chromosome 14, whole genome shotgun sequence				
Sequence ID: CM026317.2 Length: 1342940 Number of Matches: 2				
Range 1: 1061535 to 1062386		GenBank	Graphics	▼ Next Match ▲ Previous Match
Score	Expect	Identities		Gaps
893 bits(483)	0.0	738/855(86%)		42/855(4%)
				Strand
				Plus/Plus
Query 1	ATGGCGCCCTATAGCATGTGTACTCTTGGCGCCCTCTCAATCCTTGGGTTTGGGGCTTAT			60
Sbjct 1061535	ATGGCGCCCTATAGCATGTGTACTCTTGGCGCCCTCTCAATCCTTGGGTTTGGGGCTTAT			1061594
Query 61	GCTCAAGAGCGTGGCTTGGAGAACCCAGATATTTTCAACTTGACCTACACGGAATAT			120
Sbjct 1061595	GCTCAAGAGCGTGGCTTGGAGAACCCAGATATTTTCAACTTGACCTACACGGAATAT			1061654
Query 121	CTGGATAAGGTGGCAGCATCCACGGGAGTTCCAGACGAGTGATTGCCGTGGAATGAC			180
Sbjct 1061655	CTGGATAAGGTGGCAGCATCCACGGGAGTTCCAGACGAGTGATTGCCGTGGAATGAC			1061714
Query 181	ACTATGAGCGGCTTTCTCG-----GAACGAGACGGGACG			216
Sbjct 1061715	ACTATGAGCGCTTTCTCGGAACGAGACGGACGATAGTGTTCAGACCGAGACGGGACG			1061774
Query 217	AGCCTATCGAGCGTGGTGCATTGTCAACCTTGGAAAGCGTGACCTGTCCGGCGGGAG			276
Sbjct 1061775	AGCCTATCGAGCGTGGTGCATTGTCAACCTTGGAAAGCGTGACCTGTCCGGCGGGAG			1061834
Query 277	GCTCACAAATCGGTACCAATGACATGCTCAGGCGCTTCATGATCTGTGTTGAA			336
Sbjct 1061835	TCTCACAAATCGGTACCAATGACATGCTCAGGCGCTTCATGATCTGTGTTGAA			1061894
Query 337	GCATATGGACAGCGTGGCAGCGATTAGTGGTCTGT--CA-AGA-C--CAGGCAACG			390
Sbjct 1061895	AAATATGGACAGCGTGGCAGCGATTAGTGGGTATGTTACACTGATCTGTCGGCGACT			1061954
Query 391	AGCGTATCTATTGTGGGATCGAATGCTCGCGGTCCTCCGG--CGGATGA--CGACAGAG			448
Sbjct 1061955	AGGAAATCGAATGATTAATAAACCTGCTGTC--AGGAGAGACAGATCAGTGACAGAG			1062012
Query 449	CTTGCCCA-AGCGCGCAGCAGTGACACACTTTGAGGCGGTCAATTATCGT-AGCGT---			503
Sbjct 1062013	CTTGCCCAAG-AGCGAGGTGACACTTTCAATGGTGCAACTTTCTGACCTGCAC			1062071
Query 504	C--CGGAATATTTTCTCTGTCTGTGGGCCCCGAATTGAGGTGAGGGAAGACATGATATA			561
Sbjct 1062072	CATCAGGTACTTTTCTCTGTCTGTGGGCCCCGAATTGAGGTGAGGGAAGACATGATATA			1062131
Query 562	GGGATTCACACGGAATGGGACGGAATCTGTACCCGTAATCGCTTAATCGCTGGGACC			621
Sbjct 1062132	GGGATTCACACGGAATGGGAGGGAATCTGTGACCCGGAATCGCTTAATCGCTGGGACC			1062191
Query 622	TACGATCTTTGCCAGATGGCGGGGAGTCTCAATGGGTACTTCAACTTTGATGGTCT			681
Sbjct 1062192	TACGATCTTTGCCAGATGGCGGGGAGTCTCAATGGGTACTTCCGGTATGACGGTCT			1062251
Query 682	TATTCGAATGGAGGGGATGAGCTCTCGGGGAATGAGCACTCTGGTCTGATGATTGCT			741
Sbjct 1062252	TATTCGGATGGATATAAGACGAGCTCTCACGGATATGGACATTATGGTCTGATCAAT			1062311
Query 742	TGCCGGGAGGCAAGCTGACTATCACTAGCACAGATCGCGCAACTTGGGCGATTGGATAT			801
Sbjct 1062312	TGCCGGGAGGCAAGCTGACTATCACTAGCACAGATCGCGCAACTTGGGCGATTGGATAT			1062371
Query 802	ACCAGCCCCCACTAA 816			
Sbjct 1062372	ACCAGCCCCCACTAA 1062386			

B.

Results for linear 816 residue sequence "KX434998.1 Foc TR4 BRIP40340 secreted in xylem 1 (SIX1) gene, complete cds" starting "ATGGCGCCCT"

1	ATGGCGCCCTATAGCATGTGTACTCTTGGCGCCCTCTCAATCCTTGGGTTTGGGGCTTATGCTCAAGAGSCTGCGGTTGAGGGAACCCAGATATTTTTCACCTTG	
1	10 20 30 40 50 60 70 80 90 100	
1	TACCGCGGGATATCGTACCATGAGGAACCGCGGAGAGTTAGGAACCCAAACCCGAATACGAGTTCTCCGAGCCAACTCCTTGGGGTCTATAAAAAAGTTGAAC	>>>F>>> 162 to 181
106	ACCTACACGGAATATCTGGATAAGGTGGCAGCATCCCCAGGAGTTCCAGACAGAGTGATTGCGTGGAATGACACTATGAGCGGGTTTCTGGGAACGAGAGG	
106	110 120 130 140 150 160 170 180 190 200	
106	TGGATGTGCTTATAGACCTATTCCACCGTGTGAGGGTGCCTCAAGGGTCTGCTCACTAAACGGCACCTTACTGTGATACTCGCGAAAGGACCCCTTGCTCTGC	
211	GGCAGCAGCTATCGAGGCGTGGTGCATTGTCAACCTTGGAAAGCGTGACCTGTGCGGGGGAGGCTCACAACTACGCTCACCAATGAGCATGCTCCAGGGCG	
211	220 230 240 250 260 270 280 290 300 310	
211	CGGTGCTGATAGCTCCGACACGCGTACAGTTGGAACCTTTCGCACTGGGACAGCGGCCCTCCGAGTGTGTTAGCGCAGTGAGTTACTGTACGAGGTCGCG	>>>R>>> 366 to 383
316	CTTCATGATCTGTGTGTTGAAGCATATGGCAGGCTGGGAGCGATTAGTGGTCTGTGTCAAGACCAGGCAACGAGGCGTATCTATTGTGGGAATCGGAATGTC	
316	320 330 340 350 360 370 380 390 400 410	
316	GAAGTACTAGACACAACCTTCTGATACCGTGTCCGACGCTCGCTAATCACCCAGCACAGTTCTGGTCCGTTGCTCCGCATAGATAACACCCCTTAGGCTTACAG	
421	GCTGGGTCCCGCGGATGACGACACGAGCTTGCCCAAGCGGCGAGCAGTGCACCACTTTCGAGGCGGTCAATTATCGTAGCGTCCGGAATATTTTCTGCTCTGT	
421	430 440 450 460 470 480 490 500 510 520	
421	CGACCCAGGSCCGCTTACTGCTGCTCAGCGGGTTCGCGGCTGTCACGTGGTGAAGCTCCGCGAGTTAATAGCATCGCAGGSCCTATAAAAAAGCAGACACA	
526	GGGCCCCGAATTGAGGTGACGGAGAGACATGATATAGGATTACACAGGAATGGGACGGAATCTGCTACCTGAATCGCTTAATCGGCTGGGACCTACGATTCT	
526	530 540 550 560 570 580 590 600 610 620	
526	CCCGGGGCTTAACCTCACTGCTCTGCTACTATATCCCTAAGTGTGCTTACCTGCTTAGACCATGGGACTTAGCGGATTTAGCGGACCCCTGGATGCTAAGA	
631	TTGCGCCAGATGGCGGGCAGTCTCAATGGGTACTTCAACTTTGATGGTCTTATCGAATGGAGAGGGATGAGCTCTCGGGGAAGTGGACACTCGTGGTCAATGC	
631	640 650 660 670 680 690 700 710 720 730	
631	AAGCGGCTTACCGCGCGTCAGAGTTACCCATGAAGTTGAACCTACCACGAATAAGCTTACCTCTCCCTACTCGAGAGGCCCTTCACTGTGAGCACCAAGTACG	
736	ATTGCTTGGCCGGGAGGCAAGCTGACTATCACTAGCACAGATCGCGCAACTTGGGCGATTGGATATACCGCCCCCACTAA	
736	740 750 760 770 780 790 800 810	
736	TAACGAACGGGCCCTCCGTTGCTAGTATAGTATGCTGCTAGCGGTTGAACCGCTAACCTATATGGTGGGGGTGATT	

Supplementary Figure S4. Forward and reverse primers binding site (A) and multiple sequence alignment of SIX7a (B) for *Foc* STR4 of *Foc*STR4F/*Foc*STR4R.

A.

Results for linear 663 residue sequence "KM503196.1 Foc STR4_SIX7" starting "ATGCAGGTTA"

```
1 ATGCAGGTTATGAAGTACCTTTACCTCCTTTTCCATTTGCGCCTGTTTGGAGTGCTATACCTGGACTTGATCTC
1      10      20      30      40      50      60      70
1 TACCTCCAACTACTTTCATGGAATGAGGAAAAGGTAAAGCGGGACAAACGCTCACGATATGGACCTGAAC TAGAG
76 TTTCCAAAGGCAAGGGCTATGCTTTAGCACCACTCAAGAGCAGCAGGACCACCAGAAAGGCCTACTGAGGTGACA
76      80      90      100     110     120     130     140
76 AAAGGTTCCGTTCCCGATACGAAATCGTGGTTGAGTTCTCGTCGTCCTGGTGGTCTTTCCGGATGACTCCACTGT
151 TTTGACATCACCGAGAATGTCAACACGTTCAACGAGTCACGCGCGCATCCACACCATGGACTCAGGGGTAGGACTCTCG
151      160     170     180     190     200     210     220
151 AAACGTGTAGTGGCTCTTACACTGTGTCAAGTGGCTGCGGGCTAGGTGTGTACCTGAGTCCCACATCCTGAGAGC
226 AATATTAGATACCAATGGCGCGCATACTACAGTACAGGCGCAAACTACATTCGTTGAGGTTGAGGTTTTCGGT
226      230     240     250     260     270     280     290
226 TTATAATCTCTATGTTTACCGCGGTATGATGTATGTTGCTCGCTGTTTGATGTAAGCAACTCCAAGTCCAAAAGCCA
      >>>F>>> 310 to 329
301 ACTCGCGAGCGGCAACTACTCTTCTGCTTCCGGATGCTCCCGCAACAGCTCAATGGCGCCCTATCAATACCGACCTC
301      310     320     330     340     350     360     370
301 TGACGGCTCCGCTTCATCAGAACGAAGGCTACGAGGGGCTTGCCAGTTACCGGCGGATAGTTATCGCTGCAG
376 CTTAGGCCCAATGAAGGGTCACTGGCGGTGGTGTAGGGGGCTGGGGTCTGGGTGACTCCGGTCTGCTTCAAACT
376      380     390     400     410     420     430     440
376 GAATCCGGGTTACTTTCCAGTGACCGCCACCAAGATCCCGCGACCCAGCCCACTGAGGCCAGAGCGAGATTGA
451 TTTGCTCGAGAGATATTAGGTATCGSCTCCGGATTCAAGTAAGCCCAAGCACTCTTACCCGCTTGAAGTCATT
451      460     470     480     490     500     510     520
451 AAACGAGCTCTCTATAATCCATAGCCGAGGCCCTAAGTTGCATTGCGGTTCGTGAGGATGGGGGAATTCAGTAA
      >>>R>>> 538 to 554
526 CCTGGGAGGCAATACGCCAACCGCTTAATGAATGCCGTCGCTACGCGAAAACCCCTCAGATGATTATAAGCCC
526      530     540     550     560     570     580     590
526 GGACCTCCGTTATGCGGTTGGCGAATTACTTACGGGACGAGTCGGGTTTGGGGAGTCTACTAAATATTCGGG
601 AGGGGCGCTTGCTGATTTCGTTTTCATAGTTTTTAACACAGCAGAGTTTGTAGTAATCTGTAG
601      610     620     630     640     650     660
601 TCCCGGGAACGACTAAAAGCAAAAGTATCAAAATTTGTGTGCTCTCAACATCATTTAGACATC
```

B.

Fusarium oxysporum f. sp. cubense isolate VCG0120 chromosome 14, whole genome shotgun sequence
Sequence ID: **CM028826.1** Length: **1838343** Number of Matches: **1**

Range 1: 1288728 to 1289395		GenBank	Graphics	▼ Next Match	▲ Previous Match
Score	Expect	Identities		Gaps	Strand
1090 bits(590)	0.0	644/669(96%)		7/669(1%)	Plus/Plus
Query 1	ATGCAGGTTATGAAGTACCTTTACCTCCTTTTCCATTTGCGCCTGTTTGGAGTGCTATA				60
Subjct 1288728	ATGCAGATTATGAAGTACCTTTACCTCCTTTTCCATTTGCGCCTGTTTGGAGTGCTATA				1288787
Query 61	CCTGGACTTGATCTCTTTCCAAAGGCAAGGGCTATGCTTTAGCACCA---ACTCAAGAGCA				117
Subjct 1288788	CCTGGACTTGATCTCTTTCCAAAGGCAAGGGCTATGCTTTAGCACCACTCCGGCTCAACACCA				1288847
Query 118	GCAGGACCCACGAAAGGCTACTGAGGTGACATTTGACATCACCAGAAATGTCACACAG				177
Subjct 1288848	CCACGACCAACACCCCGCGCTAGAGAGGTGACATTTGACATCACCAGAAATGTCACACAG				1288907
Query 178	TTACCGAGCGCGCATCCACACATGAGTCAAGGTTAGGACTCTCGAATATTAGATAC				237
Subjct 1288908	TTACCGAGCGCGCATCCACACATGAGTCAAGGTTAGGACTCTCGAATATTAGATAC				1288967
Query 238	CAATGGCGCGCATACTACAGTACAGGCGACAAACTACATTCGTTGAGGTTGAGGTTTTTC				297
Subjct 1288968	CAATGGCGCGCATACTACAGTACAGGCGACAAACTACATTCGTTGAGGTTGAGGTTTTTC				1289027
Query 298	GGTACTGCCGAGGCGCAAGTAGTCTTGCTTCCGGATGCTCCCGCAACAGGTCAATGGCGC				357
Subjct 1289028	GGTACTGCCGAGGCGCAAGTAGTCTTGCTTCCGGATGCTCCCGCAACAGGTCAATGGCGC				1289087
Query 358	GCATCAATAGCGACCTCTTAGGCCC AATGAAGGGTCACTGGCGGTGGTGTAGGGGGC				417
Subjct 1289088	GCATCAATAGCGACCTCTTAGGCCC AATGAAGGGTCACTGGCGGTGGTGTAGGGGGC				1289147
Query 418	TGGGGTGGGTGACTCCGGTCTGCTTCAAACTTTTGGTCGG--A--GAGATATTAGGTAT				474
Subjct 1289148	TGGGGTGGGTGACTCCGGTCTGCTTCAAACTTTTGGTCGGCGGAGGAGATATTAGGTAT				1289207
Query 475	CGGCTCCGATTCAACGTAAAGCCAGGACTCTCAACCCCTTGAAGTCATTCTGGGAGG				534
Subjct 1289208	CGGCTCCGATTCAACGTAAAGCCAGGACTCTCAACCCCTTGAAGTCATTCTGGGAGG				1289267
Query 535	CAATACGCGCAACCGCTTAATGAATGCCGCTCGTACGCGCAAAACCTTCAGATGATTAT				594
Subjct 1289268	CAATACGCGCAACCGCTTAATGAATGCCGCTCGTACGCGCAAAACCTTCAGATGATTAT				1289327
Query 595	AMGCCAGGGGGCTTGCTGATTTCGTTTTCATAGTTTAAACACAGCAGAGTTTGTAGTA				654
Subjct 1289328	AMGCCAGGGGGCTTGCTGATTTCGTTTTCATAGTTTAAACACAGCAGAGTTTGTAGTA				1289386
Query 655	AATCTGTAG 663				
Subjct 1289387	AATCTGTAG 1289395				