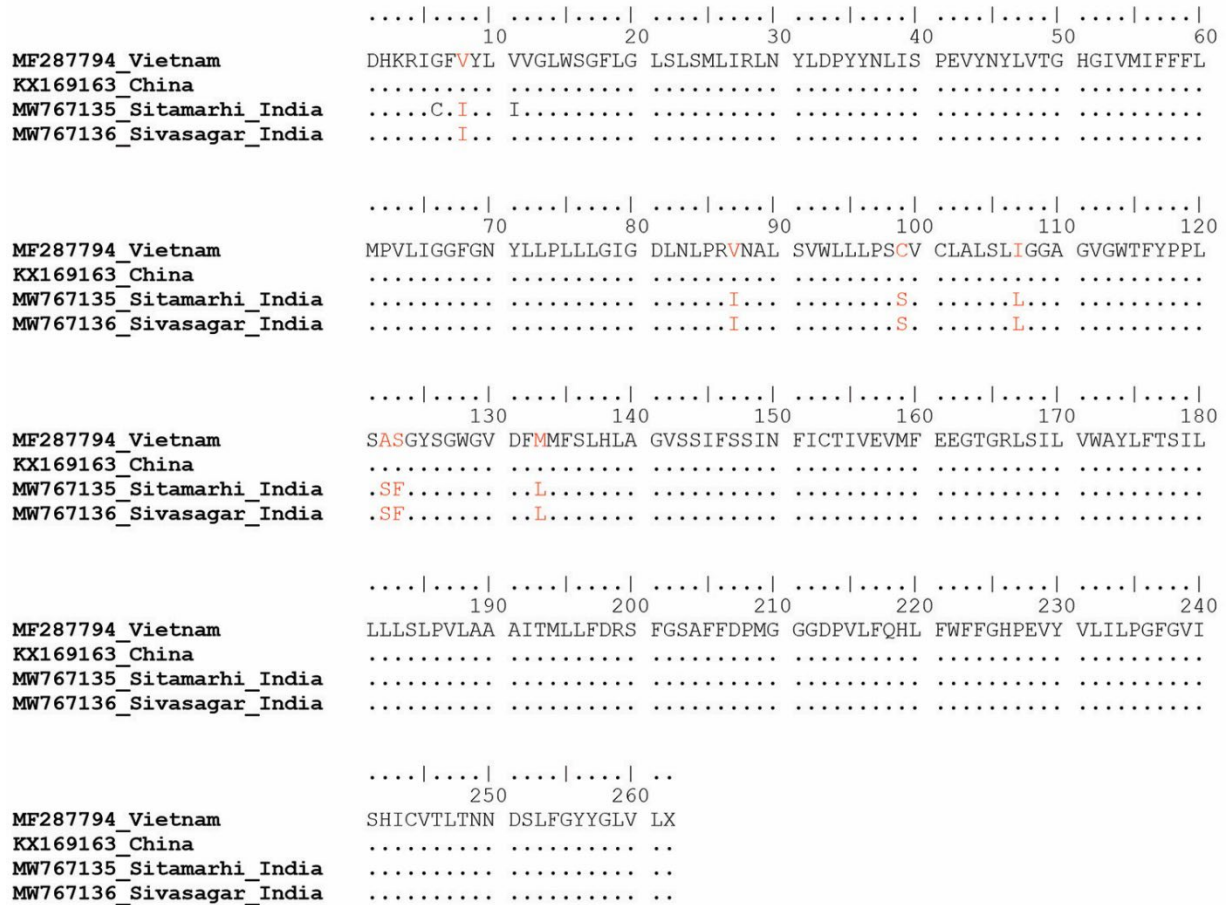


Fasciolopsis buski Detected in Humans in Bihar and Pigs in Assam, India

Appendix 2



Appendix 2 Figure 1. Alignment of the ITS2 gene region highlighting genetic variations (red) between *F. buski* isolates from India and from China and Vietnam.

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          |.....|.....|.....|.....|.....|.....|
          10      20      30      40      50      60
MN970005_Vietnam GCTTATAAAC TATCAGACG CCCAAAAAGT CGTGGCTTGG GTTTTGCCAG CTGGCGTGAT
EF612489_Vietnam .....
China .....
DQ351842_Meghalaya_India .....C.....A
MW771525_Sitamarhi_India .....C.....A
MW771526_Sivasagar_India .....C.....A
KF564866_UP_India .....C.....A
DQ351841_Meghalaya_India .....C.....A
KF781306_Meghalaya_India .....C.....-C..A

          |.....|.....|.....|.....|.....|.....|
          70      80      90     100     110     120
MN970005_Vietnam TTCCTCTATG ATTATTCATG TGAGGTGCCA GAACTATGGC GTTTCCTAA TGTATCCGGA
EF612489_Vietnam .....
China .....
DQ351842_Meghalaya_India C.....
MW771525_Sitamarhi_India C.....
MW771526_Sivasagar_India C.....
KF564866_UP_India C.....
DQ351841_Meghalaya_India C.....
KF781306_Meghalaya_India C.....

          |.....|.....|.....|.....|.....|.....|
          130     140     150     160     170     180
MN970005_Vietnam CGCGTCCTTG TCTCGGAGA AGGCTGTGAT GAGGTGCGGT AGCGGAATCG TGGTCTAATG
EF612489_Vietnam .....
China .....
DQ351842_Meghalaya_India .....A...G...G...T...
MW771525_Sitamarhi_India .....A...G...G...T...
MW771526_Sivasagar_India .....A...G...G...T...
KF564866_UP_India .....A...G...G...T...
DQ351841_Meghalaya_India .....A...G...G...T...
KF781306_Meghalaya_India .....A...G...G...T...

          |.....|.....|.....|.....|.....|.....|
          190     200     210     220     230     240
MN970005_Vietnam ATTACTGTGC ACGTTCTGCT GCTGTGTCCT CATCGTCGGC TTGATGCGAG ATTAGGTATC
EF612489_Vietnam .....
China .....
DQ351842_Meghalaya_India .A.....C.T...T...T...C.T...C...
MW771525_Sitamarhi_India .A.....C.T...T...T...C.T...C...
MW771526_Sivasagar_India .A.....C.T...T...T...C.T...C...
KF564866_UP_India .A.....C.T...T...T...C.T...C...
DQ351841_Meghalaya_India .A.....C.T...T...T...C.T...C...
KF781306_Meghalaya_India .A.....-C.T...T...T...C.T...C...

          |.....|.....|.....|.....|.....|.....|
          250     260     270     280     290
MN970005_Vietnam GTGTCTGAGG CTTTGGCCAT ACACAGACTG CAAATTGTGT GGTCTAATTT CC
EF612489_Vietnam .....
China .....
DQ351842_Meghalaya_India .....T.A...C.T.G...
MW771525_Sitamarhi_India .....T...C.T.G...
MW771526_Sivasagar_India .....T...C.T.G...
KF564866_UP_India .....T...C.T.G...
DQ351841_Meghalaya_India .....T...C.T.G...
KF781306_Meghalaya_India .....T...C.T.G...

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Appendix 2 Figure 2. Alignment of the *cox1* gene region highlighting genetic variations (red) between *F. buski* isolates from India and from China and Vietnam.

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.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
10    20    30    40    50    60
MW767135_Sitamarhi_India GATCATAAGC GTATTTGTTT TATTATTTA ATAGTTGGGC TTTGAGAGGG GTTTTAGGG
MW767136_Sivasagar_India .....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....
MF287794_Vietnam .....G.....G.....G.....G.....TT .G..G.....G.....G.....G.....G.....
KX169163_China .....G.....G.....G.....G.....TT .G..G.....G.....G.....G.....G.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
70    80    90    100   110   120
MW767135_Sitamarhi_India TTGTCATTAA GTATCTGAT ACGGTTGAAT TACTGGATC CTTATTATAA TTTAATTCT
MW767136_Sivasagar_India .....G.....G.....T..T..A..A ..T.....G.....G.....G.....G.....G.....
MF287794_Vietnam .....G.....G.....T..T..A..A ..T.....G.....G.....G.....G.....G.....
KX169163_China .....G.....G.....T..T..A..A ..T.....G.....G.....G.....G.....G.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
130   140   150   160   170   180
MW767135_Sitamarhi_India CCTGAGGTTT ATATTATTT GGTACAGGA CATGGTATG TAATGATTT TTTCTTTTG
MW767136_Sivasagar_India .....G.....G.....T.....T.....A.....G.....T.....C.....G.....G.....
MF287794_Vietnam .....G.....G.....T.....T.....A.....G.....T.....C.....G.....G.....
KX169163_China .....G.....G.....T.....T.....A.....G.....T.....C.....G.....G.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
190   200   210   220   230   240
MW767135_Sitamarhi_India ATGCCTGTGT TAATAGCTGG GTTGGTAAT TACTGTTAC CTTTGTGCT TGGTATAGT
MW767136_Sivasagar_India .....G.....G.....T.....T.....G.....T.....A.....G.....G.....G.....
MF287794_Vietnam .....G.....G.....T.....T.....G.....T.....A.....G.....G.....G.....
KX169163_China .....G.....G.....T.....T.....G.....T.....A.....G.....G.....G.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
250   260   270   280   290   300
MW767135_Sitamarhi_India GATTTGAATC TTCCCTGTAT TAATGCTTGG AGGCTTGGT TGTGTGTGC TTTAGTGTT
MW767136_Sivasagar_India .....T.....A.....G.....A.....A.....G.....A.....A.....A.....CT..C...
MF287794_Vietnam .....T.....A.....G.....A.....A.....G.....A.....A.....A.....CT..C...
KX169163_China .....T.....A.....G.....A.....A.....G.....A.....A.....A.....CT..C...

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
310   320   330   340   350   360
MW767135_Sitamarhi_India TGCTTGGCTT TGAGTTTGT AGGAGTGTCT GGGGTAGGTT GAACTTTTTA TCCCTCTTG
MW767136_Sivasagar_India .....T.....A.....G.....G.....T..T.....G.....G.....G.....G.....G.....
MF287794_Vietnam .....T.....A.....G.....G.....T..T.....G.....G.....G.....G.....G.....
KX169163_China .....T.....A.....G.....G.....T..T.....G.....G.....G.....G.....G.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
370   380   390   400   410   420
MW767135_Sitamarhi_India TCTAGTTTTG GTTATTCTGG TTGGGGAGTT GATTTTTGA TGTTTTCTTT GCATTGGCG
MW767136_Sivasagar_India .....GC..CA.....G.....G.....A.....G.....G.....G.....G.....G.....G.....
MF287794_Vietnam .....GC..CA.....G.....G.....A.....G.....G.....G.....G.....G.....G.....
KX169163_China .....GC..CA.....G.....G.....A.....G.....G.....G.....G.....G.....G.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
430   440   450   460   470   480
MW767135_Sitamarhi_India GGGGTTTCTA GTATTTTGG GCTATTAA A TTTATTGTA CTATAGTGA AGTGATGTT
MW767136_Sivasagar_India .....A.....T.....T.....T.....T.....T.....T.....G.....T.....G.....T.....
MF287794_Vietnam .....A.....T.....T.....T.....T.....T.....T.....T.....G.....T.....G.....T.....
KX169163_China .....A.....T.....T.....T.....T.....T.....T.....T.....T.....G.....T.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
490   500   510   520   530   540
MW767135_Sitamarhi_India GAGGAAGGAA CAGGACGTTT AAGTATTTTA GTTTGAGCTT ATTTGTTTAC TCTATTTTG
MW767136_Sivasagar_India .....T.....T.....G.....G.....G.....G.....G.....G.....G.....G.....G.....
MF287794_Vietnam .....T.....T.....G.....G.....G.....G.....G.....G.....G.....G.....G.....
KX169163_China .....T.....T.....G.....G.....G.....G.....G.....G.....G.....G.....G.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
550   560   570   580   590   600
MW767135_Sitamarhi_India TTGCTTTTGT CTTTGGCGGT TTTGGCTGCT GCTATAACAA TGTGTTGTTT TGATCGTAGG
MW767136_Sivasagar_India .....A.....T.....A.....A.....T.....T.....A.....A.....A.....T.....T.....
MF287794_Vietnam .....A.....T.....A.....A.....T.....T.....A.....A.....A.....T.....T.....
KX169163_China .....A.....T.....A.....A.....T.....T.....A.....A.....A.....T.....T.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
610   620   630   640   650   660
MW767135_Sitamarhi_India TTTGGCTCTG CCTTTTTTGA TCCTATGGGG GCGGAGATC CAGTGTATT TCAGCATTGG
MW767136_Sivasagar_India .....G.....A.....G.....G.....G.....G.....G.....G.....G.....G.....G.....
MF287794_Vietnam .....G.....A.....G.....G.....G.....G.....G.....G.....G.....G.....G.....
KX169163_China .....G.....A.....G.....G.....G.....G.....G.....G.....G.....G.....G.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
670   680   690   700   710   720
MW767135_Sitamarhi_India TTTTGGTTTT TTGGGCATCC GGAGGTTTAT GTTTTGATT TGCCGGGGTT TGGTGTATT
MW767136_Sivasagar_India .....C.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....
MF287794_Vietnam .....C.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....
KX169163_China .....C.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
730   740   750   760   770   780
MW767135_Sitamarhi_India AGACATATTT GTGTRACTT AACTAATAAA GATTCCTTGT TTGTTATTA TGGTCTGTT
MW767136_Sivasagar_India .....T.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....
MF287794_Vietnam .....T.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....
KX169163_China .....T.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....

....
MW767135_Sitamarhi_India TTGG
MW767136_Sivasagar_India ....
MF287794_Vietnam ....
KX169163_China ....

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Appendix 2 Figure 3. Alignment of the translated cox1 gene region highlighting genetic variations (red) between *F. buski* isolates from India and from China and Vietnam.