

LE_HBa0169D11, 85.0 cM, Chr. 6

Christopher Martin and Douglas Maxwell, University of Wisconsin Madison

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Primer Name	Sequence (5'-3')
CMTY4A-F2	CCCAAGATGCTCACTGTCAATGTC
CMTY4A-R1	GTTCCGAAGCTAGTTTATGTGTTCC

Cerasiforme partial sequence_Ty4AR1: 324 bp;

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1      CCCAAGATGC TCACTGTCAA TGTCCATTAG CTTCATCTCA AAATCAGCAA TCTTGTCTTG
61     GGCTGCAATA CATAATAGTT ATGCAAATAA GTTAAAAC TA GACCATAGTA ACAGAGAGAC
121    TGAATCCATA ATCAAAATAA AATCAATAAA TCTATCATAA AAGACACGAC TCAGTCCCAA
181    TTATACCAAT TTCAAGCAAA ATCAAGCTAG TTTAAATTAT TCTATCGATC TATAGACAGT
241    GAAGTAATCA TTTCTAAAAT TCATAATTTA GAATCAAACA NGATTCCAAA CTACAAATTA
301    NTGTTCGCTT CAATTTTCCT CACA
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Gc171 complete sequence_TY4AF2-R1: 470 bp;

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1      CCCAAGATGC TCACTGTCAA TGTCCATTAG CTTCATCTCA AAATCAGCAA TCTTGTCTTG
61     GGCTGCAATA CATGATAGTT ATGCAAATAA GTTAAAAC TA GACCATAGTA ACAGAGAGAC
121    TGAATCCATA ATCAAAATAA AATCAATAAA TCTATCATAA AAGACACGAC TCAGTCCCAA
181    TTATACCAAT TTCAAGCAAA ATCAAGCTAG TTTAAATTAT TCTATCGATC TATAGACAGT
241    GAAGTAATCA TTTCTAAAAT TCATAATTTA GAATCAAACA CGATTCCAAA CTACAAATTA
301    CTGTTCGCTT CAATTTTCCT CACATTTGAC ATGTTTAATA AGTAATCAAA AGCAAAAAAG
361    TGTCAATATT TTGGGACCAG GAGGTATCAA TTTCAACAAT ATATATAGCA GATGTTATAG
421    TCTCTAGATC CTATTTATAA TTATGGAAAC ACATAAACTA GCTTCGGAAC
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HUJ-VF partial sequence Ty4AR1: 412 bp;

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1      CCCAAGATGC TCACTGTCAA TGTCCATTAG CTTCATCTCA AAATCAGCAA TCTTGTCTTG
61     GGCTGCAATA CATGATAGTT ATGCAAATAA GTTAAAAC TA GACCATAGTA ACAGAGAGAC
121    TGAATCCATA ATCAAAATAA AATCAATAAA TCTATCATAA AAGACACGAC TCAGTCCCAA
181    TTATACCAAT TTCAAGCAAA ATCAAGCTAG TTTAAATTAT TCTATCGATC TATAGACAGT
241    GAAGTAATCA TTTCTAAAAT TCATAATTTA GAATCAAACA CGATTCCAAA CTACAAATTA
301    CTGTTCGCTT CAATTTTCCT CACATTTGAC ATGTTTAATA AGTAATCAAA AGCAAAAAAG
361    TGTCAATATT TTGGGACCAG GAGGTATCAA TTTCAACAAT ATATATAGCA GA
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Conclusions

Partial sequence was obtained for both Cerasiforme and HUJ-VF, and complete sequence was obtained for Gc171 using standard sequencing methods. Upon alignment all tested sequences were identical. Therefore, this locus is not the location of Ty-4.