MK000001=P10

Marker: P10
Type:
Description: Carrot chloroplast
Reference: B.S. Vivek as RFLP [Vivek, B.S., Q.A. Ngo, and P.W. Simon. Evidence for maternal inheritance of the chloroplast genome in cultivated carrot (Daucus carota L. ssp. *sativus*). Theor. Appl. Genet. 98:669-672. 1999.], then Jim Bradeen converted to PCR Marker. Described in Doug's "Carrot DNA 4" page 39.
Primers: P10B1fin .....5'-AAG ATT AGG ATC CTC CGC AAT-3'
P10B2fin .....5'-GGG TTC GAA TCC CTC TCT TT-3'
PCR Reaction: 20 µl: [0.2 µg/ml DNA; 1 µM each primer; 5 U/µl Taq; 2 mM $MgCl_2$]
PCR Program: 35 cycles of {94°C 0:30; 55°C 0:30; 72°C 1:00}; 4°C hold.
Screening Method: Detected by agarose gel after *Bgl*II digestion:
5 µl PCR reaction + 25 µl master mix (=3 µl Buffer D, 0.3 µl BSA, 0.25862 µl *Bgl*II, 21.44138 µl H_2O) at 37°C 2hr, 70°C 10min.
Product Sizes: No *Bgl*II site = 490 b.p.
*Bgl*II site = 198 and 291 b.p.
Example: 

Genbank reference: DQ898156 from 7962 to 8451, SNP @ b.p. 8160..8165
Sequence Information:

```
>VC000366 P10 Chloroplast BglII fragment from Jim Bradeen \PCR&SEQ\Chloroplast
P10\SubFrag1bR.seq
TAAACCTCGATTCAAACATTGAAAGTCTTNATTGGGTAGCTGCGAGAAATCCAAATATGGCTCACCCCGTATTCCCCATATCTGCTCTTTTGA
AACACCTTAATAGGGGTTAAGATTAGGATCCTCCGCAATATCTAATTGGAGGTATGAAAGAAATTATTGGTAATAAAAGACTCTTGTGACAAT
TGAATTTTAATTTCTGTGAAATTTTTTTATGTTTCTAGAAAGCACTTCATTTATTGGTGTCAA

AACATTTGGT ATAAAAAAAT GGAGGATCTA TTATCTTTTC TCAAATTTTT TTTTCAAAAA AGATCT
TGGAGATTGT GTAATGCTTA CTCTCAAACT TTTCGTTTAC ACAGTAGTGA TATTCTTTGT

TTCTCTATTTATTTTTGGATTCCTATCTAATGATCCGGGGCGTAATCCTGGCCGTGAAGAATAAAAAGGGAGTTTTCATTTTCCTTGCTTGAT
TTTTCAATTTTCTTAGTATTTTTTATCTATTCCACATGTTTAACTAGGAAACATTCAAAAGGATTGGCTAAATTTGAAAGAGAAATCAAATAT
AAAGTCATCAACAAAAACGGAAAGAGAGGGATTCGAACCCTCGGNACGAATAACTCGTACAACGGATTAGCAATCCGNCGCTTTAGTCCACTC
AGCATCTCTTCCAATTGAAAAAGACAATTACTATGTTACATTACACATGAAATACG
( AGATCT = Bgl II site )
```

Corresponding sequence in GenBank for this region from gb|DQ898156.1| Daucus carota chloroplast, complete genome:

```
Query  3     AACCT-CGATTCAAACATTGAAAGTCTTNATTGGGTAGCTGCGAGAAATCCAAATATGGC  61
             |||||  ||||||||||||||||||||| |||||  ||||||||||||||||||||||||
Sbjct  7852  AACCTTCGATTCAAACATTGAAAGTCTTGATTGGATAGCTGCGAGAAATCCAAATATGGC  7911

Query  62    TCACCCCGTATTCCCCATATCTGCTCTTTTGAAACACCTTAATAGGGGTTAAGATTAGGA  121
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7912  TCACCCCGTATTCCCCATATCTGCTCTTTTGAAACACCTTAATAGGGGTTAAGATTAGGA  7971

Query  122   TCCTCCGCAATATCTAATTGGAGGTATGAAAGAAATTATTGGTAATAAAAGACTCTTGTG  181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7972  TCCTCCGCAATATCTAATTGGAGGTATGAAAGAAATTATTGGTAATAAAAGACTCTTGTG  8031
```

```
Query  182   ACAATTGAATTTTAATTTCTGTGAAAttttttATGTTTCTAGAAAGCACTTCATTTATT  241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8032  ACAATTGAATTTTAATTTCTGTGAAATTTTTTTATGTTTCTAGAAAGCACTTCATTTATT  8091

Query  242   GGTGTCAAAACATTTGGTATaaaaaaaTGGAGGATCTATTATCTTTTCTCAAAttttttt  301
             |||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Sbjct  8092  GGTGTCAAAACATTTGGTATAAAAAAATGGAGGATCTATTATCTTTTCTCATTTTTTTTT  8151

Query  302   ttCAAAAAAGATCTTGGAGATTGTGTAATGCTTACTCTCAAACTTTTCGTTTACACAGTA  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8152  TTCAAAAAAGATCTTGGAGATTGTGTAATGCTTACTCTCAAACTTTTCGTTTACACAGTA  8211

Query  362   GTGATATTCTTTGTTTCTCTATTTATTTTTGGATTCCTATCTAATGATCCGGGGCGTAAT  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8212  GTGATATTCTTTGTTTCTCTATTTATTTTTGGATTCCTATCTAATGATCCGGGGCGTAAT  8271

Query  422   CCTGGCCGTGAAGAATAAAAAGGGAGttttcattttccttgcttgatttttcaattttct  481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8272  CCTGGCCGTGAAGAATAAAAAGGGAGTTTTCATTTTCCTTGCTTGATTTTTCAATTTTCT  8331

Query  482   tagtatttttttATCTATTCCACATGTTTAACTAGGAAACATTCAAAAGGATTGGCTAAAT  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8332  TAGTATTTTTTATCTATTCCACATGTTTAACTAGGAAACATTCAAAAGGATTGGCTAAAT  8391

Query  542   TTGAAAGAGAAATCAAATATAAAGTCATCAACAAAAACGGAAAGAGAGGGATTCGAACCC  601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8392  TTGAAAGAGAAATCAAATATAAAGTCATCAACAAAAACGGAAAGAGAGGGATTCGAACCC  8451

Query  602   TCGGNACGAATAACTCGTACAACGGATTAGCAATCCGNCGCTTTAGTCCACTCAG-CATC  660
             |||| |||||||||||||||||||||||||||||| |||||||||||||||| ||||
Sbjct  8452  TCGGTACGAATAACTCGTACAACGGATTAGCAATCCGCCGCTTTAGTCCACTCAGCCATC  8511

Query  661   TCTTCCAATTGAAAAAGACAATTACTATGTTACATTACACATGAAATACG  710
             ||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8512  TCTCCCAATTGAAAAAGACAATTACTATGTTACATTACACATGAAATACG  8561
```