http://www.vcru.wisc.edu/simonlab/sdata/MK000062.pdf

MK000062=A/321:A/392

Marker: A/231:A/392
Type: Codominant PCR
Description:
Reference: Euphytica 127: 353–365, 2002. PCR-based markers to differentiate the mitochondrial genomes of
petaloid and male fertile carrot (Daucus carota L.) Inga C. Bach, Annette Olesen & Philipp W. Simon,
Primers: cmt-1 (a).....5'-GCAAGAAGGAAAGCTGTTAGAG-3'
cmt-2 (b) .....5'-GGTATCCCTCTTCTGTTTCGG-3'
PCR Reaction: 20 µl: [0.4 µg/ml DNA=8 ng; 0.4 µM each primer=8 pMol each; 0.025 U/µl Taq=0.5 U; 1.5 mM $MgCl_2$=30 nMol; 0.1 mM each dNTP=2 nMol]
PCR Program: 94°C 2:00; 35 cycles of {94°C 1:00; 55°C 1:00; 72°C 2:30}; 72°C 7:00
Screening Method: Product size by agarose gel
Product Sizes: 321 in Sp cytoplasm; 392 in N cytoplasm
Example:
Diagram of how it works:

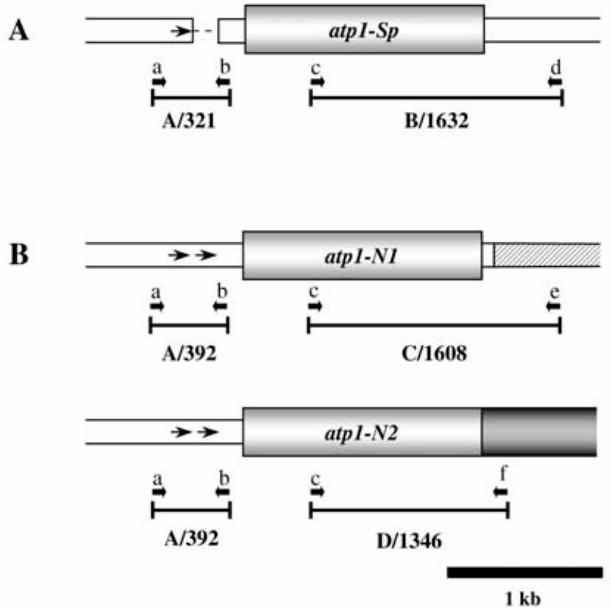

Figure 1. Structures of mtDNA atp1 genes and flanking regions in line K826A with SpC cytoplasm (A) and line K831B with N cytoplasm (B). Open reading frames (ORFs) are indicated by large shaded boxes and intergenic regions by open boxes. Nonhomologous regions are indicated by darker shading (ORFs) or crosshatching (intergenic regions). Thin arrows indicate the sites of a 71 bp fragment that forms a direct repeat in the fertile line. The lack of this repeat upstream from atp1-Sp is indicated by a dotted line. Thick arrows indicate the annealing sites and orientations of the primers cmt-1 (a), cmt-2 (b), atp1-d1 (c), cmt-3 (d), cmt-4 (e) and cmt-5 (f). PCR amplification products serving as markers are indicated by bars labeled A/321, A/392, B/1632, C/1608 and D/1346.
Genbank reference: The DNA sequences of the atp1-Sp,atp1-N1 and atp1-N2 loci have been assigned GenBank Accession Nos. AF301602, AF301604 and AF301603, respectively.
Sequence Information:
Map Location:
Published Reference:
Other Information:
Primer Location (lab specific): Box 0 X0
PCR Program Name (lab specific):