mitfa^{b692}

Nature of the mutation

The *b692* allele contains a single T-to-G point mutation that substitutes isoleucine by serine at position 215 in the first helix of the helix-loop-helix dimerization domain (Lister et al., Developmental Biology 237: 333-344, 2001).

Genotyping assay

Genotyping of the *b692* allele is based on the RFLP assay (**R**estriction **F**ragment **L**ength **P**olymorphism; Botstein *et al.*, Am. J. Hum. Genet. 32: 314-331, 1980). This method is used to detect a mutation that either creates or abolishes a site recognized by a specific restriction enzyme. In the RFLP assay, a sequence of interest is first PCR-amplified and then the PCR product is subjected to restriction enzyme digestion. The presence or absence of the mutation is determined by the resulting restriction pattern. The *b692* mutation creates a site recognized by the BsrDI restriction enzyme.

Primers:
MIT_01: 5' GCA AAA GAG AGA CAA AAG AAG GAC 3'
MIT_02: 5' CTT ACG GAT CAT TTG ACT TGG G 3'

PCR program (53_30_30):

1. 94ºC for 3 min
2. 94ºC for 30 sec
3. **53**ºC for **30** sec
4. 72ºC for **30** sec
5. Go to step 2 (above) for 39 cycles
6. 72ºC for 5 min
7. 8.0ºC hold
8. END

Product size: 234 bp

Digestion of the PCR product with the BsrDI restriction enzyme:

Product type	Product digestion	DNA fragments after digestion (bp)
PCR product derived from the WT template	unaffected	234 bp
PCR product containing the mutation	cleaved	185 bp and 49 bp

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