

**CRIME AND ANIMAL GENETICS:
USE OF CANINE MITOCHONDRIAL DNA AS SUPPORTING EVIDENCE**

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Hairs of suspected canine origin left at the scene of an attempted capital murder case were used to obtain mitochondrial DNA. Sequences derived from PCR products amplified from this DNA were then compared to those obtained from three dogs belonging to a suspect.

Originally, DNA was extracted from all six samples using a Proteinase K extraction. There were no follicles on the unknown evidentiary samples and attempts at STR analysis were unsuccessful.

Mitochondrial DNA was successfully isolated and amplified from the samples and specific canine primers were used to amplify a 295bp product from Hypervariable Region I.

The PCR products were sequenced in both directions and compared to known published sequence and those in GenBank.

In the region amplified, there are 23 known single nucleotide polymorphisms (SNPs) and the allele frequencies have been calculated by Savolainen et al. (1997).

The sequence from the three unknown evidentiary samples were identical to the sequence of the suspect's three dogs. The sequence showed variation from the published consensus sequence at two polymorphic sites. Since the three known dog samples and the three unknown dog samples were identical in sequence, the suspect's dogs could not be excluded as being the donors of the evidentiary hair samples submitted. Furthermore, the identity of the 6 sequences was consistent with information provided that the three dogs are related.