

A rough calculation of the heating and deformation of the sphere caused by infrared radiation of a few mW cm⁻² for a few milliseconds gives an estimate for the membrane deformation in the order of 1 nm. A mechanical stimulus of this amplitude is sufficient to elicit a response from insect mechanoreceptors⁶. This proposed mechanism of transferring infrared radiation to mechanical action is used for photoacoustic spectroscopy⁷, an ultra-sensitive measuring technique in which an infrared beam thermally excites absorbing matter, in turn displacing the membrane of a loudspeaker.

Infrared detectors have previously been observed in crotalid and boid snakes, where infrared radiation warms up a thin membrane innervated by fibres of the trigeminal nerve. These act as true thermoreceptors⁸. In contrast, the stimulus for the sensory cell in the infrared receptors of *Melanophila* is a mechanical one, and the sensillum seems to function according to a photomechanical principle.

**Helmut Schmitz, Horst Bleckmann
Manfred Mürtz***

Rheinische Friedrich-Wilhelms-Universität Bonn,
Zoologisches Institut, Poppelsdorfer Schloss and
*Institut für Angewandte Physik, Wegelestrasse 8,
D-53115 Bonn, Germany
e-mail: Bleckmann@uni-bonn.de

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Pet cat hair implicates murder suspect

DNA fingerprinting has been widely used as a forensic tool for over a decade^{1,2}, with simple tandem repeat (STR) loci³ being increasingly used to compare genotypes^{4,5}. Genomic and mitochondrial DNA, extracted from human or animal hairs collected at crime scenes, can be genotyped using the polymerase chain reaction (PCR)^{6–8}. By characterizing STR loci in domestic species, including cats and dogs^{9,10}, individual animals can be identified with high statistical confidence^{1,11,12}. As an example we describe a homicide case where the composite STR genotype of a hair linked to a crime scene matched that of the suspect's pet cat.

The case concerned a 32-year-old woman who disappeared from her home in Richmond, Prince Edward Island, Canada, on 3 October 1994. Her abandoned car was dis-

Table 1 Comparison of suspect (Snowball) and jacket hair (Evidence) genotypes

STR Locus	Allele Size (bp)		Allele size difference (bp)	STR match window* (bp)
	Snowball	Evidence		
FCA 026	147.83, 143.73	148.11, 143.73	0.28, 0.0	< 0.37
FCA 043	126.38, 120.52	126.29, 120.50	0.09, 0.02	< 0.59
FCA 080	259.27, 253.39	259.20, 253.14	0.07, 0.25	< 0.30
FCA 088A	121.91, 110.50	121.91, 110.50	0.0, 0.0	< 0.42
FCA 126	143.41, 141.08	143.41, 141.08	0.0, 0.0	< 0.53
FCA 132	152.73, 150.69	152.73, 150.69	0.0, 0.0	< 0.27
FCA 149	132.02, 128.05	131.80, 128.07	0.22, 0.02	< 0.29
FCA 058	229.03	229.24	0.21	< 0.36
FCA 090	93.54	93.54	0.0	< 0.46
FCA 096	210.95	211.00	0.05	< 0.25

*Match window gives the maximum allowable variation to declare a match, and was defined as the maximum pairwise allele size difference in a 70-member feline pedigree, comparing the migration at each locus of all alleles that are identical by descent¹⁴.

covered within days, and blood found inside was shown to match the victim. Three weeks later, a man's leather jacket stained with the victim's blood was discovered in woods, 8 km from her home. In the lining several white domestic cat hairs were found (A. E. Evers, Royal Canadian Mounted Police).

The victim's body was uncovered in a shallow grave on 6 May 1995, and the victim's estranged common-law husband was arrested and charged. The suspect lived with his parents and a pet cat; a white American shorthair named Snowball. We were asked to determine whether genomic DNA from the cat hairs found in the jacket matched Snowball's DNA profile.

Our laboratory had isolated and characterized nearly 400 dinucleotide STR loci from domestic cat DNA when constructing a linkage map of that species^{10,13}. We extracted and amplified DNA from the root of one of 27 hairs from the jacket and typed the DNA on the basis of ten feline dinucleotide repeat STR loci that were selected for optimal performance in forensic analysis¹⁴. We electrophoresed the fluorescently labelled PCR products in 6% denaturing polyacrylamide gels using a PE Applied Biosystems ABI 373A Automated DNA Sequencer. We similarly amplified DNA extracted from a blood specimen collected from Snowball (January 3 1995 by subpoena). Composite STR genotypes of the hair and Snowball's blood on the same gel were judged to match at all ten loci (seven heterozygous and three homozygous STR loci were resolved; Table 1).

The likelihood of a match between the hair genotype and a random individual was estimated from the frequency of the composite genotype in the population at large using allele frequency estimates from two STR population surveys: 19 unrelated cats from Prince Edward Island and nine cats from around the United States¹⁴. Although small, the island sample was adequate (95% confidence) to detect any STR allele present at a frequency of 9.5% or higher. The two populations showed appreciable allelic variation and remarkable population genetic similarity (as opposed to geographic population substructure). For example, 62% of the

detected STR alleles were present in both populations and the same alleles were most common for nine of the ten selected loci (all except FCA 088A) in both populations¹⁴.

The 10 STR loci were selected to reside on different linkage groups to ensure that there was no association between alleles at different loci. In addition, the distribution of outcomes of Fisher's Exact Tests on all pairwise combinations of 72 alleles between the 10 loci did not depart from expectations of independence in the island population sample (with Bonferroni correction for multiple tests). The incidence of the composite hair genotype for the seven heterozygous loci, estimated using the product rule and minimum allele frequency estimates for rare alleles^{1,11,12}, was 2.2 × 10⁻⁸ and 6.9 × 10⁻⁷ for the island and the US population databases, respectively.

The results of our analysis were presented and admitted to the Supreme Court of Prince Edward Island. The jury convicted the defendant of second-degree murder on 19 July 1996. The case represents a legal precedent for the introduction of automated STR genotyping of pet animal hairs in forensic cases that can be connected to the suspect in capital cases.

Marilyn A. Menotti-Raymond

Victor A. David*, Stephen J. O'Brien

Laboratory of Genomic Diversity and *SAIC,
National Cancer Institute,
Frederick, Maryland 21702-1201, USA

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