EXHIBIT 2

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DNA fingerprints from fingerprints

Forensic scientists regularly generate genetic profiles from old blood stains, seminal stains, vaginal swabs, hair, bone, urine and cigarette butts[1–6]. We show that an individual's genetic profile can now also be generated from swabs taken from objects touched by hands, providing a new tool for crime scene investigations. Our findings also demonstrate the need for caution when handling exhibits and when interpreting results.

We swabbed specific areas of hands and objects with cotton cloth dampened with sterile water, using disposable forceps. We extracted[7] and quantified (ACES 2.0+ program, Gibco BRL) DNA from these swabs, and typed for a short tandem repeat locus using the polymerase chain reaction[7]. We compared the results with independent typings of blood or buccal samples from participating individuals.

Initial tests showed that we could readily obtain correct genetic profiles from swabs taken directly from the palm of a hand (13 of 13). DNA yields varied from 2 to 150 ng (average 48.6 ng). Dry hands and those that had been washed recently tended to provide the least DNA.

Swabs of objects handled regularly by specific individuals all provided genetic typings that matched the user. Objects included: leather briefcase handles ($n=3$, mean 75 ng DNA), pens ($n=3$, mean 1.6 ng), a car key ($n=1$, 1.1 ng), a personal locker handle ($n=1$, 3.7 ng) and telephone handsets ($n=5$, mean 10.3 ng). One of the telephone handsets also clearly displayed the genetic profile of a known secondary (minor) user.

Furthermore, a number of pre-cleaned objects held for a relatively short period of time (15 min) including: plastic knife handles ($n=6$, mean 17.8 ng DNA), a mug ($n=1$, 6.8 ng), a glass ($n=1$, 34 ng) as well as new vinyl gloves worn for 20 to 90 min ($n=8$, mean 51 ng) gave the genetic profile of the holder or wearer. We found alleles in addition to those of the wearer in samples from two of the gloves, which could be due to secondary transfer. We also found that swabs of the inside of worn (1 min) condoms ($n=4$), where no ejaculation occurred, also provide the wearer's genetic profile (mean 11.2 ng DNA). This is relevant to some sexual offence investigations.

DNA yields from swabs of polypropylene tubes held for varying lengths of time (5 s, 30 s, 3 min, 10 min), did not differ significantly, indicating that substantial transfer of material occurs during initial contact.

Objects handled by many individuals all produced profiles with multiple alleles of varying intensity. To determine the effect of multiple handlers, we exchanged polypropylene tubes between individuals (2 or 3, 10 min each) with different genotypes. Although the material left by the last holder was usually present on the tube, that of previous holders was also retrieved to varying extents. The strongest profile obtained was not always that of the person who last held the object, but was dependent on the individual. We regularly observed profiles of previous holders of a tube from swabs of hands involved in these exchanges, showing that in some cases material from which DNA can be retrieved is transferred from object to hand (secondary transfer).

Also, hands swabbed before and after a one-minute handshake revealed the transfer of DNA from one individual to another in one of the four hands tested. Thus genetic profiles from objects handled by several people or from minute blood stains on touched objects may be difficult to interpret.

There are many cases in which the genetic profile of individuals who may have handled or touched particular objects associated with a crime could be extremely important to an investigation. Our methods have already been used at our laboratory to provide evidence in attempted murder, rape, armed robbery, extortion and drug-trafficking cases.

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How many replicons make a nodule?

Allan Downie, in his commendable News and Views discussion[1] of our work[2], suggests that a second, non-chromosomal symbiotic replicon could be present in the bacterial *Rhizobium* species NGR234. So far, our as-yet unpublished work on physical mapping and random sequencing of the NGR234 genome by V. Viprey, C. Freiberg and X. P. has produced no evidence of another plasmid. Further, the electrophoretic methods we used could visualize the twin symbiotic plasmids (relative molecular mass (M_r) 1×10^9) of *R. meliloti*, but in the event consistently demonstrated only a single plasmid of M_r $3.1\times10^8 \pm 2\times10^7$ in NGR234 (refs 3, 4). Thus, although Morrison *et al.*[5] reported that NGR234 contains two plasmids of M_r 3×10^8 and 4.5×10^8, it seems unlikely that a second plasmid exists. It is true, however, that some nodulation and other symbiotic genes map to the chromosome[6]. (Incidentally, the *fixABC* cluster is present on pNGR234*a*.)

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Unique morphology of the human eye

Human eyes have a widely exposed white sclera surrounding the darker coloured iris, making it easy to discern the direction in which they are looking[1]. We compared the external morphology of primate eyes in nearly half of all primate species, and show that this feature is uniquely human. Humans have the largest ratio of exposed sclera in the eye outline, which itself is elongated horizontally. We suggest that these are adaptations to extend the visual field by allowing greater eye movement, especially in the horizontal direction, and to enhance the ease of detecting the gaze direction of another individual.

We measured three parameters in 88 primate species: an index of exposed sclera size (SSI) in the eye outline, the width–height ratio (WHR) of the eye outline and the sclera coloration. Human eyes have the largest