

# PCR DNA typing for forensics

SIR — The first admission by a British court of forensic evidence using the polymerase chain reaction (PCR)<sup>1,2</sup> suggests that acceptance of this test could quickly become general outside the United States<sup>3</sup>. In actual casework, great care must be exercised in the areas of chain integrity (continuity), quality control and the choice of the population database used in the probability calculations. Otherwise, unreliable conclusions may be drawn and the expert witnesses accused of presenting worthless evidence. The PCR procedure has had only limited forensic application, but in individual cases it has allowed DNA analysis otherwise inaccessible to standard procedures. This is so when the amount of DNA is limited, or when the DNA is degraded because of environmental factors, contains a mixture of DNA coming from various subjects or is contaminated by handling before reaching the laboratory.

Yet PCR analysis was admitted by the Italian courts in April 1991 (Corte d'Assise, L'Aquila) as part of the trial evidence in the murder of a seven-year-old girl (the Balsorano-Avezzano murder, 1990). On 23 August 1990, C. C. was found killed in a wooded area near the family house. The police investigation pointed to the victim's maternal uncle as the suspect. The major evidence consisted of hair roots and blood spotting found on the accused's vest and underpants.

The investigators had DNA prints prepared from the victim's and the accused's blood. The victim's profile matched those from the hair-root cells and bloodstains. The DNA was examined by *in vitro* amplification using the PCR of different polymorphic sites, including VNTRs loci (APOB, D1S80, HLADQalfa, D2S44), microsatellite markers (APOCII, 3'CACA distrophin, CA/GTVNDR18) and two allele site specific RFLPs (XV2C, KM19, CKMM, APOCII/BanII/AvaII). In addition, a 49 bp portion from a 3.4-kb Y chromosome-specific tandem repeat was amplified for sex determination of the biological traces, and provided no evidence of specific Y-material.

The PCR results determined that DNA profiles from the victim's blood specimen and traces matched with  $1.7 \times 10^{-11}:1$  odds against the match arising by chance in the population. This forensic case was also investigated by direct sequencing of the CA/GT strand of the amplified microsatellite VNDR18. The victim's blood pattern matched that of hair-root cells found on the uncle's vest. The suspect received a life sentence.

It has been argued that the DNA

typing of small-sized forensic samples should be based on different means, including the determination of amplified DNA fragment length differences, hybridization with allele-specific oligonucleotide probes, and direct DNA sequencing<sup>4</sup>. The 1990 Balsorano-Avezzano murder proves that this complex protocol provides reliable, probative, not unduly prejudicial, and helpful biological evidence to the jury.

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## Chauvinism

SIR — A recent study tends to support the hypothesis of 'national publication bias', according to which journals prefer to publish papers from their own country<sup>1</sup>. This may be true for the journals published in the West but is certainly not true for those published elsewhere. There is also the problem of the 'impact factor'<sup>2</sup>.

Most of the scientific journals published in India or other developing countries do suffer simply because of a preconceived notion that the large number of papers published in them have a low impact factor rating. This may or may not be true. Fortunately, these journals are striving hard to improve their image by internationalizing their editorial boards to increase what is called their 'internationality factor'<sup>3</sup>. As national publication bias and impact factor are to some extent interrelated, this could very adversely affect scientists, especially in developing countries. This fact should be of some concern to the whole scientific community.

As professional career decisions and even election to fellowships of the national academies in developing countries also depend on impact factor rating, as in the West, scientists from these countries must publish in journals with a high impact factor rating, which may or may not be a true reflection of the capability of a scientist.

Nearly all the journals with high impact factor ratings are published in the West and, because they suffer from national publication bias, authors from

developing countries are at a disadvantage; a very vicious circle indeed. In my view, university authorities and scientific academies should think of ways to minimize the harmful effects of national publication bias and low impact factor. Editors of journals with a high impact factor rating may also have to change some of their policies to ensure that science remains free of national bias and is truly free and international in outlook.

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## Modern myth

SIR — You remark: "Perhaps biologists... look forward to the time when interesting questions can be answered" (*Nature* **352**, 11; 1991), in relation to Walter Gilbert's article (*Nature* **349**, 99; 1991)<sup>2</sup>, which includes the astonishing statement: "Thus I expect that... half of the total knowledge of the human organism will be available in five to seven years, and all of it by the end of the decade" (*Nature* **349**, 99; 1991). But it is not information we should seek, but understanding.

It is a modern myth that the DNA of an organism contains all the information necessary to produce that organism. This is not so. Some components of the body, such as the phospholipid bilayer and the structure of the mitochondrion, do not seem to be coded by genes, but are built onto structures transmitted in the cytoplasm of the ovum. Widely different morphologies can be produced from similar genomes, such as some castes of social insects, which depend on the physiological regime within which the genome is expressed. Similarly, correct expression of the information in the human genome depends on many aspects of the external environment and on all the myriad micro-environments created by the contortions of morphogenesis, to which multiple copies of the same genome become exposed in the cells of the embryo. The number of different expressions of one genome is potentially possibly infinite.

Although the complete sequencing of the human genome will be a very major achievement, with profound implications for the future health of mankind, it will fall very far short of making available all there is to be known about the human organism.

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