Merck, SmithKline and patents

SIR — The position Merck has taken — and publicly demonstrated — on the patenting of genes and gene fragments, as well as access to genomic-based inventions for use as research tools (clones, genes and their expressed proteins, and recombinant cell lines for example) has been broadly misrepresented by Dr George Poste from SmithKline Beecham Pharmaceuticals[1].

Merck & Co. Inc. recognizes a role for intellectual property protection for genomic inventions in the advancement of biomedical research and the development of new gene-derived therapeutics and diagnostics. But we draw an important distinction between the patentability of genomic inventions and the accessibility of patented genomic research tools to all scientists for research purposes — a distinction not recognized by Poste. Merck believes that patentability and accessibility are mutually compatible. Together, patents and appropriate access maintain incentives for commercial investment in genomic research, while promoting open exchange of scientific information, thereby speeding identification of disease-related genes and development of gene-derived therapies.

Poste misrepresents the Merck position when he states that "Merck claims that in most cases genes and ESTs [expressed sequence tags] are 'research tools' that should be placed in the public domain and should not be subject to patenting", inaccurately citing a publication in *Nature*[2]. This is not Merck's position, and furthermore confuses patentability with dissemination of basic scientific information.

Merck believes that the requirements of patentability for biotechnology inventions should be the same as for non-biotechnology inventions. Under US patent law, the invention must fall within the definition of patentable subject matter, and must be novel, non-obvious and have utility[3]. As Poste pointed out, patenting of genomic inventions, provided that function and utility are demonstrated, has been widely endorsed, and Merck wholeheartedly agrees. But, in line with patent law, Merck does not believe that patents should be awarded to either genes or ESTs for which the function or utility is speculative or prophetic.

The patent provision of the US Constitution clearly states its purpose, which is "[t]o promote the Progress of Science and the useful Arts, by securing for limited Times to Authors and Inventors the exclusive Right to their respective Writings and Discovers..."[4]. Granting patents to genes or gene fragments of unknown or speculative utility would turn this principle on its head, actually denying future inventors the exclusive rights to their discoveries. Thus patents granted for genes or gene fragments based on their unknown future potential would have a destructive impact on the incentives for the industry to research and develop new drugs and therapies based on genomics science. Scientists and financiers, public or private, could invest years of work and hundreds of millions of dollars to identify, say, the gene that expresses a protein that plays an important role in causing Alzheimer's disease only to find that this particular gene (or fragment thereof) had been locked up years earlier by a speculative patent.

Although Merck seeks patent protection for internally discovered basic research tools, it is a strategy to ensure our continued ability to use those research tools and assays without requiring rights from third parties. What Poste missed — and thus misrepresented — is our allied position on the accessibility of genomic inventions as research tools. Merck's policy is to negotiate non-exclusive licences for rights under patents to our internally discovered research tools for research purposes by academic scientists at no charge, and to industrial sector entities on reasonable terms as appropriate and consistent with the advancement of biomedical research. Merck's policy is clear and consistent with the principles of intellectual property protection.

In line with our policy, Merck, in 1994, initiated the Merck Gene Index project to develop a collection of human ESTs, with associated cDNA clones, as a resource publicly available to scientists in both the public and private sectors worldwide. This cooperative effort has already become the largest single contributor of sequence entries — currently more than 75% of the ESTs — to GenBank, the central repository of publicly available gene sequence information at the National Center for Biotechnology Information (NCBI). Curiously, Poste failed to include this contribution among his list of predominant databases of human genetic sequence data, although Craig Venter and his colleagues cited extensive data from the Merck Gene Index project in compiling their initial assessment of human gene diversity and expression patterns[5]. (At 15 April 1996, the Merck initiative had submitted 260,000 ESTs to the public database, from more than 150,000 clones to the public EST database, dbEST.)

The Merck Gene Index project, clearly distinguishing between patentability and accessibility, makes EST data freely available with the aim of promoting the unrestricted exchange of human genomic data, thereby accelerating the rate of discovery in genomics and, we trust, stimulating patentable inventions stemming from subsequent elucidation of the entire sequence, function and utility of the gene.

Interestingly, the National Center for Human Genome Research (NCHGR) recently issued a policy statement in support of this approach. The centre maintains that submitting sequence patent applications may have a chilling effect on research and development, stating that "raw human genomic DNA sequence, in the absence of additional demonstrated biological information, lacks demonstrated specific utility and, therefore, is an inappropriate material for patent filing".

Public access to sequence data will maximize the probability of discovery of new genes and their function by allowing all who wish to engage in healthy competition to convert that data into new therapeutics. Others, however, have chosen to lock up information about gene sequences and ESTs in the hope that they will have the scientific acumen and luck to translate sequence information into successful biotherapeutics. We may not know for a decade which approach will produce more 'winners': it is Merck's contention that broad and open access means a win for science and discovery, and ultimately, the future of health care.

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1. Poste, G. *Nature* **378**, 534–536; 1995.
2. Elliston, K. & Williamson, A. *Nature* **372**, 10 (1994).
3. 35 U.S.C. §§ 100–103.
4. United States Constitution, Article I, Section 8, Clause 8 (1789).
5. Adams, M.D. *et. al. Nature* **377** Suppl., 3–174 (1995).

BSE a specific bovine disease?

SIR — It has been postulated that BSE is not a variant of scrapie accidentally acquired by *Bos taurus* but more probably a specific bovine disease associated with cows.

Scrapie has been known for more than 200 years, but a French veterinary surgeon in southern France, M. Sarradet, described as early as 1883 "a case of scrapie in an ox" (*Rev. Vétérinaire* **3**, 310–312; 1883).

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