The *Discussion Forum* provides a medium for airing your views on any issues related to the pharmaceutical industry and obtaining feedback and discussion on these views from others in the field. You can discuss issues that get you hot under the collar, practical problems at the bench, recently published literature, or just something bizarre or humorous that you wish to share. Publication of letters in this section is subject to editorial discretion and company-promotional letters will be rejected immediately. Furthermore, the views provided are those of the authors and are not intended to represent the views of the companies they work for. Moreover, these views do not reflect those of Elsevier, *Drug Discovery Today* or its editorial team. Please submit all letters to Rebecca Lawrence, News & Features Editor, *Drug Discovery Today*, e-mail: Rebecca.Lawrence@drugdiscoverytoday.com

Gene patents: are they socially acceptable monopolies, essential for drug discovery? – Reply ▲

Initial letter: Williamson, A.R. (2001) *Drug Discov. Today* 6, 1092–1093

Response from Alan R. Williamson

The contributors to the debate stimulated by my article in the *Discussion Forum* [1] raise several points that I would like to respond to.

Are gene sequences too simple as intellectual property?

Jack Heinemann voices valid concerns about the weaknesses of gene patents [2]. He is right to stress the complexities that arise in defining a gene. However, the over-simple 'one-gene, one protein, one function' concept suits both those filing patents and those granting patents. No doubt more sophisticated filings will be made as the field develops. Heinemann raises several grounds for challenging patents that might occupy the courts in the future. (He might find himself called as an expert witness in such cases.) His list of the weaknesses of the gene patents that are currently being granted lends weight to my argument against them being granted. I maintain that it would be better to stem the flow of such patents now than to depend on the lengthy and expensive process of legal actions in the future.

Patent law does not have to be changed for gene patents

Richard Binns agrees with me that unduly broad claims should not be granted by patent offices [3]. I agree with him that patent law does not have to be changed for gene patents and I hope that we are both right in that regard. I was not calling for a change in the law in my claim [4] that 'society would benefit from immediate change in the *policy* of patent offices to limit the allowance of patents on genes to specified uses with only narrow claims'. Patent offices have changed their position on the criteria for granting gene patents but they have not moved far enough in my view. Although I welcome the new requirement set by the United States Patent and Trademark Office (USPTO) for evidence for 'specific, credible and substantial' gene function before granting a patent, time will tell how rigorously these criteria will be applied.

Are gene patents really so obvious?

The case for allowing a dominant claim to composition of matter of the DNA sequence of the gene remains weak. Isolation and sequencing of a piece of DNA is no longer a creative step. If one considers the complexities of gene definition raised by Heinemann then truly defining a gene might not be obvious. However, patents are being granted on DNA sequences based upon the primary criterion that they code for a protein that has some defined function. Binns is right to stress that functional characterization might not be routine, which is why I state that granting a patent that claims a defined gene use might be justified, but then only a use patent should be granted.

Gene patents give access to information

This is true, but the application of Bermuda Rules, the 24 h release policy for all sequence data generated by the publicly funded genome project, affords better access. The alternative to a gene patent would be a trade secret, which is precluded for publicly funded sequencing subject to Bermuda Rules and is highly unlikely to be of much use in industry given the available draft sequence of the human genome (approximately 50% finished sequence progressing to 100% by April 2003). In the unlikely event that a company could keep the identity of a gene sequence secret for long enough to produce specific compounds acting on the product of a gene, any patent claiming those compounds would need to disclose the nature of the gene; then isolation and sequencing of the gene would be obvious to any competitor.

Gene patents encourage scientific progress

A case can be made that gene patents have stimulated the biotechnology industry but, given the proven inventiveness of scientific founders, there would probably be an equally viable industry in the absence of gene patents. A large and thriving biotechnology industry existed before extensive gene patenting. I acknowledged that patents on genes encoding therapeutic products were important to the rise of the early

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biotechnology business, but I also pointed out that a composition of matter patent on the product of the gene would have sufficed.

The public Human Genome Project (HGP) was not driven by the desire for gene patents. The business plan for the commercial genome sequencing effort did include patenting of genes as a value generator, but it was not claimed to be the major reason for investment. Binns wonders whether the public HGP would have grown as rapidly without the stimulus of the commercial genome sequence project – probably not. The rapid escalation of the HGP to produce a draft sequence was debated in 1995 but it was considered to be premature [5]; full-scale production sequencing began in March 1999. The announcement of the commercial effort did help to accelerate the flow of funds to the HGP. There was also a reciprocal benefit to the commercial project that was able to incorporate all public sequence data, freely available from the Internet under Bermuda Rules, into their draft sequence. Only the public HGP will produce a finished sequence that will be the definitive version of the human genome sequence and the most useful source in which to search for novel drug targets.

Gene patenting maintaining competitiveness in the EU

I welcome the agreement from Patrick Nef [6] that developing drugs is sufficiently difficult that it is in the public interest that 'companies with exclusive rights on a particular gene target are ready to make them available to others for a reasonable fee'. I hope that we can look to Hoffmann-La Roche to set an example in this regard. Nef doubts that a policy of not granting gene patents in the EU would encourage pharmaceutical R&D in Europe. It would be interesting to know whether other EU pharmaceutical companies share his doubts.

I am not swayed from my argument that a lack of gene patents would not hurt pharmaceutical R&D. I do not think that Nef makes a good case for gene patents being value generators for pharmaceutical companies. Successful, patent-protected products are the only way for a pharmaceutical company to recover the huge costs of drug discovery and development. Freedom to explore any gene target would be assured in the absence of gene patents; secrecy is not a viable option for reasons stated previously. For academia few gene patents prove to have commercial value, whereas investors in biotechnology companies are more impressed by the 'value-added' to gene patents through genuine innovation.

Nef adds to Heinemann's list of grounds on which to challenge gene patents in the future. However, he rightly acknowledges the costly (and I would add complicated) nature of such a challenge in the courts. Nef points to key differences in the practice of granting gene patents in the EU versus the USA. This supports the view that we need a uniform treatment of gene patent applications worldwide.

References

1 Williamson, A.R. (2001) Gene patents: are they socially acceptable monopolies, essential for drug discovery? *Drug Discov. Today* 6, 1092–1093

2 Heinemann, J. (2002) Gene patents: are they socially acceptable monopolies, essential for drug discovery? – Reply. *Drug Discov. Today* 7, 23–24

3 Binns, R. (2002) Gene patents: are they socially acceptable monopolies, essential for drug discovery? – Reply. *Drug Discov. Today* 7, 102–103

4 Williamson, A.R. (2001) Gene patents: socially acceptable monopolies or an unnecessary hindrance to research? *Trends Genet.* 17, 670–673

5 International Human Genome Sequencing Consortium (2001) Initial sequencing and analysis of the human genome. *Nature* 409, 860–921

6 Nef, P. (2002) Gene patents: are they socially acceptable monopolies, essential for drug discovery? – Reply. *Drug Discov. Today* 7, 103–104

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Finding new antibiotics: the power of computational methods ▼

Antibiotics have been highly successful for the treatment of bacterial infections. Their extensive use, however, has led to the rapid evolution of antibiotic resistance. The antibiotics that are currently available act on a relatively small number of cellular processes such as protein synthesis or peptidoglycan biosynthesis. New agents that act on novel gene products within previously untargeted biochemical pathways would circumvent many of the known resistance mechanisms and provide new therapeutic options. How then, can this be accomplished?

An important question to be answered when choosing potential targets is whether the biochemical pathway to be targeted is unique to bacteria and, if so, how widespread is it among bacteria? A biochemical pathway that is common to both bacteria and humans is not ideal because of the potential for side effects. Similarly, the extent of conservation of a biochemical pathway between bacterial species will influence the spectrum of activity of the antibiotic to be designed. The large and rapidly increasing number of available microbial genome sequences is being used to answer these questions and thereby facilitate the identification of new bacterial targets for antibiotic development.

A powerful computational approach that uses bacterial genome sequence information is to compare the identified genes in all bacterial pathogens to determine which genes are shared by various species (see Read *et al.* [1] for a recent review). For example, a comparison of the sequences of the respiratory tract pathogens *Streptococcus pneumoniae*, *Haemophilus influenzae* and *Neiserria meningitidis* indicated that *S. pneumoniae* has a much greater capacity to utilize sugars than the other

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