

Rod photoreceptor rescue or degeneration

To the editor—We read with interest the article by Picaud and colleagues¹ in the October issue of *Nature Medicine*. Evidence of rod and cone photoreceptor rescue by 1-cis diltiazem was quantified using techniques of immunohistochemistry, electrophysiology and photoreceptor counting. Of note, the authors described a considerable photoreceptor rescue as demonstrated by opsin antibody staining, but only a moderate rescue as demonstrated by photoreceptor cell counts.

We have previously shown that an antibody against opsin that recognizes the N terminal of the opsin molecule (similar to the antibody used by Picaud *et al.*) labeled only the rod outer segments but not the perikarya of normal rod cells. However, in degenerating photoreceptor cells the rod perikarya were also labeled². We believe that the immunolabeling noted in this study¹ might represent degenerating photoreceptor cells and not surviving cells as claimed.

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Picaud and Sahel reply—Diltiazem was shown to slow down photoreceptor degeneration in the rd mouse, an animal model for retinitis pigmentosa¹. Rod cell numbers were quantified after cell labeling with the rho-4D2 antibody directed against rhodopsin. This quantification was possible because the antibody labeled surviving rod cell bodies. Given their own experience with a rhodopsin antibody that failed to label rod cell bodies², Edward and Tso suggest that these labeled cells were perhaps degenerating photoreceptors.

However, it has been reported previously that rod cell body staining is not obtained with all rhodopsin antibodies³ but that rho-4D2 antibody does label rod cell bodies in the normal retina³ and

in other conditions⁴. Therefore, we believe our rod cell count did estimate surviving photoreceptors and not degenerating cells.

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Celera: financial optimism, scientific skepticism

Genome sequencing pioneer Craig Venter last month left Wall Street bewitched, his critics bothered, and much of the press bewildered with news that his company, Celera Genomics, has placed sequence data in its database “covering 90% of the human genome.”

Celera’s shares were already in favor with investors who had, for the previous few weeks, been buying heavily into genomics companies as a potentially lucrative investment. Within hours of the announcement, the shares shot up in value by almost 40%, from what had already been a record high of \$186 to \$258, before settling back later in the day to \$242.

Those who argue that Venter’s ‘shotgun’ approach to sequencing has limitations that can best be met by close collaboration with publicly funded, clone-by-clone strategies claimed that their perspective had been vindicated. This was based on Venter’s admission that he had made heavy use of public data in reaching his self-declared “milestone.”

But many were left asking whether it was reasonable that whereas Celera—like the rest of the research community—enjoys free access to the public data, the arrangement is not reciprocal. A statement from the company, although confirming that it eventually anticipated all the data being published openly in the scientific literature, also emphasized that the data were being made available “under a non-redistribution agreement” to Celera database subscribers.

The mass media seems confused by the significance of the company’s statement that it had “compiled DNA sequence covering 90% of the human genome.” A number of newspaper articles, including, for example, one in the *Financial Times* of London, subsequently reported that the company “had mapped 90% of the human genome.” Some claimed that this gave it a substantial lead over publicly funded sequencing efforts, which are due to produce their own ‘rough draft’ of the genome in the summer. Few reported that this 90% included data obtained by Celera from the public databases, or that the company’s own sequenced databases—covering 81% of the estimated 3.2 billion base pairs—needed the public data to be properly ‘finished’.

Despite the reservations, the figures produced by Venter at his press conference were impressive. For example, he stated that the company’s statistical analysis and comparison with known genes suggested that “greater than 97% of all human genes are represented in our database” (even if, as others points out, some are present in highly fragmented form).

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