

## References

- 1 White, A.R. *et al.* (2003) Monoclonal antibodies inhibit prion replication and delay the development of prion disease. *Nature* 422, 80–83
- 2 Paramithiotis, E. *et al.* (2003) A prion protein epitope selective for the pathologically misfolded conformation. *Nat. Med.* 9, 893–899
- 3 Moroncini, G. *et al.* (2004) Motif-grafted antibodies containing the replicative interface of cellular PrP are specific for PrP<sup>Sc</sup>. *Proc. Natl. Acad. Sci. U. S. A.* 101, 10404–10409
- 4 Peden, A.H. *et al.* (2004) Preclinical vCJD after blood transfusion in a PRNP codon 129 heterozygous patient. *Lancet* 364, 527–529

# Abundant A-to-I editing in the human transcriptome

Nicole Johnston, [nicolejohnston@yahoo.com](mailto:nicolejohnston@yahoo.com)



RNA editing by ADAR (adenosine deaminases acting on RNA) enzymes convert adenosine to inosine (A-to-I) in precursor mRNAs and plays a crucial role in vertebrate and invertebrate development. If ADAR-mediated editing is knocked out, the organism dies. Evidence of this editing has been found in inflamed tissues, malignant gliomas, epileptic mice, suicide victims experiencing chronic depression, and in individuals with amyotrophic lateral sclerosis [1], implicating the process in a number of diseases.

## New targets

Previously, the glutamate and serotonin receptors were the only known ADAR substrates. Recently, however, a report from Compugen (<http://www.cgen.com>), based in Tel Aviv, Israel, describes identification of 12,723 A-to-I editing sites in 1637 different genes using computational methods. Among these, 26 novel

substrates were validated experimentally.

‘Previously, only two targets were known,’ says Compugen scientist and spokesman, Eli Eisenberg. ‘But there are three different enzymes that do that editing,’ he explains. ‘It can’t be that three enzymes only have two targets. Other evidence suggests that there are many more editing sites.’

## Hunting for novel substrates

Putting that theory to the test, bioinformatics specialists at the company developed a computational approach designed to overcome recognized difficulties associated with identifying unknown ADAR substrates.

ADAR substrates consist of imperfectly matched dsRNA stems that are formed when an exon containing an adenosine to be edited base pairs with a complementary region of pre-mRNA, which can be thousands of nucleotides apart. Compugen’s approach entailed searching for mismatches in potential double-stranded regions. Human expressed sequence tags (ESTs) and cDNAs were aligned with the genome and organized into gene groups and partial gene groups. The algorithm they developed then honed the search for A-to-I editing sites.

In humans, they discovered that editing sites are typically found in noncoding regions of RNA, particularly among Alu

repeats, transposable elements unique to primates and responsible for >10% of our genome. Two Alu regions oppositely oriented within a gene can form dsRNA. The ADAR enzyme recognizes the dsRNA stem and then changes some of the adenosines to inosines.

‘The editing prefers to attack sites that are not perfectly paired... and is related to the stability of the dsRNA,’ explains Eisenberg. Furthermore, it was found to occur in a variety of organs. ‘A couple of years ago, this was thought to be restricted to the nervous system – all edited mRNAs before were found in the brain,’ says biologist Gordon Carmichael, also at the University of Connecticut Health Center, Farmington, Connecticut, USA (<http://www.uchc.edu>). ‘This shows us that [this RNA editing] is way more prevalent and it’s in messages we didn’t think it would be in.’

The Compugen team reasons that such widespread editing contributes to greater diversity of the human transcriptome than could be achieved by alternative splicing alone.

But Robert Reenan, a biologist also at the University of Connecticut Health Center, suspects that stability might not be solely responsible. ‘It certainly is possible that, rather than just reflecting an effect on the stability of the RNA secondary structure, that it’s a reflection of the enzyme’s preference,’ he says.

**Broad impact**

Nonetheless, the findings are being hailed a significant discovery. 'This is really a tremendous contribution in terms of identifying additional candidate substrates,' says Charles

Samuel, a biologist at the University of California in Santa Barbara, USA (<http://www.ucsd.edu>).

'RNA editing is significantly broader in its biological impact than we thought,' adds Carmichael. 'It's not

just a local phenomenon, it's a broad one.'

**Reference**

- 1 Levanon, E.Y. *et al.* (2004). Systematic identification of abundant A-to-I editing sites in the human transcriptome. *Nat. Biotechnol.* 22, 1001–1005

# Promising Phase I results against new HIV target

Jo Whelan, [jo.whelan@tiscali.fr](mailto:jo.whelan@tiscali.fr)

The first in a new class of potential antiretroviral drugs known as maturation inhibitors has shown promising results in early Phase I clinical trials. PA-457 acts against a different viral target from existing HIV treatments, and could therefore be useful against the increasing problem of drug-resistant HIV isolates.

'This compound seems to work by a brand new type of mechanism,' says Christopher Aiken of Vanderbilt University School of Medicine (<http://www.vanderbilt.edu>), whose lab is working on the antiviral action of betulinic acid derivatives. 'It is apparently not targeting the protease, but is inhibiting maturation by specifically blocking the cleavage of one of the sites in the Gag protein. This is a very vulnerable Achilles' heel for HIV, because if you block it then the virus is really crippled, and that is why the compound is so potent *in vitro*.'

**Specific**

PA-457 (3-O-(3',3'- dimethylsuccinyl)-betulinic acid) is thought to disrupt a late step in the processing of the viral protein known as Gag, preventing the capsid precursor protein (p25) from being converted to the mature capsid protein (p24) [1]. Specifically, cleavage of the proteins SP1 and CA at their junction site in the Gag precursor

PR55<sup>Gag</sup> is delayed, causing an intermediate protein to accumulate [2]. SP1 is essential for the correct formation of the viral capsid, and failure to release it means that the cores of virus particles shed from HIV-infected cells are mis-shapen and non-infectious.

As yet there is no direct evidence that PA-457 binds to Gag. 'There is a lot of indirect evidence that it does, but no one has yet convincingly demonstrated its effect in a cell-free system,' says Aiken. 'However, it is very specific to HIV-1, so we know it is not a general cytotoxic effect that is blocking viral activity. It may be that the compound is activated by modification within the cell.'

**Clinical trials**

PA-457 strongly inhibits the replication of wild-type and drug-resistant strains of HIV-1 *in vitro* [1]. Resistance to currently approved antiretroviral drugs is increasingly common: an estimated 5–10% of infected people are resistant to all available reverse transcriptase and protease inhibitors, and this group is growing rapidly. Because it acts on a different viral target, researchers are optimistic that PA-457 might provide a new treatment option for resistant strains. 'It is promising because the sequence that the drug appears to be targeting is extremely highly conserved in HIV-1 isolates,' Aiken comments.

'Even if this compound turns out to have disadvantages, there may be others that can hit the same target.'

PA-457 is being commercialized by Panacos Pharmaceuticals, Gaithersburg, Maryland (<http://www.panacos.com>). In a preliminary Phase I clinical trial, reported by Panacos at the XV International AIDS Conference in Bangkok in July 2004, it showed good oral bioavailability and favourable pharmacokinetics, suggesting that it will be suitable for once-daily oral dosing. It was also well tolerated at all the doses given (up to 250 mg as a single oral dose). Panacos also presented preclinical studies which it says suggest that PA-457 is unlikely to cause drug–drug interactions when given in combination with currently approved HIV therapies. A multiple-dose Phase I study is now underway in uninfected volunteers, and Panacos anticipates that a Phase II study in HIV-infected patients will begin before the end of 2004.

**References**

- 1 Li, F *et al.* (2003) PA-457: A potent HIV inhibitor that disrupts core condensation by targeting a late step in Gag processing. *Proc. Natl. Acad. Sci. U. S. A.* 100, 13555–13560
- 2 Zhou, J. *et al.* (2004). The sequence of the CA-SP1 junction accounts for the differential sensitivity of HIV-1 and SIV to the small molecule maturation inhibitor 3-O-(3',3'-dimethylsuccinyl)-betulinic acid. *Retrovirology* 1, 15