

then determined the directions of individual magnetic moments using a technique known as magnetic force microscopy. Statistical analysis of these directions confirmed that a spin-ice state, characterized by a preponderance of the two in, two out configuration, had indeed been created.

Conventional spin ice lends itself well to experimentation. Its disordered spin arrangements have been imaged by neutron scattering, and applying magnetic fields to it has revealed disordered phases that respond to neutron scattering and bulk measurements as if they consisted of stacks of independent chains or sheets — so as if they have only one or two dimensions, rather than three. Phase transitions that, like the liquid–liquid or liquid–gas transitions in more complex matter, involve no change in structural symmetry have also been observed<sup>6</sup>. In such ‘symmetry-sustaining’ transitions, what is ordered remains ordered, and what is disordered remains disordered.

But experiments on conventional spin ice raise interesting questions. First, what is the true origin of the two in, two out rule? The dipolar interaction between magnetic moments is long-range, so any explanation that considers only near neighbours must be incomplete. This question has largely been answered: remarkably, the standard model of spin ice predicts that the two in, two out rule emerges from the many-bodied dipolar interaction of some  $10^{23}$  magnetic moments<sup>7,8</sup>. Second, is there a ‘true’ ordered ground state (Fig. 1d)? The question is also pertinent to normal ice<sup>9</sup>, as such a minimum-energy state is required by the third law of thermodynamics, which states that entropy approaches zero as temperature tends to absolute zero. An ordered ground state is also predicted by the standard model of spin ice, but is not observed experimentally. Finally, what microscopic factors drive phase transitions in an applied magnetic field? This question, too, remains essentially open.

Artificial spin ice could, in principle, help to supply further insight into these problems. It could, for example, be engineered to have different, controllable interactions and then be subjected to temperature changes or magnetic fields to mimic the behaviour of conventional spin ice. Direct imaging with magnetic force microscopy could be used to identify and understand individual defects in the spin-ice state. Such defects (Fig. 1c) cannot be imaged by neutron scattering on conventional spin ice, but might be crucial in determining its properties.

Bringing spin ice to room temperature could also inspire technological applications. In magnetic-memory media, information is encoded into the magnetic moments of ferromagnetic grains. The drive to increase the density of memory bits in such media will mean smaller, more strongly magnetized elements that are more closely spaced<sup>10</sup>. This trend will amplify the dipolar interaction and its consequences<sup>11</sup>. Experiments with spin ice,

however, show how to create a dense array of magnetic elements, which, although they interact, retain many states in which information could potentially be encoded.

This is for the future. As a replica of conventional spin ice, artificial spin ice is not perfect: the two in, two out configuration is maintained only approximately, and the system should actually prefer an alternative, ordered state<sup>12</sup> (Fig. 1d). Its failure to find this state might reflect the inefficiency of the energy-minimization protocol involving magnetic field cycling. Despite its limitations, however, Schiffer and colleagues’ invention<sup>1</sup> does emphasize the potential of designed magnetic arrays, not only as model systems for the study of disorder, but also as the basis of technological applications. ■

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1. Wang, R. F. *et al.* *Nature* **439**, 303–306 (2006).
2. Harris, M. J., Bramwell, S. T., McMorrow, D. F., Zeiske, T. & Godfrey, K. W. *Phys. Rev. Lett.* **79**, 2554–2557 (1997).
3. Ramirez, A. P., Hayashi, A., Cava, R. J., Siddharthan, R. & Shastry, B. S. *Nature* **399**, 333–355 (1999).
4. Pauling, L. *J. Am. Chem. Soc.* **57**, 2680–2684 (1935).
5. Lieb, E. H. *Phys. Rev. Lett.* **18**, 692–694 (1967).
6. Sakakibara, T., Tayama, T., Hiroi, Z., Matsuhira, K. & Takagi, S. *Phys. Rev. Lett.* **90**, 207205 (2003).
7. Melko, R. G. & Gingras, M. J. P. *J. Phys. Cond. Mat.* **16**, R1277–R1319 (2004).
8. Isakov, S. V., Moessner, R. & Sondhi, S. L. *Phys. Rev. Lett.* **95**, 217201 (2005).
9. Singer, S. J. *et al.* *Phys. Rev. Lett.* **94**, 135701 (2005).
10. Moser, A. *et al.* *J. Phys. D* **35**, R157–R167 (2002).
11. Martin, J. I. *et al.* *J. Magn. Magn. Mater.* **256**, 449–501 (2003).
12. De’Bell, K., Maclsaac, A. B., Booth I. N. & Whitehead, J. P. *Phys. Rev. B* **55**, 15108–15118 (1997).

## CANCER BIOLOGY

# Signatures guide drug choice

Julian Downward

**Cancer drugs are increasingly designed to target specific cell-signalling pathways. When, and in what combination, these drugs should be used might be judged by analysing the gene expression signature of the tumour.**

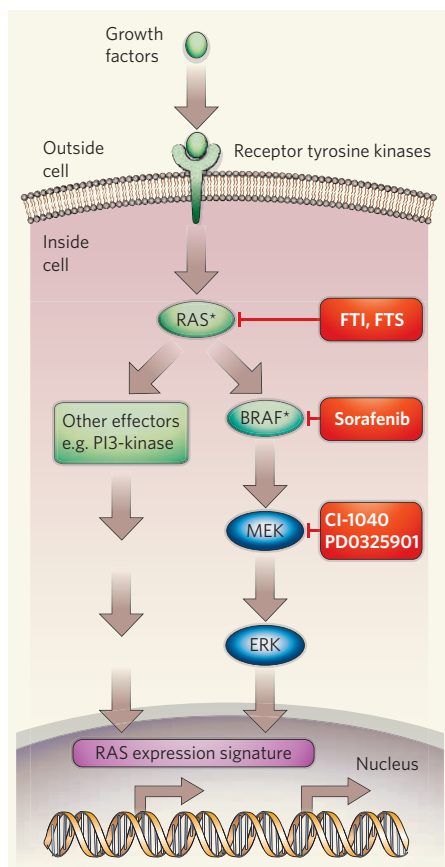
Current approaches to the design of drugs against cancer assume that almost all tumours escape normal growth regulation by usurping a few of the dozen or so key cell-signalling pathways. However, pathways can be activated at different points, so it is not always easy to tell which signalling mechanism has been activated by looking for mutations in known cancer-associated genes (oncogenes, or tumour-suppressor genes). If the gene at the top of a signalling cascade is unaffected, for instance, one cannot assume that the pathway is not involved, as a factor further downstream might have been activated. It can thus be hard to predict the best treatment for a particular tumour. Two papers in this issue<sup>1,2</sup> address this problem in different ways, and provide a potential strategy for choosing the most effective combination of therapies based on the gene expression signature of a tumour.

Tumour cells seem to rely heavily on the continued activation of one or two pathways — a phenomenon termed oncogene addiction — whereas normal cells use a broader range of signals<sup>3</sup>. This, combined with the damage accrued through the reckless lifestyle of the cancer cell, provides an Achilles’ heel that might be exploited therapeutically by targeting pathways activated by oncogenes such as RAS, SRC and MYC. The RAS pathway (Fig. 1), for example, can be activated in many different ways in tumours, including mutation of the RAS oncogene itself (seen in 40% of lung

cancers) and of the BRAF oncogene, the next factor in the pathway (mutated in some 60% of melanomas)<sup>4</sup>. Thus, looking for evidence of an initiating mutation can make it hard to identify all tumours in which this pathway has been activated.

Equally, looking for a single downstream indicator of pathway activation, such as phosphorylation of the enzyme ERK (one of the final steps in the RAS pathway), can also be problematic. Negative feedback loops, such as the induction of phosphate-removing enzymes that target ERK, can attenuate the steady-state phosphorylation of ERK. In addition, branching of the pathway can mean that other targets might be more important in certain circumstances (Fig. 1).

One step in the RAS pathway that is being targeted by candidate drugs is MEK, an enzyme that is directly activated by BRAF, and that is thought to be responsible for much of the downstream signalling from RAS (Fig. 1). To see whether MEK inhibitors could be useful for treating all tumours with aberrant RAS signalling, Solit *et al.* (page 358)<sup>1</sup> tested human tumour cell lines carrying mutations in BRAF or RAS for sensitivity to these drugs. Cells bearing an activating BRAF mutation were extremely sensitive to MEK inhibitors, both *in vitro* and when transplanted into immunodeficient mice. By contrast, cells with an activating RAS mutation showed much lower and more variable sensitivity to these inhibitors.



**Figure 1 | Oncogene activation, transcription signatures and drug sensitivity.** Growth factors activate RAS through receptor tyrosine kinases, leading to stimulation of the BRAF, MEK and ERK cascade, but also of other pathways, including that involving phosphatidylinositol (PI) 3-kinase. Activation of the RAS pathway in tumours can occur through mutation or overexpression of the components shown in green. Bild *et al.*<sup>2</sup> define unique gene expression signatures for five oncogenic pathways, including that for RAS. These can be used to assess the level of activity of each pathway in a cancer cell and the sensitivity to drugs targeting those pathways (red). Solit *et al.*<sup>1</sup> show that activating mutations (\*) in BRAF make the cells sensitive to inhibitors of MEK, whereas those in RAS do not, presumably because it can signal through an alternative pathway.

The fact that the mutational status of BRAF predicts sensitivity to inhibition of MEK suggests that all oncogenic signalling from BRAF is mediated through the activity of its direct target MEK. However, signalling from RAS bifurcates to several downstream targets in addition to BRAF and MEK, including key pathways such as that involving phosphatidylinositol 3-kinase. Thus, inhibition of MEK may not be sufficient to inhibit cell proliferation triggered by these pathways, at least in some situations<sup>5</sup>. The clear implication is that the MEK inhibitors being developed as potential drugs<sup>6</sup> should be tested on tumours bearing activating BRAF mutations, such as melanomas, and not on tumours with activating RAS mutations, such as pancreatic and lung carcinomas. Indeed, the mutational

status of BRAF should be used to stratify patients in any such trials.

What, then, of situations in which pathway activation might not be caused by a single oncogenic mutation? Bild *et al.* (page 353)<sup>2</sup> used microarrays to analyse the gene expression profiles of human mammary epithelial cells in which five key oncogenic pathways had been activated — by mutational activation of the MYC, RAS, SRC or  $\beta$ -catenin proteins, or by loss of the Rb tumour-suppressor gene. In each case, the authors defined a signature of a hundred or so genes whose expression correlated with activation of the specific pathway.

Similar individual signatures have been characterized before<sup>7–10</sup>, but here Bild *et al.* used them simultaneously to analyse the activation state of each of the pathways in a range of human and mouse tumours. The signatures successfully predicted the activating mutation in several mouse models of cancer and in human lung cancers bearing RAS mutations. In addition, predictions of the degree of deregulation of each pathway could be used as a basis for categorizing tumours into clusters that showed marked correlations with clinical outcome. For example, in lung cancer, deregulation of MYC, RAS, SRC and  $\beta$ -catenin together correlated with particularly poor patient survival.

The signatures for RAS and SRC pathway activation accurately predicted the *in vitro* sensitivity of a broad range of human tumour cell lines to drugs targeting the mutationally activated versions of these proteins. However, the RAS signature did not correlate with the levels of activated RAS protein in the cell, presumably because the same signature of gene

expression can be achieved by activation of upstream or downstream components of the pathway. One might conclude that analysis of gene expression signatures is a more reliable predictor of pathway activation across different tumour types than analysing the mutation state or expression level of a given oncogene. This would be particularly true for complex branching pathways such as the RAS one.

So from a single microarray (which can analyse the expression levels of all the genes involved at once) it should be possible to determine the extent to which different signalling pathways are activated and what combination of pathway-specific drugs might, where available, be most effective. In favourable cases, such as those in which BRAF is mutated, the state of a single oncogene may be sufficient to predict response to a single drug, although this will probably be the exception rather than the rule. The foundations may have been laid for the development of truly rational combination therapies for multigene cancers. ■

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1. Solit, D. B. *et al.* *Nature* **439**, 358–362 (2006).
2. Bild, A. H. *et al.* *Nature* **439**, 353–357 (2006).
3. Weinstein, I. B. *Science* **297**, 63–64 (2002).
4. Downward, J. *Nature Rev. Cancer* **3**, 11–22 (2003).
5. Mao, J. H. *et al.* *Genes Dev.* **18**, 1800–1805 (2004).
6. Sebolt-Leopold, J. S. & Herrera, R. *Nature Rev. Cancer* **4**, 937–947 (2004).
7. Neiman, P. E. *et al.* *Proc. Natl Acad. Sci. USA* **98**, 6378–6383 (2001).
8. Huang, E. *et al.* *Nature Genet.* **34**, 226–230 (2003).
9. Pavay, S. *et al.* *Oncogene* **23**, 4060–4067 (2004).
10. Sweet-Cordero, A. *et al.* *Nature Genet.* **37**, 48–55 (2005).

## ATMOSPHERIC CHEMISTRY

# Biogenic bromine

Ross J. Salawitch

**Among other effects, bromine released by biological processes in the oceans apparently reduces ozone levels in the troposphere. This source may be a link between atmospheric composition and climate change.**

Bromine compounds from organic halogens (halons) used in fire extinguishers and from methyl bromide, which has anthropogenic and natural sources, cause about half of the chemical loss that results in the Antarctic 'ozone hole' in the stratosphere. Low levels of ozone in the atmosphere's lowermost layer, the troposphere, during the polar spring result from bromine released from melting sea ice and 'frost flowers'. But it is also becoming evident that bromine produced by natural processes in the ocean can influence the composition of both the troposphere and the stratosphere. Much research is being devoted to understanding the sources and sinks of

these organic bromine compounds, and their effects in the atmosphere.

Yang *et al.*<sup>1</sup>, for example, writing in the *Journal of Geophysical Research*, present simulations of how the troposphere is affected by the inorganic bromine molecules that are released when biogenic organic bromine decomposes. They calculate that levels of tropospheric ozone are reduced by 5–30%, depending on location and season, relative to a simulation that does not take bromine into account. Two mechanisms are involved. One is the direct catalytic loss of ozone in a reaction involving bromine monoxide (BrO). The other is reduced production of ozone; this is caused