

A wet and altered Mars

John F. Mustard

Has Mars always been cold and dry or was it once warm and wet? Reanalysis of spacecraft data reveals a signature from the surface rocks that indicates their composition has been altered in the presence of water.

Two years ago, Bandfield *et al.*¹ published interpretations of data from an instrument on the Mars Global Surveyor spacecraft that caused many planetary scientists to rethink their ideas about the geological evolution of the red planet. On page 263 of this issue, Wyatt and McSween² describe how they have reinterpreted the same data and arrived at a fundamentally different view. So what's going on?

Bandfield *et al.* reported that the mineralogy of volcanic regions on Mars was best explained by the existence of two very different rock types — basalt in the southern highlands and andesite in the northern plains. The mineral make-up of a volcanic rock reflects the composition of its source region and whether it has undergone melting or crystallization. On Earth, basalt (which is dominated by the minerals plagioclase and high-calcium pyroxene) is the typical rock of the ocean floor; it is formed by partial melting of mantle rocks beneath the Earth's crust and extrusion of the melt to the surface. Andesite, a more silica-rich rock, is most commonly formed by partial melting of mantle in the presence of the water released as oceanic crust descends into the mantle along subduction zones.

Bandfield and colleagues' conclusion, that there are large areas of both andesite and basalt on Mars, precipitated a number of questions. Has recycling of crust occurred on

Mars? Are there significant quantities of water in the mantle? Are the mineralogical divisions due to some other magmatic process?

Wyatt and McSween's reinterpretation² of the data leads to a very different, but no less intriguing, conclusion. Their calculations also produce a mineralogy that is consistent with basalt for the southern highlands. But for the northern plains, their inferred composition consists of typical basalt minerals plus clays and sheet silicates that are characteristic of low-temperature aqueous alteration — in other words, basalt weathered in the presence of water. It happens that the distribution of this altered basalt corresponds well with the vast areas of the northern plains in which water, debouched from enormous outflow channels that emanate from the southern highlands, may once have been concentrated into an ocean (Fig. 1)^{3,4}. The spatial coincidence is not perfect, and there are concentrations of altered basalt in the southern highlands that are not correlated with enclosed basins or water-related features. Yet the association is strong enough to take the implications seriously.

If Wyatt and McSween's solution is correct, a key question is when the basalt alteration took place. The timing would affect the specific mineralogy of the alteration, as well as the prospects for potential habitats for life. If the volcanic material was erupted into an ocean (or ice, if the ocean was

frozen), then we might expect copious hydrothermal activity to have occurred, which would have provided abundant energy sources and habitats for life. Furthermore, the alteration could have been widespread in places and penetrated deep into the crust. If, on the other hand, the oceans were created well after the volcanic rocks were in place, then without heat sources the amount of chemical exchange would have been far less. In this case, the alteration would have been relatively weak and mainly confined to the surface, and the habitats for life would have been far less favourable.

A third alternative is that the altered basaltic rocks are sedimentary in origin, with the alteration occurring at some unspecified time and location upstream from the basin, and the altered rocks subsequently being transported to their present location. In this case, the association of the altered basalt with the ocean basin would be purely a consequence of sediment transport. Certain geomorphological features in the northern plains suggest that interaction between volcanoes and water or ice may have occurred. But these features are sparse relative to the extent of alteration mapped by Wyatt and McSween². So the question of when and how the alteration occurred remains unresolved.

One might ask how such distinctly different conclusions^{1,2} can be derived from the same data set. The analyses were conducted with spectra acquired by the thermal emission spectrometer (TES) on Mars Global Surveyor, which is still in operation. Crystal-lattice vibrations in minerals modify the thermal emission spectra from surfaces in distinct ways that can be used to identify minerals and their mixtures. However, the signature from the surface of Mars is relatively weak and, compared to that from terrestrial rocks, bland. As Wyatt and McSween show², there are several possible solutions for the TES observations that fit the data equally well. Which is the right one? In fact, the solutions differ only subtly. It turns out that high-silica glass and some clay minerals have very similar spectral properties in the TES wavelength range. Bandfield *et al.* used the glass spectra, Wyatt and McSween did not. But this made a big difference to the interpretations of rock type and thus of geological history.

One source of uncertainty in these new results is that the surface of Mars is quite commonly covered to a variable extent by mobile materials such as dust and sand. True exposures of the crust are rare, although abundant rocks of likely local origin were observed at the Viking landing sites, which are in the northern plains. Poleward of 30°, both north and south, there is a patchy and discontinuous layer of cemented dust and soil, 1–10 m thick, which was formerly ice-rich⁵. This layer becomes more continuous with latitude, until it covers most of the

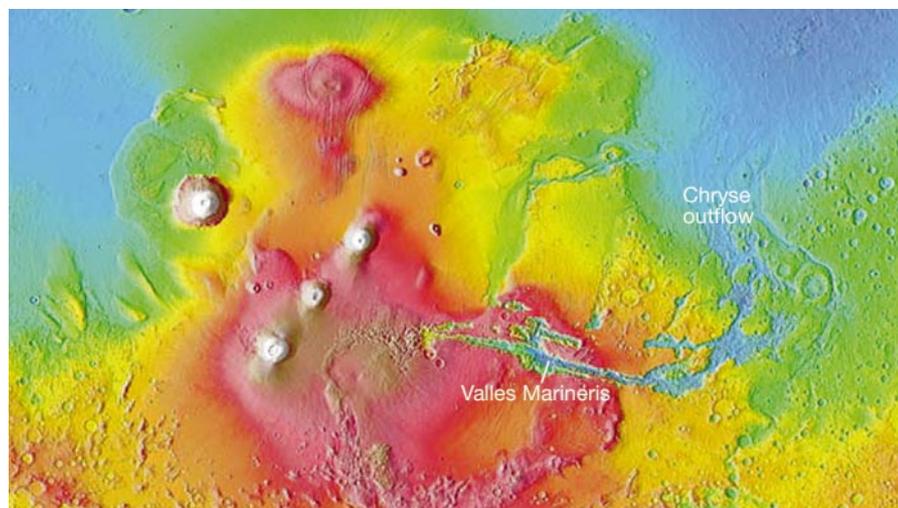


Figure 1 Mars in relief. This shaded topographic map is of the part of Mars known as the Tharsis province, and shows the major volcanoes, the Valles Marineris and the Chryse outflow regions. Colour indicates elevation, where blue is lowest and white is highest. Wyatt and McSween² report that volcanic rocks in the northern plains (blue) have been altered in the presence of water, whereas those in the southern highlands have not.

surface at latitudes above 60° (ref. 6). Water in this layer may be responsible for the alteration suggested by Wyatt and McSween, and poleward of 60° may obscure the signatures of the underlying bedrock.

To see beneath the mantle, we need to measure spectra from isolated, small exposures of bedrock, and that is not possible with the current generation of sensors, which offer only coarse spatial resolution. However, a new series of sensors, with increased spatial resolution and covering complementary wavelength regions, is scheduled to fly to Mars in 2003–2006. By combining all these

sources of data, it should be possible to identify true exposures of the martian crust and determine their mineral compositions. ■
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1. Bandfield, J. L., Hamilton, V. E. & Christensen, P. R. *Science* **287**, 1626–1630 (2000).
2. Wyatt, M. B. & McSween, H. Y. Jr *Nature* **417**, 263–266 (2002).
3. Parker, T. J. *et al.* *J. Geophys. Res.* **E98**, 11061–11078 (1993).
4. Head, J. W. *et al.* *Science* **286**, 2134–2137 (1999).
5. Mustard, J. F., Cooper, C. D. & Rifkin, M. L. *Nature* **412**, 411–414 (2001).
6. Kreslavsky, M. A. & Head, J. W. *J. Geophys. Res.* **E105**, 26695–26711 (2000).

Cancer

New-age tumour suppressors

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The discovery of a gene that is inactivated in stomach cancers illustrates the value of mouse models for finding tumour-suppressor genes that are switched off by mechanisms other than mutation.

Tumour-suppressor genes form a crucial part of our natural anticancer defences. When these genes become inactive, tumours often develop. Most cells have two copies (alleles) of every gene, and the classical view of a tumour suppressor is that loss of function only occurs when both copies are inactivated genetically. First, a mutation takes place in one allele in a developing tumour cell; next, the remaining normal allele is knocked out by 'loss of heterozygosity' (LOH) — the cell loses a large part of the chromosome on which the normal allele resides¹.

These ideas led to the discovery of a whole generation of tumour suppressors, including the well-known retinoblastoma protein and p53 (see ref. 2 for a review). However, although LOH is often seen in certain chromosomal regions in human and mouse cancers, the rate of discovery of the tumour suppressors in those regions seems to have slowed substantially. This may be because many tumour-suppressor genes take alternative routes to inactivation. Writing in *Cell*, Li *et al.*³ describe how they identified *RUNX3* — which they find to be switched off in human gastric cancers — as just such a gene.

Why have the new-generation tumour suppressors been so difficult to identify? One reason may be the strategy that is typically used: find the characteristic region of LOH in a particular tumour; narrow down that region as much as possible by 'deletion mapping'; and hunt for inactivating mutations within genes in the corresponding region on the matching, undamaged chromosome. This allows the discovery of classical tumour suppressors, which have genetic alterations in both alleles. But tumours are more resourceful than we once thought, and as well as genetic mechanisms, they use an

armoury of epigenetic mechanisms (which do not involve irreversible changes in DNA) to silence genes that impede rapid cell growth. For example, we now know that tumour-suppressor genes can be silenced by mechanisms such as the reversible modification of the regulatory promoters with methyl groups, either on both alleles, or on just one when the other has been deleted⁴.

In addition, there may be not one but several genes with overlapping functions within the LOH region of interest. One example of this might be provided by a region on human chromosome 3 that is frequently lost in lung tumours⁵; pinpointing the critical gene in this section has proved extremely difficult. A strong candidate is infrequently mutated but is often silenced by promoter methylation⁶. To add to this already complicated scenario, 'haploinsufficient' tumour-suppressor genes show loss of function after only one of the two alleles is altered⁷. This raises the spectre of large regions of LOH containing many genes, with one or more key genes being haploinsufficient and therefore hard to find by traditional means, because the corresponding alleles on the undamaged chromosome are not necessarily mutated. Clearly we need to find other approaches.

Functional studies in mice are proving extremely useful here, and lie behind the clever detective work of Li *et al.*³. *Runx1*, *Runx2* and *Runx3* are related mouse genes that encode gene-transcription factors with an impressive list of alternative names and functions⁸; for example, their human counterparts are known to be involved in leukaemias and certain congenital abnormalities. Li *et al.* studied the precise role of *Runx3* by knocking out the gene in mice.

They found that the *Runx3*-deficient

animals died shortly after birth, probably because they couldn't feed properly — the epithelial cells that made up their stomach lining had multiplied excessively. In other words, *Runx3* is involved in keeping cell numbers under control, a typical feature of a tumour suppressor.

A similar effect is seen in mice that lack the transforming growth factor- β 1 (TGF- β 1) protein, which controls cell numbers by inhibiting cell proliferation and inducing cell death. This fact — together with the finding that Smad proteins, which transmit cellular signals coming from TGF- β s, interact directly with the Runx proteins⁹ — led Li *et al.* to investigate the TGF- β 1 signalling pathway in cells from the *Runx3*-deficient mice. The TGF β 1-induced inhibition of proliferation was only modestly affected in *Runx3*-deficient gastric epithelial cells. But the ability of TGF- β 1 to induce cell death was strongly impaired. Moreover, when the authors reintroduced a functional copy of the *Runx3* gene into gastric tumour cells that lacked the protein, tumour growth was inhibited — a strong sign that the authors had identified a gene that suppresses gastric cancers in mice.

Li *et al.* also looked at the expression of the human *RUNX3* gene in patients with gastric cancer. They found that the loss of function of this gene — as a result of deletion of one allele followed by methylation-induced silencing of the other — correlated with the progression of cancer, with all of the eight most advanced tumours studied showing deletions. But the authors' search for the mutational hallmarks of a classical tumour-suppressor gene was unsuccessful. They detected just one *RUNX3* mutation, a 'missense' mutation that alters the encoded protein's structure but may leave some of its functions intact, in 119 tumours. So *RUNX3* is by no means a classical tumour suppressor.

In humans, *RUNX3* is located on the short arm of chromosome 1, in a region designated 1p36 that has long been of interest to cancer researchers. Is *RUNX3* the critical tumour-suppressor gene in this region? No doubt studies of gene expression and promoter methylation, and mutation hunting, will soon provide the solution. In the meantime, there are other questions to answer, not least how *RUNX3* works to keep cell numbers in the stomach under control.

The interaction between the RUNX and SMAD proteins, downstream targets of TGF- β signalling, may be important here. But the answer will not be straightforward. Although SMAD proteins can inhibit cell proliferation, they also induce tumour invasion and metastasis^{10,11}. Moreover, in genetically engineered animal models, TGF- β can inhibit early stages of tumour development but stimulate later tumour progression and metastasis¹⁰. Perhaps the loss of *RUNX3* blocks some of the inhibitory