

Now that both charm and beauty particles have been discovered, the Kobayashi–Maskawa theory has become an integral part of the standard model, although several of its predictions are still being tested. One was proved correct last year: the neutral beauty mesons and their antiparticles mix together just as the neutral kaons do (see my report in News and Views, *Nature* 329, 394; 1987). The crucial test will be to produce particles containing the sixth quark — ‘truth’ or ‘top’.

But the ratio of  $\eta_{00}$  to  $\eta_{+-}$  is also very important. Superweak theory predicts equality, with only a slight mixing of CP-odd in the  $K_S^0$  wavefunction and of CP-even in the  $K_L^0$  given by a mixing parameter  $\varepsilon$  which is known to be non-zero (see Fig. 1). Kobayashi–Maskawa theory predicts CP violation both in the wavefunctions and directly in the decay process, via a parameter  $\varepsilon'$  which is zero in superweak theory. The decay rates are modified so that  $\eta_{00} = \varepsilon - 2\varepsilon'$ ;  $\eta_{+-} = \varepsilon + \varepsilon'$ .

The problems of measuring a difference between  $\eta_{00}$  and  $\eta_{+-}$  are formidable. Each CP-violating decay of  $K_L^0$  to two pions is masked by 3,000 normal  $K_L^0$  decays. Experiments need large statistics, and extremely clean identification of the two-pion final states to reduce systematic errors caused by contamination from CP-conserving decays. The CERN NA31 collaboration (and a competing collaboration at Fermilab, Chicago; Woods, M. *et al.*, *Phys. Rev. Lett.* 60, 1695; 1988) uses proton beams with hundreds of gigaelectron volts of energy to produce fast kaons whose decay products travel forward, close to the beam direction, inside a long vacuum tank with a detector at the end. At these high energies a single detector can measure charged pions and the  $\gamma$ -rays from neutral pions with good precision, and at the same time identify and reject electrons, muons and extra pions from the unwanted decays.

Using samples of one million  $K_L^0 \rightarrow \pi\pi$  and 10 million  $K_S^0 \rightarrow \pi\pi$  decays, the CERN group finds  $\eta_{00}/\eta_{+-} = 0.980 \pm 0.004$  (statistical)  $\pm 0.005$  (systematic); or the real part of  $\varepsilon'/\varepsilon = (3.3 \pm 1.1) \times 10^{-3}$  (with combined errors). This is only three standard deviations away from equality of  $\eta_{00}$  and  $\eta_{+-}$ , but in close agreement with predictions from Kobayashi–Maskawa theory. Figure 2 shows how the errors on the real part of  $\varepsilon'/\varepsilon$  have been reduced in successive experiments since 1972. Further improvements are still needed, of course, both to confirm this result and to measure the size of the phase angle in Kobayashi–Maskawa theory which fixes the strength of CP-violation and which is one of the basic parameters in the standard model. □

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## Ore deposits

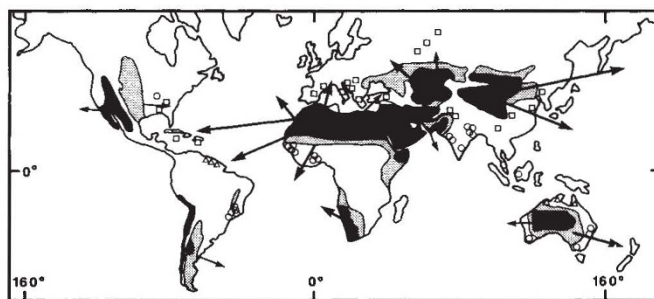
# Bauxites gathering dust

K. Pye

BAUXITE ores, consisting of oxides and oxyhydroxides of aluminium and iron mixed with variable amounts of clay, quartz and heavy minerals, provide the main source of aluminium and their genesis is therefore of considerable commercial interest. Three main modes of origin are traditionally proposed for bauxites and laterites: *in situ* weathering and leaching of bedrock to leave aluminium- and iron-rich residues; Al/Fe enrichment of sediments or weathering residua by movement of groundwater; or deposition

and petrographic data strongly suggest that wind-borne (aeolian) material has been introduced at the top of the profile. This is consistent with the continental dune trends and occurrence of a zone of kaolinite and quartz-rich sediments in the adjacent part of the Indian Ocean that indicate a dominant movement of sand and dust westwards and north-westwards across Western Australia.

The possibility that other bauxite deposits in Australia have also been significantly influenced by aeolian processes



Main dust trajectories (arrows) and location of principal bauxite deposits on □, karst; △, clastic sedimentary rocks; ○, igneous and metamorphic rocks. Bold areas are arid; stippled are semi-arid.

of Al/Fe-rich sediment reworked from pre-existing bauxites or lateritic soils. These processes are not mutually exclusive, and some bauxites have complex histories involving all three<sup>1,2</sup>. On page 819 of this issue<sup>3</sup>, Brimhall *et al.* present the first substantive evidence, based on work in the Darling Downs area of Western Australia, that deposition of wind-blown dust can also contribute to metal enrichment in bauxites. These findings will aid the interpretation of bauxites elsewhere, and provide further evidence that the transport of wind-blown dust is a process of geological, climatological and economic significance.

There are about 900 million tonnes of bauxite reserves in the Darling Downs area<sup>4</sup>, representing almost a quarter of Australia's reserves and making it one of the largest deposits in the world. The bauxite near Jarrahdale contains a large amount of quartz sand and an abraded heavy mineral suite, suggesting that it developed by weathering of a former fluvial sedimentary cover<sup>5</sup>. Another interpretation<sup>6</sup> is that it formed by *in situ* weathering of the underlying Archaean bedrock, although this idea does not account for the abraded heavy mineral suite.

The more rigorous chemical mass-balance approach adopted by Brimhall *et al.*<sup>3</sup> in their study in this issue demonstrates that *in situ* weathering cannot fully account for the concentration of elements in these profiles, and their mineralogical

warrants investigation. The Mitchell Plateau deposits lie beneath the north-westerly dust trajectory, and the deposits in Victoria, northern New South Wales and southern Queensland lie in the path of a south-easterly dust trajectory towards the Tasman Sea (see figure). The important deposits at

Weipa on Cape York Peninsula and at Gove in the Northern Territory do not lie downwind of an obvious dust source, although some deflation and westwards reworking of lateritic soils on Cape York could have occurred. North Queensland and the Northern Territory today experience a seasonally wet tropical climate, but during the Pleistocene<sup>6</sup> conditions were much drier for long periods, with dust blowing possibly on a larger scale.

The main dust trajectories are apparently correlated with the location of bauxite deposits in other parts of the world too (see figure). The deposits in Guinea, Sierra Leone and Ghana are in the area affected by dust trajectories from the Sahara. Deposition of iron-rich Harmattan dust could have significantly influenced the composition of soils in

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northern Nigeria<sup>7</sup>. Similarly, the karst bauxites of southern Europe occur in an area influenced by northerly dust transport from the Sahara. There is increasing evidence that widespread *terra rossa* soils in southern Europe contain a significant amount of weathered dust<sup>8,9</sup> which has been locally reworked.

Transport of Saharan dust as far as the Caribbean and South America has also been documented<sup>10,11</sup>, and it is possible that the parent material for the Jamaican karst bauxites was partly aeolian. Fine-grained dust, which is transported great distances, is typically enriched in aluminium and iron relative to silicon because of a high content of clay minerals and amorphous aluminosilicate material

compared with the coarser local dust. Furthermore, the relatively low rate of dust accumulation at great distance from the dust source could favour further aluminium and iron enrichment by leaching of silicon in suitable topographic traps.

The importance of aeolian dust in the formation of other near-surface residua and precipitates, including some calcretes<sup>12</sup>, gypcretes<sup>13</sup>, desert varnish<sup>14</sup> and red beds<sup>15</sup>, is now well-established. Following the new work of Brimhall *et al.*, bauxites need to be re-evaluated to assess the importance of dust deposition and aeolian reworking in their genesis. □

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## Reverse genetics

# Anti-sense RNA as a tool to study plant gene expression

Conrad Lichtenstein

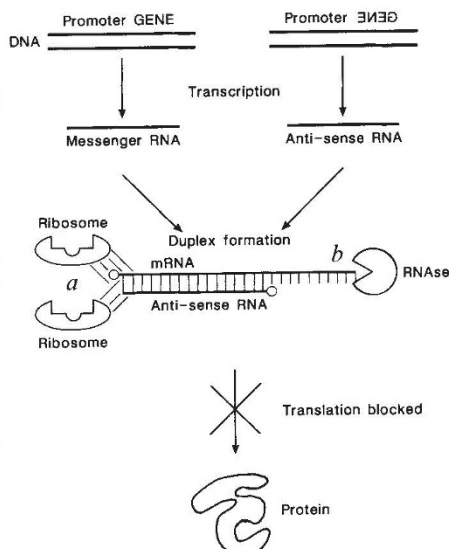
ANTI-SENSE RNA, regulatory RNA that can inhibit gene expression, is complementary to a given messenger RNA species, with which it pairs, forming double-stranded RNA. In one way or another (see later) this duplex RNA formation blocks expression of the protein gene product. Anti-sense RNA is a natural mechanism for gene regulation in bacteria but has also been used experimentally (see ref. 1 for a review). On page 866 of this issue<sup>2</sup>, van der Krol and co-workers report on the use of such RNA to block gene expression in plants in a dramatic and beautiful way. By insertion of an anti-sense gene suppressing expression of an enzyme required for pigment synthesis, they generate transgenic plants with altered flower colour.

With the advent of recombinant DNA technology, genetic engineering meant introducing new and different genes into organisms. A later development was to manipulate the existing genes within an organism. One way to achieve this 'gene surgery' exploits existing cellular machinery for genetic exchange by homologous recombination. Here, a cloned DNA sequence is mutated *in vitro* and then reintroduced back into a cell where it recombines with and so replaces a target gene, providing that there is a reasonable stretch of common DNA sequence.

This reverse-genetics technology is a powerful tool to elucidate the genetic function of an unknown piece of DNA. It also has evident applications to gene therapy, for removing undesirable genes or replacing defective ones and for protein engineering. Although the principle has been successfully applied in the study of bacteria and yeast, it is less well-suited to plants and animals where transforming

DNA integrates randomly into non-homologous sequences rather more frequently than into the homologous target sites. Much research is devoted to overcoming this problem; various strategies allow a direct selection for homologous recombination<sup>3</sup> or screen to weed out the random from the targeted events in a population of genetically transformed cells<sup>4</sup>.

Alternative approaches to manipulating gene expression, using anti-sense RNA, are concurrently being developed (see figure). Here, anti-sense genes are constructed *in vitro* by reversing the orientation of a portion of transcribed DNA, usually including the region encoding the protein, and placing this next to a transcriptional-control sequence, a promoter. This gene cassette is then delivered to the



a, Prevention of initiation of translation; b, RNA degradation.

target cell, resulting in genetic transformation and inhibition of expression of the target gene. Thus, unlike homologous recombination, anti-sense RNA does not allow gene replacement, only gene turn-off. As this may not be completely effective, it is a possible disadvantage, but could be useful when a reduction in gene expression is desired. It also provides the potential for selective control of gene expression in specific tissues or at specific stages in development by an appropriately regulated promoter. Its chief advantage is that it can be used against invading nucleic acids to engineer virus resistance; clearly homologous recombination cannot be used in these circumstances.

How does anti-sense RNA regulate gene expression? Much can be learned by studying bacteria which have, not surprisingly, already invented the use of anti-sense RNA<sup>1</sup>. In bacteria one likely mechanism is by blocking translation. Evidence for this is seen, for example, in an experiment in which resistance to the RNA coliphage SP was engineered into *Escherichia coli*<sup>5</sup>. The gene for the maturation protein was found to be the best target for anti-sense RNA with this phage. The greatest inhibitory effect was observed with a sequence encompassing the 24-base non-coding region plus a 216-base coding region of the sequence. Significantly, even a 19-base sequence covering only the ribosome-binding site exerted a strong inhibitory effect on phage proliferation, suggesting that the presumed duplex RNA which forms in this region prevents ribosome recognition and hence initiation of translation into the protein. In the natural examples in bacteria it is significant that the anti-sense gene also spans this ribosome binding-site region.

From micro-injection studies of anti-sense RNA into unfertilized eggs of frogs it can be seen that only sequences including the region spanning the site of initiation of translation are effective at reducing translation of the gene product, suggesting a mechanism similar to that in prokaryotes<sup>6</sup>. In other studies, where anti-sense genes were stably incorporated into the nuclear genome of cultured mammalian cells, there is evidence that an anti-sense RNA:messenger RNA duplex is formed within the nucleus but cannot be transported to the cytoplasm and hence is not available for translation. In this latter experiment, the region spanning translation initiation was not required and other regions were equally effective<sup>7</sup>. Other evidence suggests that the anti-sense RNA:messenger RNA duplex which forms in the nucleus is highly unstable and rapidly degraded<sup>8</sup>.

The first published demonstration of the use of anti-sense RNA-mediated suppression of gene expression in plants was using a transient expression system, electroporation, of plant protoplasts with