check in response to the DNA-synthesis block? The authors speculate that it's a survival mechanism: during S phase there are likely to be DNA strand breaks and stalled replication forks that will lead to p53 stabilization. At this point in the cell cycle E2F-1 levels are high. E2F-1 and p53 comprise a lethal concoction, so to prevent cells from apoptosing every time they divide, p53 must be kept in check. How this occurs now needs to be worked out.

Cath Brooksbank

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Arabidopsis produces a simple type of fruit known as a silique, which develops from the ovaries alone (an organ in which *PISTILLATA* is never expressed). Apples, on the other hand, form pome fruits with seeds embedded in fleshy tissue derived from sepals, petals and anthers. Somehow *PISTILLATA* must block the development of pome tissue — a block that is relieved in normal apples by fertilization.

Seedless fruit varieties are more attractive to consumers and, because they crop without the need for pollinators, they do not depend on insect species during flowering. The identification by Yao and colleagues of the source of seedlessness opens the way for producing seedless strains of commercial apple varieties, whether by conventional breeding or by genetic-manipulation techniques. It may also lead to pipless pears (another pome fruit) and, who knows, perhaps even the stoneless plum.

Christopher Surridge
Senior Editor, Nature

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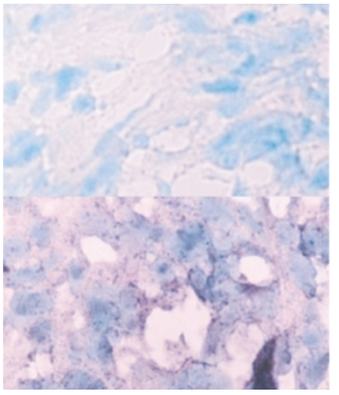

APOPTOSIS

Silent but deadly

Cancer cells find many ways to cheat death, but one puzzle is how they do so in malignant melanoma, where p53 — a key trigger of apoptosis — is often functional. The answer, revealed by Scott W. Lowe and colleagues in *Nature*, is that they switch off a gene further down the death pathway.

Lowe and co-workers surveyed several tumour types for loss-of-function mutations in *Apaf-1*. This potential tumour-suppressor gene encodes the co-activator for caspase-9, a downstream effector of p53. In malignant melanoma samples (top panel in the figure) the authors found that the levels of Apaf-1 messenger RNA were reduced, and experiments with melanoma cell lines confirmed that in these 'Apaf-1-negative' cells the p53-dependent response to chemotherapeutic drugs was compromised.

Lowe and co-workers showed that several melanoma cell lines contain only one copy of *Apaf-1*, and they concluded that this allele is transcriptionally silenced — perhaps by DNA methylation. To test this possibility they added a methylation inhibitor to melanoma cells, and observed an 8–20-fold increase in the levels of Apaf-1 protein and RNA in the Apaf-1-negative cells, but little effect on cells expressing normal levels of Apaf-1.

These results, say the authors, "imply that *Apaf-1* loss contributes to the aggressive nature and extreme chemoresistance of metastatic melanomas". And, although other anti-apoptotic mutations might be involved, these data raise the possibility that such cancers may one day be treated with chemotherapeutic drugs.

Alison Mitchell

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HUMAN GENOME

APOPTOSIS

Apoptotic molecular machinery: vastly increased complexity in vertebrates revealed by genome comparisons.

Aravind, L. *et al*. *Science* **291**, 1279–1284 (2001)

The apoptotic machinery evolved from signalling pathways present in the common ancestor of plants, animals and fungi. Analysis of the human, fly and nematode genomes now reveals an increase in both the number and complexity of apoptosis-related proteins in vertebrates.

DNA REPAIR

Human DNA repair genes.

Wood, R. D. *et al*. *Science* **291**, 1284–1289 (2001)

This catalogue groups 130 repair genes on the basis of function — for instance, base-excision repair, nucleotide-excision repair or mismatch repair — or sequence homology to known repair genes in other organisms. A strong message is the likelihood of clinical applications relating to human DNA repair genes.

MEMBRANE DYNAMICS

A genomic perspective on membrane compartment organization.

Bock, J. B. *et al*. *Nature* **409**, 839–841 (2001)

The authors compared four protein families involved in membrane traffic (SNAREs, Rabs, coats and members of the Sec1 family) in four different organisms (yeast, worm, fly and human). There was no difference in the basic machinery between the unicellular yeast and multicellular flies or worms. But humans have about twice as many genes in each of these families. The final (?) count is 35 SNAREs, 60 Rabs and 53 coat complex subunits.

CYTOSKELETON

Genomics, the cytoskeleton and motility.

Pollard, T. D. *Nature* **409**, 842–843 (2001)

The search for new cytoskeletal proteins yielded mixed results depending on the protein family. The author found seven highly divergent actin genes and seven new Arp genes. But the search yielded essentially no new myosins and kinesins in addition to the 40 or so known members of each of these families. One explanation is that it is much harder to assemble the genes of large multi-domain proteins.

CELL CYCLE

Can sequencing shed light on cell cycling?

Murray, A. W. & Marks, D. *Nature* **409**, 844–846 (2001)

The authors were disappointed to find only a few new cyclins and no new Cdks and spindle checkpoint proteins. No need to be disappointed — this could simply mean that they've done an excellent job in the past!