IN THE NEWS

Dung DNA set to foil ivory poachers

Elephant dung could be more valuable than ivory — to the elephants at least. A test that compares DNA from illegal ivory with maps of genetic variation based on dung samples might hold the key to tracking down poachers.

The ban on ivory trading has driven poachers into forests, where their activities are more difficult to detect. Tom Milliken of TRAFFIC, an organization that monitors trade in ivory, thinks the dung-based maps could help to pinpoint poaching hotspots: "…the largest uncertainty in our chain is where it is coming from, and this method will help with that" (news@nature.com).

The group that constructed the map, from the University of Washington in Seattle, took skin and dung samples from 16 African countries. "…the most important breakthrough is the ability to get it (DNA) from feces because we can sample many countries very quickly now," said Samuel Wasser, who led the study (Reuters.com). Because forest elephants live in isolated communities, genetic variation is sufficient to distinguish between animals from different areas. "We have incredible precision at telling one forest location from another," Wasser explained (*newscientist.com*).

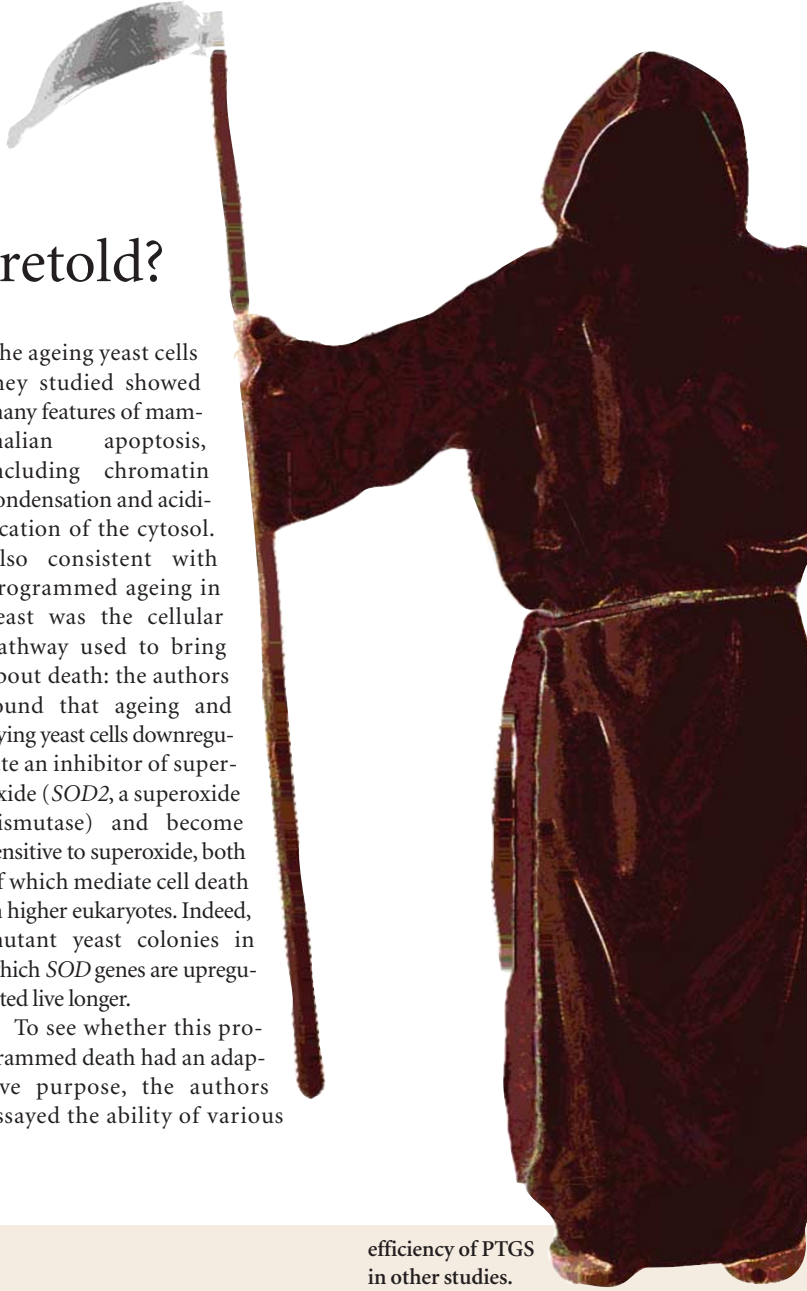
But there is room for improvement, as the map isn't as good at distinguishing man-made boundaries: "Right now, it's probably not precise enough because it might not tell us if a consignment comes from one side of a national border or another," commented Julian Blanc of the World Conservation Union (*The Guardian, UK,* 28 September, 2004). However, increased accuracy should make the map a valuable tool in the future.

But this requires more dung, and Wasser has a plea for those who patrol the areas affected: "…please, just ask them to pick up the poop," (news@nature.com).

Louisa Flintoft

AGEING

Yeast: a death foretold?



A new study adds fuel to the controversy over whether yeast cells undergo programmed cell death by suggesting that it occurs for the good of the species.

Death spares no one, not even yeast cells. But the how and why of death in *Saccharomyces cerevisiae* is dividing the community. In a recent paper, Paola Fabrizio and colleagues propose that the death of older yeast cells occurs to allow younger cells to thrive — in essence, therefore, they suggest that apoptosis occurs in yeast as an adaptive process that benefits other members of the group. This conclusion is controversial for two reasons — first, because it presupposes that death is actually programmed in yeast and that it occurs by apoptosis, and second, because it invokes the maligned theory of 'group selection', which runs counter to the well-established idea that selection occurs at the level of the individual.

Fabrizio and colleagues first addressed how cell death occurs. The ageing yeast cells they studied showed many features of mammalian apoptosis, including chromatin condensation and acidification of the cytosol. Also consistent with programmed ageing in yeast was the cellular pathway used to bring about death: the authors found that ageing and dying yeast cells downregulate an inhibitor of superoxide (*SOD2*, a superoxide dismutase) and become sensitive to superoxide, both of which mediate cell death in higher eukaryotes. Indeed, mutant yeast colonies in which *SOD* genes are upregulated live longer.

To see whether this programmed death had an adaptive purpose, the authors assayed the ability of various

RNA SILENCING

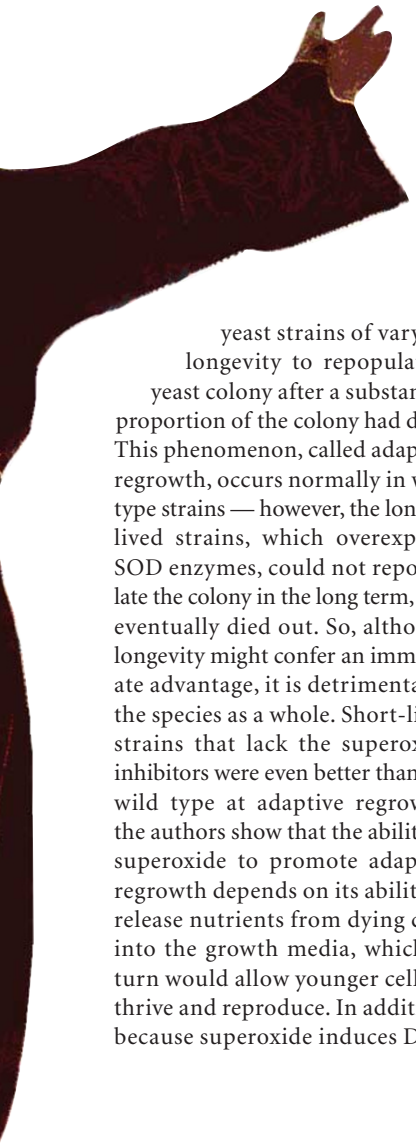
Simple, but effective

An important question about silencing by small RNAs concerns why some target genes are regulated at the level of transcription, whereas others are regulated post-transcriptionally. Phillip Zamore and colleagues suggest that the simple system that operates in the yeast *Schizosaccharomyces pombe* could help to find the answer.

Argonaute (Ago) proteins are crucial for the execution of gene silencing by small RNAs. Many species express multiple Ago proteins, and some of these induce silencing at the transcriptional level (transcriptional gene silencing (TGS)), whereas others specifically mediate post-transcriptional gene silencing (PTGS). Yeasts are poor relations in this respect; for example, *S. pombe* encodes a single Ago protein, Ago1, which functions in TGS. However, despite lacking other members of the Ago family, previous studies have hinted that PTGS also occurs in this species.

To confirm this, the authors replaced the *S. pombe adh1* gene with an *adh1*:GFP fusion. They then used a GFP hairpin RNA to induce silencing of the transgene. An intron was included in the hairpin construct, a strategy that had been shown to increase the efficiency of PTGS in other studies. Expression of the hairpin decreased GFP fluorescence, indicating successful silencing of the fusion gene. To test whether this was mediated by TGS or PTGS, the authors measured both the total levels of *adh1*:GFP mRNA and the levels of its transcription. Overall, *adh1*:GFP mRNA levels decreased in cells expressing the hairpin, but the rate of transcription remained the same, indicating that silencing was post-transcriptional.

As Ago1 is the only *S. pombe* Ago protein, is it responsible for PTGS as well as TGS? Silencing of *adh1*:GFP was abolished in *Ago*$^{-}$ mutants, confirming that this is the case. Interestingly, the authors went on to show that proteins that interact with Ago1 to mediate TGS are not required for PTGS,



yeast strains of varying longevity to repopulate a yeast colony after a substantial proportion of the colony had died. This phenomenon, called adaptive regrowth, occurs normally in wild type strains — however, the longer-lived strains, which overexpress SOD enzymes, could not repopulate the colony in the long term, and eventually died out. So, although longevity might confer an immediate advantage, it is detrimental to the species as a whole. Short-lived strains that lack the superoxide inhibitors were even better than the wild type at adaptive regrowth; the authors show that the ability of superoxide to promote adaptive regrowth depends on its ability to release nutrients from dying cells into the growth media, which in turn would allow younger cells to thrive and reproduce. In addition, because superoxide induces DNA mutations, its presence favours the selection and growth of mutants that are better adapted to the environment.

The results were not peculiar to laboratory strains, as the same phenomena occurred in three strains newly collected from the wild. Computational simulations tell a similar story — that a population that undergoes premature death and has a high mutation frequency is more likely to adapt to a changing environment.

So in yeast, at least, apoptosis is an altruistic act, as not dying damages the chances of survival of the whole group. If the theory stands up to scrutiny then what consequences does it have for humans? Should we thwart any attempt to extend our lives for the sake of our species? Whatever the eventual answer, this is a debate that isn't being laid to rest.

Tanita Casci

References and links

ORIGINAL RESEARCH PAPER Fabrizio, P. *et al.* Superoxide is a mediator of an altruistic aging program in *Saccharomyces cerevisiae*. *J. Cell Biol.* **166**, 1055–1067 (2004)

WEB SITE

Longo's laboratory: http://www.usc.edu/programs/pibbs/site/faculty/longo_v.htm

suggesting that Ago1 functions as part of distinct complexes to mediate the two types of silencing.

The fact that both TGS and PTGS are mediated by Ago1 in *S. pombe* indicates that it is not simply the availability of specialized Ago proteins that determines which pathway is used to silence specific genes. Gene-specific characteristics are also likely to be important, such as the chromosomal context of the gene or its rate of transcription. The simple system provided by silencing in *S. pombe* should be a useful tool for dissecting these requirements.

Louisa Flintoft

References and links

ORIGINAL RESEARCH PAPER Sigova, A., Rhind, N. & Zamore, P. D. A single Argonaute protein mediates both transcriptional and post-transcriptional silencing in *Schizosaccharomyces pombe*. *Genes Dev.* **18**, 2359–2367 (2004)

WEB SITE

http://www.umassmed.edu/bmp/faculty/zamore.cfm?start=0&

IN BRIEF

PLANT DEVELOPMENT

The *PLETHORA* genes mediate patterning of the *Arabidopsis* root stem cell niche.

Aida, M. *et al. Cell* **119**, 109–120 (2004)

In *Arabidopsis thaliana*, root stem-cells are maintained by a small set of organizing cells, known as the quiescent centre (QC), the location of which depends on auxin accumulation. By using a promoter-trap screen, the authors identified two putative transcription factors, *PLETHORA 1* (*PLT1*) and *PLT2*, which are required for QC specification and for maintaining root stem-cells during embryonic pattern formation; in addition, evidence indicates that their expression in the QC responds to auxin.

DEVELOPMENTAL BIOLOGY

Foxa2 is required for transition to air breathing at birth.

Wan, H. *et al. Proc. Natl Acad. Sci. USA* **101**, 14449–14454 (2004)

A fundamental adaptation faced by a newborn mammal is the ability to breathe in air through its lungs. Now, by knocking out gene function in the epithelial cells of the developing mouse lung, Wan and colleagues show that *Foxa2*, which encodes a forkhead transcription factor, is a master gene required for lung maturation at birth. This finding could inform treatments for premature babies and for individuals with lung disease or injury.

DEVELOPMENTAL BIOLOGY

Hmx2 and *Hmx3* homeobox genes direct development of the murine inner ear and hypothalamus and can be functionally replaced by *Drosophila Hmx.*

Wang, W. *et al. Dev. Cell* **7**, 439–453 (2004)

The authors show that the roles of mouse homeobox genes *Hmx2* and *Hmx3* in the development of the vestibular system are overlapping and distinct, but that their roles in the central nervous system (CNS) are interchangeable. Moreover, the single fly *Hmx* can rescue the CNS and inner-ear phenotype in double-knockout mice, despite differences in morphology. The authors propose that evolution of complex organs such as the vertebrate inner ear might involve cooption of primitive genetic programmes to new locations, not just from acquisition and modification of protein domains.

GENE EXPRESSION

Genome-wide mRNA surveillance is coupled to mRNA export.

Hieronymus, H. *et al. Genes Dev.*, 1 November 2004 (doi:10.1101/gad.1241204)

The authors found evidence to suggest that there are links between DNA and RNA surveillance and mRNA export. A screen of annotated, non-essential *Saccharomyces cerevisiae* genes identified new factors required for mRNA export, including Rrp6, an mRNA surveillance factor, and Lrp1, a DNA-repair protein. The authors found that Lrp1 can mediate mRNA degradation and requires Rrp6 for nuclear localization to the genes that encode their target mRNAs.