EDITORS' CHOICE

edited by Gilbert Chin

PALEOECOLOGY

Long-Lasting Consequences

The high Arctic of North America includes a vast coastline and numerous islands stretching from Alaska to Greenland. Lakes and ponds in this region provide valuable environmental records in the form of plankton communities preserved in sediment. It has generally been thought that these lakes and other areas of the high Arctic were pristine and unaffected by humans until very recently. Most areas saw only nomadic Inuit whalers until the past century, and only during the summers.

An excavated whale-bone house.

Douglas *et al.* show, however, that on Somerset Island, and perhaps elsewhere, these nomadic visits significantly and indelibly altered a pond ecosystem as early as 800 years ago. Where the Inuit camped and processed whales, they often dumped carcasses in nearby lakes and ponds, fertilizing the lakes and changing the nitrogen balance and plankton community. These changes have persisted long after the departure of the Inuit, illustrating the persistent effect even temporary human habitation can have on the environment. — BH

Proc. Natl. Acad. Sci. U.S.A. **101**, 1613 (2004).

ECOLOGY/EVOLUTION

Revealing Relationships

Rafflesia, a genus of 16 species of parasitic plants inhabiting the tropical rainforests of Southeast Asia, harbors the world's largest flower—a giant 1 m across that attracts pollinating flies with its odor of rotting carrion. Despite its iconic status, *Rafflesia*'s evolutionary history has remained uncertain; unraveling the phylogenetic relationships of parasitic plants is often tricky because many morphological and genetic features are lost or much modified in the transition to the parasitic life-style.

Barkman *et al.* used a comparison of mitochondrial DNA (mtDNA) sequences to place *Rafflesia* in its phylogenetic context among the angiosperms. Plant mtDNA tends to have lower mutation rates than other components of the plant genome and hence can yield more reliable phylogenies. Their approach places *Rafflesia* close to the Malpighiales, an order of flowering plants that includes the passion flowers—confirming at last the relationship first noted by Robert Brown (of Brownian motion) in 1822. Such analyses, applied to further groups of parasitic plants, will help to reveal the evolutionary pathways by which plants can switch from photosynthetic to parasitic mode. — AMS

Proc. Natl. Acad. Sci. U.S.A. **101**, 787 (2004).

BIOMEDICINE

The ABCs of CBS

The analysis of sequence motifs shared by diverse proteins often provides important information about protein function. One such motif is the cystathionine β-synthase (CBS) domain, a stretch of 60 amino acids that occurs—usually as tandem pairs—in more than a thousand proteins. Hereditary disease-causing mutations in CBS domains have been identified in several human proteins, including AMP-activated protein kinase (Wolff-Parkinson-White syndrome) and IMP dehydrogenase (retinitis pigmentosa), but the functional role of this structural motif has been unclear.

Image not available for online use.

A surface charge representation (negative, red; positive, blue) of modeled CBS domains in γ2.

Through biochemical analyses of CBS domains derived from several representative proteins, Scott *et al.* show that tandem pairs of CBS domains form allosteric binding sites for adenosine-containing ligands and that binding is impaired by disease-associated mutations. In the case of AMP-activated protein kinase, tandem pairs of CBS domains in the enzyme's γ2 subunit appear to provide two binding sites for AMP and ATP, a finding consistent with modeling and mutagenesis work by Adams *et al.* Localization of the nucleotide binding sites in this enzyme, which is a key player in energy metabolism, may facilitate drug development efforts in diabetes and obesity. — PAK

J. Clin. Invest. **113**, 274 (2004); *Protein Sci.* **13**, 155 (2004).

BIOCHEMISTRY

Open Access

The *Escherichia coli* protein Hfq was first identified over three decades ago as a host factor necessary for the replication of the bacteriophage Qβ; Hfq appears to alter the secondary structure of the Qβ RNA. Viruses have streamlined their genomes by relying on the existing functions of host proteins, so it was not unexpected to find the abundant Hfq as a participant in the lives of host RNAs, promoting degradation in some instances, such as *sodB* mRNA, while enhancing the stability of small regulatory RNAs, such as RyhB, in others. Geissmann and Touati have mapped these interactions in detail and find that Hfq, like its Sm and Lsm cousins, binds to an AU-rich motif just upstream of the translation start site in *sodB* mRNA. One result of this interaction is the partial opening of the neighboring stem-loop that contains the initiator codon, which allows RyhB to gain access to a complementary 9-nucleotide sequence. Formation of the short double-stranded RNA region then leads to degradation of both RNAs in a pathway that may be shared by the many other iron metabolism transcripts targeted by RyhB. — GJC

EMBO J. **23**, 396 (2004).

CHEMISTRY

To Have and To Hold

Dendrimeric polymers possess a highly branched regular structure that can contain a variety of subnanometer-

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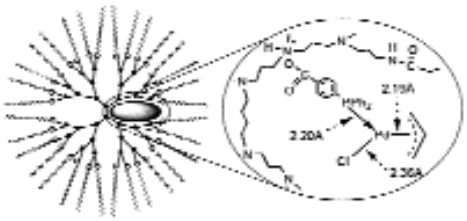
CREDITS: (TOP) JUNKO HABU; (BOTTOM) SCOTT *ET AL.*, *J. CLIN. INVEST.* **113**, 274 (2004)



The encapsulated Pd catalyst.

scale voids between their chains. This structure is reminiscent of binding pockets in enzymes; and, in principle, metal complexes incorporated into dendrimers could show improved catalytic activity because of favorable ligand interactions with the side groups of polymer chains and a high density of active sites. However, the number of systems in which dendrimer incorporation has improved catalytic activity are few.

Ooe *et al.* show that encapsulation of an allylic palladium catalyst, $[PdCl(C_3H_5)]_2$, by a fifth-generation dendrimer (one formed by five rounds of adding branches) can improve yields in the Heck reaction, which couples an aryl halide to a compound with a double bond. The dendrimer arms contain amino acid groups, and 4-diphenylphosphinobenzoic acid was added to stabilize the active Pd(0) species through a phosphine ligand interaction. Stabilization was achieved at a ratio of P to Pd of unity, even though in solution, high P/Pd ratios typically stabilize Pd(0). The authors argue that the amino acid groups that bind the phosphine ligand donor produce a favorable polar environment around the Pd center. For the coupling of iodobenzene to *n*-butylacrylate, yields were >90%. — PDS

J. Am. Chem. Soc. 10.1021/ja038455m (2004).

CHEMISTRY

Wrapping Phosphorus in Vinyl

The vinyl group, CH_2=CHX, has one of the most extensively developed chemistries. However, when X is phosphorus, many simple examples of vinyl compounds are unknown or have not been reproduced synthetically. Monkowius *et al.* report on the synthesis of the tetra(vinyl)phosphonium cation, $[(CH_2=CH)_4P]^+$. Synthesis from trivinylphosphine led to unwanted polymerization reactions, so the authors focused on a strategy in which all four vinyl groups were formed in the last step of synthesis. They prepared the 2-acetoxyethyl precursor, $[P(CH_2CH_2OAc)_4]^+I^-$, which, upon heating in the presence of base, produced the tetravinyl cation. They have used this species as a highly reactive precursor for a number of reactions. — PDS

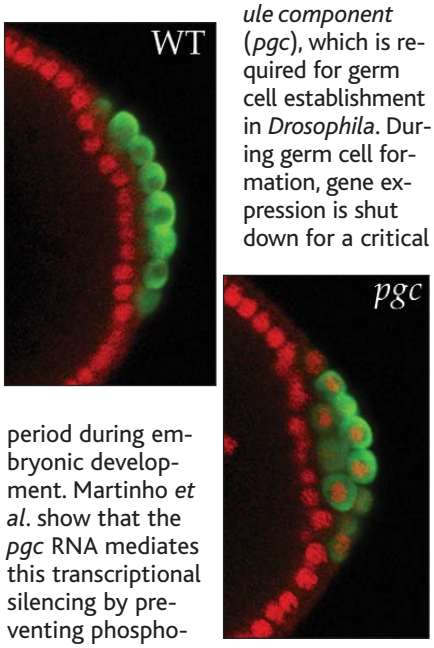
J. Am. Chem. Soc. 10.1021/ja0399019 (2004).

DEVELOPMENT

Repressing RNA

Recent discoveries have demonstrated that noncoding RNAs play important roles in an increasingly wide range of biological processes. Although the functions of micro RNAs (miRNAs) are still being explored, the involvement of specific noncoding RNAs in the formation of germ plasm and germ cells has been appreciated for several years, yet, unlike miRNAs, their mode of action has for the most part not been well defined.

One such noncoding RNA is *polar granule component* (*pgc*), which is required for germ cell establishment in *Drosophila*. During germ cell formation, gene expression is shut down for a critical period during embryonic development. Martinho *et al.* show that the *pgc* RNA mediates this transcriptional silencing by preventing phosphorylation of the C-terminal domain (CTD) Ser2 residue of RNA polymerase II, an important event that is required for the transition from the pre-initiation transcription complex to the actively transcribing elongation complex. The authors speculate that *pgc* may function like another noncoding species, the 7SK small nuclear RNA, found in humans, that acts to sequester factors required for the phosphorylation of the CTD Ser2. — GR



Transcription activation (red) in germ cells (green) in wild-type (left) and *pgc* RNA-deficient (right) embryos.

Curr. Biol. **14**, 159 (2004).

CREDITS: (TOP) OOE *ET AL., J. AM. CHEM. SOC.* 10.1021/JA038455M (2004); (BOTTOM) MARTINHO *ET AL., CURR. BIOL.* **14**, 159 (2004)

Repressing RNA

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