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In This Issue

FEATURE ARTICLE, BIOCHEMISTRY

SNAREs can force vacuole lysis

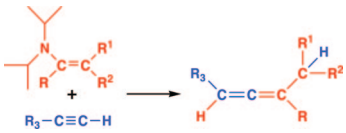
The fusion of membranes inside cells is an essential part of moving molecules between organelles. Vincent Starai *et al.* report that precise levels of SNARE proteins regulate the balance between fusion and lysis. SNARE proteins bring membranes together, but many other proteins and lipids, such as Rab family GTPases and the proteins that bind to them, are usually needed for fusion. The authors engineered yeast to overproduce the four SNARE proteins that form the complex that promotes vacuole fusion and lysis. By controlling the levels of SNAREs, the Ypt7p Rab protein, and HOPS protein complex on the vacuole surfaces, they measured the properties of fusing vacuoles. Yeast membranes with high levels of SNAREs can still fuse without the normally required Rab proteins, but often rupture. When the Rab proteins are present, much smaller amounts of SNAREs are required for fusion, and fewer vacuoles are ruptured. These results show that Rab proteins are essential for maintaining the integrity of vacuoles during fusion and for avoiding lysis. — P.D.

"Excess vacuolar SNAREs drive lysis and Rab bypass fusion" by Vincent J. Starai, Youngsoo Jun, and William Wickner (see pages 13551–13558)

CHEMISTRY

Allene formation with gold

Gold has recently come into its own as a catalyst for complex organic reactions. Vincent Lavallo *et al.* use gold to directly couple two unsaturated carbon centers to form the three-carbon allenic core through a unique "carbene/vinylidene cross coupling." Allenes are useful molecules for synthetic organic chemistry, especially in making natural products. The authors added a sterically demanding carbene to form a cationic gold complex that was then used to join enamines and terminal alkynes to form allenes. The gold complex could couple a wide variety of enamines and alkynes. The final allenes were unsymmetrically substituted and nonterminal. The reaction was also diastereoselective, which could lead to enantioselective reactions. The authors' analysis of the stages of the reactions suggests that a carbene/vinyledene cross-coupling mechanism is responsible. — P.D.



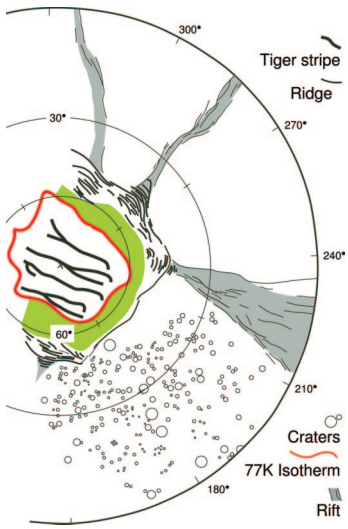
Schematic representation of the gold-catalyzed cross-coupling reaction.

"Allene formation by gold catalyzed cross-coupling of masked carbenes and vinylidenes" by Vincent Lavallo, Guido D. Frey, Shazia Kousar, Bruno Donnadieu, and Guy Bertrand (see pages 13569–13573)

GEOLOGY

Tectonics from a frigid Enceladus

Only a few bodies in the solar system are tectonically active, and Saturn's icy moon Enceladus is easily the smallest of these. Its southern hemisphere is marked by a distinct arrangement of tectonic features, intense heat flux, and geyser-like plumes. Two competing models have been proposed to explain the plumes: "Cold Faithful," which ascribes the plumes to the sublimation of liquid water in an icy H_2O shell, and "Frigid Faithful," which ascribes the plumes to the dissociation of clathrates in a clathrate-rich icy shell. Gustavo Gioia *et al.* argue that an icy shell under Frigid Faithful conditions can be modeled as a brittle elastic body stressed by the thermal expansion of a deep source of heat. The tectonic features could have formed without high temperatures, liquid water, or solid-state convection. Their Enceladus is unlikely to harbor life but is the first integrated model of the mechanics and thermodynamics of



Major tectonic features on the southern hemisphere of Enceladus.

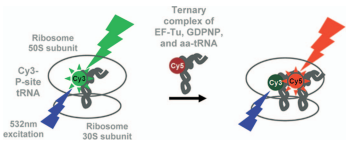
Enceladus to give a unified explanation of the salient tectonic features, geyser-like activity, and heat transport from a depth of tens of kilometers to the surface. — P.D.

"Unified model of tectonics and heat transport in a frigid Enceladus" by Gustavo Gioia, Pinaki Chakraborty, Stephen Marshak, and Susan W. Kieffer (see pages 13578–13581)

BIOPHYSICS

Fluctuations are key in mRNA translation

Ribosomes translate mRNA into protein at a rate of ≈20 amino acids per second. The low error rate in translation cannot be directly explained by the slim difference in energies between mRNA binding to correct ("cognate") tRNA or to near-cognate tRNA (which differs by one base). Tae-Hee Lee *et al.* argue, based on the results of single-molecule experiments, that induced fit between tRNA and the ribosome, aided by large, rare thermal fluctuations, gives cognate tRNA a competitive advantage. The authors labeled P-site tRNA with the fluorophore Cy3, and free, amino acid-bearing tRNA with the fluorophore Cy5, and observed aminoacyl-tRNA binding by measuring the efficiency of fluorescence resonance energy transfer (FRET) in individual molecular binding events. Cognate tRNA were much more successful in binding than near-cognate tRNA. Full translation requires hydrolysis of GTP, but the authors supplied only the analog GDPNP, which stalled translation after tRNA binding. This experimental brake allowed them, by means of FRET, to observe the dynamics of tRNA in the mid-FRET state that corresponds to GTPase activation. Lifetime histograms of this state were best fit by double exponential decays, indicating that what was previously thought of as a single state actually consists of a combination of transient and stable associations. On the basis of statistical mechanics, Lee *et al.* propose a model in which a cognate tRNA would have a slightly shorter distance to travel (in a thermal fluctuation) to achieve the stable, GTPase-activated state. This would account for the low error rate in mRNA translation. — K.M.



FRET between tRNA is a measure of location on the ribosome.

"The role of fluctuations in tRNA selection by the ribosome" by Tae-Hee Lee, Scott C. Blanchard, Harold D. Kim, Joseph D. Puglisi, and Steven Chu (see pages 13661–13665)

POPULATION BIOLOGY

Frog-killing fungus origins

A mysterious fungal disease that attacks and kills amphibians is devastating frog populations across the world. Since its identification in 1998, frustratingly little has been revealed about the pathogenesis of the fungus *Batrachochytrium dendrobatidis*; even its mode of killing remains unclear. To determine more about the nature of the threat, Jess Morgan *et al.* investigated the population genetics of the fungus. Using data from a well studied population of frogs in the Sierra Nevada of California, Morgan *et al.* sought to resolve two competing hypotheses of the fungus' origins. To determine whether the fungus was a new pathogen or whether it was an existing one that took advantage of new conditions, such as environmental change, the authors compared the genetic similarity of >100 fungal isolates from across the region. Their analysis suggests that the fungus is a relatively new pathogen to the area but that it is dividing into distinct subpopulations as it adapts. This genetic diversity cannot be explained solely by asexual reproduction. Learning more about the fungus' reproductive habits is an important step in attempting to control the pathogen. — T.H.D.


Amphibians affected by fungal pathogen.

"Population genetics of the frog-killing fungus Batrachochytrium dendrobatidis*" by Jess A. T. Morgan, Vance T. Vredenburg, Lara J. Rachowicz, Roland A. Knapp, Mary J. Stice, Tate Tunstall, Rob E. Bingham, John M. Parker, Joyce E. Longcore, Craig Moritz, Cheryl J. Briggs, and John W. Taylor* (see pages 13845–13850)