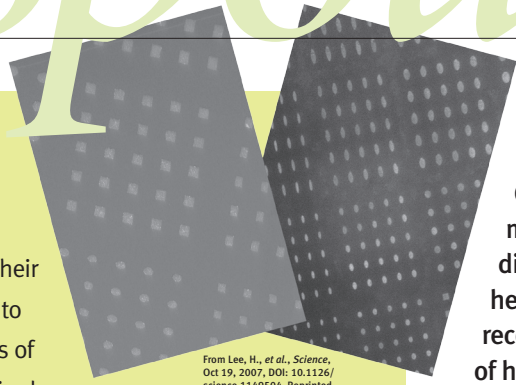
Spotlight

Mussels Stick Out



From Lee, H., *et al.*, *Science*, Oct 19, 2007, DOI: 10.1126/science.1149504. Reprinted with permission from AAAS.

Mussels are notorious for their ability to stick to nearly all types of surfaces. Inspired by the natural adhesive properties of the plaque-substrate interfacial proteins in mussels, Lee *et al.* (*Science* 2007, *318*, 426–430) now develop a simple, yet effective, method for coating surfaces. The authors observed that mussel foot protein 5 is abundant in two amino acids, 3,4-dihydroxy-L-phenylalanine (DOPA) and lysine. From this observation, they hypothesized that the catechol group of DOPA and the amine of lysine are involved in the adhesive properties conferred by this protein. The authors then tested the ability of dopamine, a neurotransmitter not found in mussel adhesive proteins, to mimic the ability to coat a wide variety of materials.

The authors' methodology is simple. Solid objects are immersed in a dilute solution containing dopamine buffered to marine pH (pH 8.5) and tested for the formation of a polydopamine layer over time. Remarkably, this simple experiment is effective and results in the deposition of a polydopamine coating on all 25 material surfaces that the authors tested.

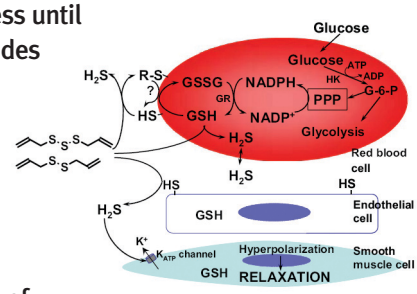
The authors then exploited the reactivity of the deposited polydopamine surface to add a second layer. Metals, self-assembled monolayers, and surface-grafted polymers can all be added to the polydopamine surface *via* secondary reactions. The simplicity and versatility of this method coupled with the capacity to add new functionalities make it an ideal general approach to modifying surfaces.

Anirban Mahapatra

Garlic and Cell Signaling

Garlic has been used for centuries for its culinary and medicinal properties. The flavor and aroma of garlic are distinctive and need no further introduction. The ascribed health properties of garlic, however, run the gamut—from the recognized association between consumption and reduction of heart-disease-associated risk factors to the largely untested notion that garlic is an aphrodisiac. Chemically, what makes garlic unique is that it is the only commonly consumed plant that contains allyl-substituted sulfur compounds. The documented medicinal properties of garlic have been attributed to these compounds, and more specifically to allicin, the predominant organic-sulfur-containing compound in garlic. Interestingly, allicin is not normally found in undamaged garlic cloves. Crushing garlic cloves brings together alliin, an amino acid, and the enzyme alliinase, both of which are present in separate compartments. Alliinase, in turn, catalyzes the conversion of alliin to allicin. Unstable allicin rapidly decomposes to allyl polysulfides such as diallyl disulfide (DADS) and diallyl trisulfide (DATS).

Despite the benefits of garlic and garlic-derived compounds in preventive cardiovascular care, little was known about the mechanisms involved in this process until now. In a new study, Benavides *et al.* (*Proc. Natl. Acad. Sci. U.S.A.* 2007; www.pnas.org/cgi/doi/10.1073/pnas.0705710104) show that the signaling molecule responsible for the cardioprotective activity of garlic is hydrogen sulfide (H_2S), which is produced as DADS and DATS react with cellular thiols. The authors report a dosage-dependent correlation between H_2S production and the ability of garlic products to cause the relaxation of blood vessels. The relaxation of blood vessels, in turn, allows an increase in blood flow and decreases blood pressure. In concluding, the authors hypothesized that the beneficial medicinal properties attributed to garlic consumption are a direct result of H_2S production. If this assertion is true, it should now be possible to test the efficacy of garlic-derived medical products by testing for the production of H_2S. **Anirban Mahapatra**



Benavides, G., *et al.*, *Proc. Natl. Acad. Sci., U.S.A.*, DOI: 10.1073/pnas.0705710104. Copyright 2007 National Academy of Sciences, U.S.A.; Epub Oct 19, 2007.

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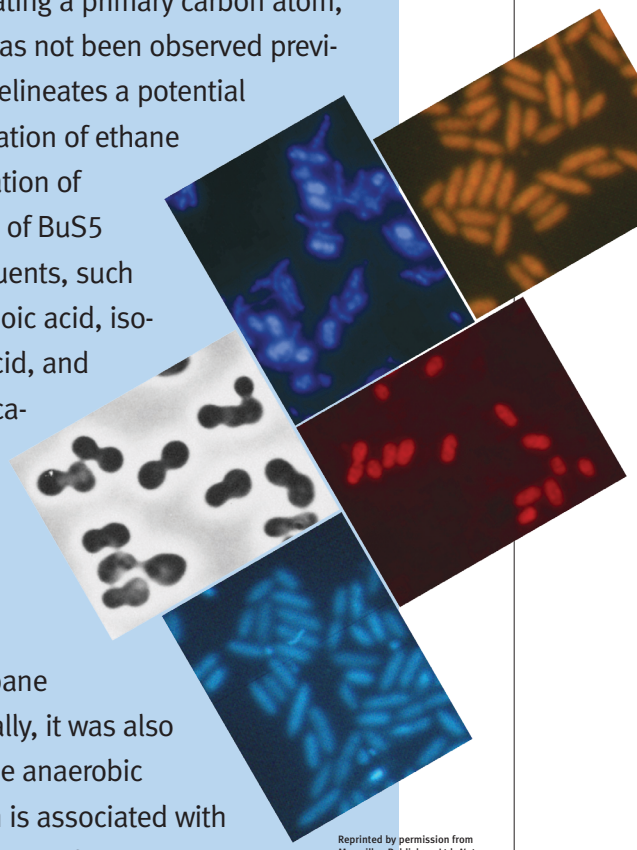
No Need for Oxygen

Biodegradation of saturated hydrocarbons, or alkanes, is an intriguing process given the low inherent reactivity of compounds of this type. Whereas aerobic oxidation of these compounds is relatively well studied, their oxidation in anaerobic environments is less well understood, especially in the case of the short-chain alkanes ethane, propane, and *n*-butane. By searching through sediments from the Gulf of Mexico and the Gulf of California, Kniemeyer *et al.* (*Nature*, published online Sept 19, 2007; DOI: 10.1038/nature06200) now report the discovery of microorganisms that can anaerobically degrade short-chain alkanes.

Enrichment cultures incubated with propane, butane, or ethane under anoxic conditions resulted in slow but definitively hydrocarbon-dependent sulfide production, an indication of the presence of sulfate-reducing microorganisms. Isolation and characterization of one of these microorganisms, strain BuS5, revealed it to be a member of the *Desulfosarcina/Desulfococcus* cluster within the Deltaproteobacteria. Notably, BuS5 utilized only propane and butane; other small molecules, such as isobutane, primary and secondary alcohols, short-chain alkanoates, lactate, fumarate, and succinate, were not consumed by this bacterium. Furthermore, upon growth with propane, the unexpected metabolite *n*-propylsuccinate was identified along with the expected product isopropylsuccinate. This suggests that the organism is capable of activating a primary carbon atom, a reaction that has not been observed previously and that delineates a potential route for degradation of ethane as well. Examination of the lipid fraction of BuS5 revealed constituents, such as isotetradecanoic acid, isohexadecanoic acid, and anteisopentadecanoic acid, that are consistent with further metabolism of the activation products of propane and butane. Finally, it was also observed that the anaerobic alkane oxidation is associated with stable carbon isotope fractionation, which is an important indicator of biodegradation. These findings substantiate previous assumptions about several phenomena attributed to biological oxidation of propane and butane and will further our understanding of the metabolism of short-chain hydrocarbons in anoxic regions of the oceans and terrestrial environments. **Eva J. Gordon, Ph.D.**



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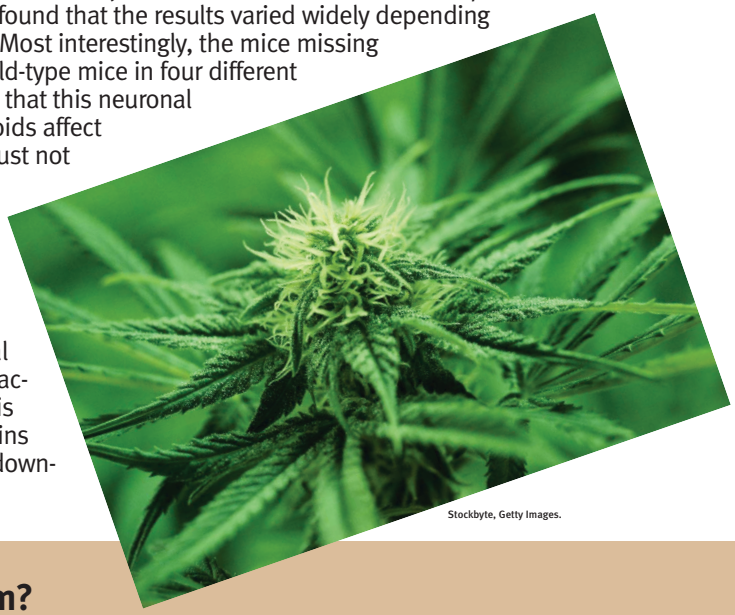
Spotlight

This Is Your Mouse on Marijuana

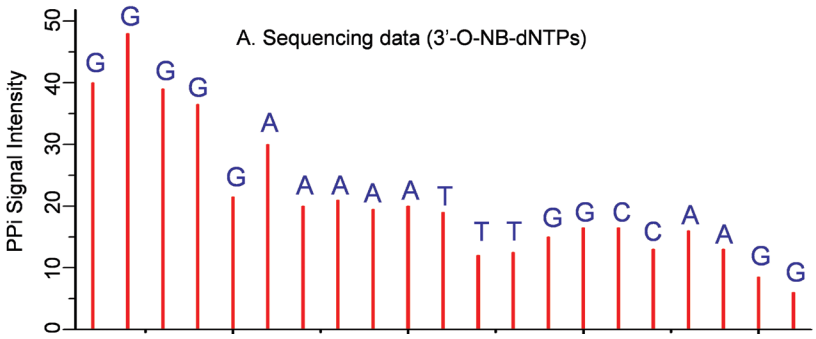
The psychoactive effects that accompany marijuana smoking are due to Δ^9-tetrahydrocannabinol (THC). This compound, as well as endogenous cannabinoids, such as anandamide, binds to the CB1 receptors found on the surface of many neuronal subtypes in the brain. Belonging to the G-protein-coupled receptor family, a ligand-bound CB1 can activate multiple signal transduction pathways within the cell. The resulting psychological and physical effects from a marijuana "high" are numerous, although the molecular mechanisms that connect these effects to cannabinoids are largely unknown. The widespread expression of the CB1 receptor in the central nervous system has led to much speculation about THC's effects and what neuronal circuits may be at work. In their new study, Monory *et al.* (*PLoS Biol.* 2007, *5*; Epub e269) produce conditional knockout mice that lack the CB1 receptor in specific neuronal populations to determine the effects of cannabinoids on various cell types in the brain. These included GABAergic neurons, principal neurons, cortical glutamatergic neurons, and dopamine receptor expressing neurons. The resulting mice were then scored for their response to THC in a battery of tests that measured motor response, pain threshold, and body temperature. The authors found that the results varied widely depending on the neurons that were targeted for CB1 deletion. Most interestingly, the mice missing CB1 in the GABAergic neurons scored almost like wild-type mice in four different response tests. This was somewhat surprising given that this neuronal subtype expresses CB1 at high levels. Do cannabinoids affect these neurons at all, or does this particular battery just not include the right litmus test? On the other hand, the mice with a CB1 loss in glutamatergic neurons of the cerebral cortex showed little response to THC in the locomotor or hypothermic tests. THC is thought to be a natural analgesic drug and, indeed, the deletion of CB1 in principal neurons showed a loss in this painkilling property. The precise neuronal populations mediating this effect, and other psychoactive effects of THC, will require more analysis, but this study points the way to how engineered mouse strains can shed light on this long-elusive receptor and its downstream targets. **Jason G. Underwood, Ph.D.**



Stockbyte, Getty Images.

mRNA Localization: Methodical or Mayhem?

The specific destination of a protein within a eukaryotic cell is often programmed by a portion of the polypeptide sequence, and as seen in many signal transduction circuits, this destination can be modulated by interacting proteins or post-translational modifications. Studies in the frog and fruit fly model systems have shown that some messenger RNAs (mRNAs) are localized during development, and this is critical to place the encoded protein in the right place at the right time. In this scenario, the protein is predelivered to its subcellular address before it is ever churned out of the ribosome. But, do these specially localized messages constitute the rare exceptions, or could this phenomenon be at work in many biological systems? In a brute-force effort, Lécuyer *et al.* (*Cell* 2007, *131*, 174–187) take on this question in a recent study and uncover some surprising results. They looked in a place where localized RNAs are already found, the first few hours in the life of a *Drosophila* embryo. Using a highly refined fluorescent *in situ* hybridization



Better Fuel for Pyros

The recent explosion of genomics data has largely been fueled by more advanced sequencing technologies. Among these methods is a tiny metabolic cascade in a test tube, termed pyrosequencing. As in traditional sequencing methods, the DNA template is bound by a primer and poised to add another nucleotide monomer. Pyrosequencing's unique trick is the addition of just one triphosphate monomer to the reaction at a time. When the correct monomer is introduced, the chain extends by one, and one molecule of pyrophosphate is liberated. Then, this pyrophosphate is the substrate for a secondary reaction, which generates ATP. This ATP fuels the firefly enzyme, luciferase, to generate light. Thus, the identity of this +1 nucleotide can be detected by the presence of the light only when the correct one of the four nucleosides triphosphates enters the reaction vessel. The reaction can continue along and make light with each new base, but as one might predict, there is a caveat. When the primer extends through a homopolymer region, several molecules of pyrophosphate are liberated, but the conversion to light seems to lose its linear nature beyond ~two nucleotides. This can be a major limitation, because genomes, particularly in higher eukaryotes, can have long regions of low complexity. Now, Wu *et al.* (*Proc. Natl. Acad. Sci. U.S.A.* 2007, *104*, 16462–16467; Epub Oct 8, 2007) present a clever solution to this problem. They synthesized special nucleoside triphosphates that possess a blocking group at the 3′ position. They demonstrated that each can be incorporated as the +1 nucleotide in a pyrosequencing reaction, but the blocking group prevents the +2 addition. Then, the specially engineered blocking moieties, *O*-allyl or *O*-(2-nitrobenzyl) can be cleaved from the elongated DNA by palladium or laser irradiation, respectively. Then the reaction is ready for extension again. The authors challenged their reversible terminators with a template rich in homopolymeric sequence and did a side-by-side comparison with conventional pyrosequencing. Their data show that while the conventional chemistry has to guess at whether the template has a run of three to five adenosines, the reversible terminators system can tabulate a perfect count. This new trick could play a key role as the next generation of sequencing machines is built and the next organisms are ushered into the genomics era. **Jason G. Underwood, Ph.D.**

protocol, they tested whopping lists of >3000 mRNAs for their localization pattern. In this high-throughput screen, more than two-thirds were found to be expressed, and a remarkable 71% of those showed subcellular localization. The mRNAs could be divided into a diverse set of localization subtypes, with the functional categories of the encoded proteins spanning the entire spectrum of cellular functions. The authors have created a public database for researchers to comb through this massive dataset. Because mRNA localization is often correlated with the encoded protein's function, this resource will be a helpful tool in assigning putative roles for genes that until now have only the bioinformatics equivalent of a serial number. These dramatic results in the *Drosophila* embryo offer ample reason to rethink the textbook protein localization paradigms. Also, in a very chicken-and-egg way, this study makes one wonder what proteins are involved in escorting each mRNA to its final destination. Jason G. Underwood, Ph.D.