

# THIS WEEK IN Science

edited by Phil Szuromi

## Jets Caught in the Act

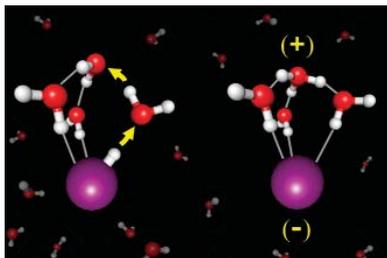
Relativistic jets of collimated plasma are produced by black holes and neutron stars. Exquisite observations of the 4-year evolution from the microquasar XTE J1550–564 synthesized by Corbel *et al.* (p. 196; see the Perspective by Rupen) show that two jets are directly related to ejecta from the black hole that was observed as an intense flare event in 1998. The knots seen in x-ray and radio wavelengths are produced by shock waves that accelerate particles to extremely high energies by synchrotron emission.

## Optical Hot Spots

Radio hot spots are concentrated regions of intense radio emission in the lobes of radio galaxies. The detailed structure of these hot spots is revealed in optical images obtained from the Very Large Telescope by Prieto *et al.* (p. 193). The bright optical emission is caused by synchrotron radiation from relativistic electrons produced by the impact of jet plasma from the galaxy with the intergalactic medium in the bow-shock region.

## Polariton Condensation in a Semiconductor

Polaritons, composite particles consisting of an electron-hole pair tied to a photon mode in a cavity, have long been sought as a semiconductor-based system for the realization of Bose-Einstein condensation. In most cases, the polaritons decay before they can thermalize into the ground state. Using 12 quantum wells to ensure a sufficient supply of excitons and a high-quality cavity to tie them to photon modes with an extended lifetime, Deng *et al.* (p. 199) report on the observation of a quantum phase transition indicative of a Bose-Einstein condensed state.



water clusters of increasing size show that the transition to the ion-pair state occurs at five water molecules. In smaller clusters, the ion pair can be created through electronic excitation.

## 129 Genome Sequence of the *Anopheles gambiae*

The enormous worldwide death rate from malaria has prompted an international consortium to sequence the genome of the principle vector, the mosquito *Anopheles gambiae*. Holt *et al.* (p. 129) present the results of the shotgun sequencing effort, which generated a sequence of 278 megabases that represents 91% of the genome. An initial functional annotation of the identified open reading frames is presented, and the authors estimate that there are 14,000 protein-encoding transcripts for which they have multiple types of evidence. The authors also performed an expressed sequence tag analysis of genes whose expression changes after the mosquito feeds.

### And in Brevia ...

A Lower Cambrian fossil (~520 million years old) described by Chen and Huang (p. 187) as a chaetognath, or arrow worm, adds to the sparse fossil record for a phylum that has survived in the oceans until the present.

## Modeling Plate Motions

The motions of plates on Earth's surface are believed to be coupled to convection in the mantle. Conrad and Lithgow-Bertelloni (p. 207) consider two subducted slab mechanisms, slab pull in the upper mantle, where the subducted slab is attached to the plate and pulls the subducting plate faster than normal toward the subduction zone, and slab suction in the lower mantle, where the subducted slab is detached from the plate and sucks the plate toward the subduction zone by enhanced mantle flow. A plate tectonic simulation with suction and pull reproduces the observed plate tectonic motions and resolves some of the difficulties in understanding the coupling of crust to mantle.

## Bypassing Silicone By-Products

A key reaction in the synthesis of silicone polymers is the addition of a silicon compound containing a Si–H group to a C=C double bond. The main industrial catalysts for these reactions are Pt compounds that suffer from the formation of various by-products, as well as deactivation of the catalysts to form colloidal Pt that discolors the final products. Markó *et al.* (p. 204) now report on a highly active and selective Pt-carbene catalyst that suppresses both of these unwanted effects.

## Comparative Genomics for *Anopheles gambiae*

The fruit fly *Drosophila melanogaster* and the mosquito *Anopheles gambiae* are separated by approximately 250 million years of evolution. An initial comparison of these genomes by Zdobnov *et al.* (p. 149) indicate that insects evolved more quickly than vertebrates; the extent of similarity between these two insects was approximately equal to that between humans and pufferfish, which diverged approximately 450 million years ago. Reorganization of significant portions of the chromosome arms has occurred between the two species, and there appears to be a reduction on noncoding regions in *Drosophila* relative to *Anopheles*. Differences in the genomes should lead to a better understanding of phenotypic controls, host-seeking preferences, and parasite susceptibility.

Christophides *et al.* (p. 159) have studied gene families and gene sets involved in innate immunity. Comparisons with *Drosophila* suggest that adaptive demands on the immune system are reflected in a lack of orthologs and an increase in species-specific gene expansions. Riehle *et al.* (p. 172) have used genomic comparisons to identify orthologous genes in the malaria mosquito that are thought to

## Adding Water to Acid

How many water molecules are needed to dissolve an acid such as HBr so that the separated H<sup>+</sup> and Br<sup>−</sup> ions form? Pump-probe spectroscopic studies by Hurley *et al.* (p. 202; see the Perspective by Robertson and Johnson) of gas-phase HBr-

regulate the complex physiologies of parasite–host interactions, development, molting, reproduction, and the osmotic challenges of blood feeding. One potential control tactic the authors suggest is to interfere in the insulin–signaling pathway used by *Anopheles* and the *Plasmodium* malaria parasite, whereby the life–span of the mosquito is shortened to prevent the development and transmission of the parasite.

Genetic mapping studies have previously identified insecticide resistance–associated loci along the mosquito chromosomes. Ranson *et al.* (p. 179) used the genome of *A. gambiae* to pinpoint genes coinciding with these loci and to examine the three major gene families involved in insecticide detoxification, the carboxylesterases, glutathione transferases, and cytochrome P450. A comparison with *Drosophila* reveals the expansion of certain families in the mosquito as a result of local duplications.



### Homing In on Us

The G protein–coupled receptors (GPCRs) in *A. gambiae* are of special interest because of their importance to the mosquito's life cycle and because odorant and gustatory receptors are likely to contribute to the extraordinary success of this mosquito as a human disease vector. Hill *et al.* (p. 176) present an initial survey of GPCRs found in the *A. gambiae* genome sequence and characterized 79 possible odorant receptors for tissue expression.

### Mosquito Gene Shuffling

A comparative study of *Anopheles gambiae* and *A. funestus*, important vectors of malaria in tropical Africa, by Sharakov *et al.* (p. 182) shows that synteny (the occurrence of genes on the same chromosome) is well preserved, but that the rates of gene shuffling resulting from inversions and synonymous substitutions have been exceptionally high. More than 70 chromosomal inversions are fixed between the two species, a rate that exceeds even that observed in *Drosophila*. Chromosome 2R specifically seems to harbor a hot spot of inversion fixation. The rapid rate of chromosome evolution reflects a similarly high rate of evolution at the sequence level. This study also suggests that positional cloning and microarray experiments may be successful only for very closely related species of mosquito.

### Clues into Chloroquine Resistance

Global resistance has made chloroquine, the traditional malaria drug, almost useless. Sidhu *et al.* (p. 210; see the Perspective by Hastings *et al.*) have investigated the correlation between chloroquine resistance among parasites and the occurrence of multiple point mutations in a gene called *pfcr*, which encodes a membrane–spanning protein. Using allelic exchange, they transferred alleles of *pfcr* from chloroquine–resistant parasites into a chloroquine–sensitive strain of *Plasmodium falciparum*. Clones of the engineered parasites displayed similar chloroquine resistance to those of the original without having had any prior exposure to the drug. The point mutations appear to confer quite specific structural recognition to chloroquine, so amodiaquine, a new antimalarial with a similar structure to chloroquine, is still effective against chloroquine–resistant parasites.

### Mosquito Resistance to Malaria

Anopheline mosquitoes are naturally resistant to *Plasmodium falciparum*. Niaré *et al.* (p. 213) take an initial step toward describing the genetics of resistance and the molecular mechanisms underlying natural refractoriness in outbred populations of mosquitoes. They identified two loci on chromosome 2, *Pfin1* and *Pfin2*, associated with resistance.

### *Plasmodium* Population Dynamics

The approach to studying the population dynamics of the malaria parasite *Plasmodium falciparum* is described by Volkman *et al.* (p. 216), who used a microarray of chromosome 2 to search for sequence polymorphisms between different parasite isolates. Most of the variation is concentrated at the chromosome ends and in few internal genes. This technology offers a rapid route to tracking the origins of infections and of new mutations involved in drug resistance and immunity.