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Bloodthirsty Hitchhikers?

NEARLY 100 YEARS AGO, FAHRENHOLZ claimed that parasite phylogeny mirrors host phylogeny (1). The report "Resolution of the early placental mammal radiation using Bayesian phylogenetics" by William J. Murphy and colleagues (14 Dec., p. 2348) brought to our minds Fahrenholz's idea, which, although in many cases not true in the strict sense, served as a hypothesis in numerous studies of coevolution. There are some striking parallels between the proposed placental mammal phylogeny and the proposed phylogeny of the mosquito genus *Anopheles* (2).

Anophelines are mammalian ectoparasites whose life cycles depend on a protein-



A female *Anopheles gambiae*.

rich blood meal required by females for egg production. Similar to placental mammals, anophelines likely originated on the ancient supercontinent Gondwana, and their basal lineages experienced rapid diversification that might have coincided with the separation of South America and Africa.

Because no sufficiently old mosquito fossil records are available, our understanding of anopheline evolutionary history depends largely on a careful analysis of their geographical distribution. Of the six *Anopheles* subgenera, *Stethomyia*, *Lophopodomyia*, *Kerteszia*, and *Nyssorhynchus* inhabit South America, *Cellia* is found in the Old World, and *Anopheles* is cosmopolitan. Remarkably, like the placental mammal clade Boreoeutheria, subgenera *Anopheles* and *Cellia* not only appear to occupy a derived (as opposed to basal) position in the anopheline phylogeny, but also are the most diverse. Phylogenetic evidence suggests that the subgenus *Anopheles*, after origination in South America and rapid dispersal throughout Laurasia, reentered the Neotropics from the north. Presumably, then, the early radiation of mammals was closely followed by radiation of anophelines, which thrived on the blood of newly emerging taxa. If this was the case, further studies of *Anopheles* phylogeny might shed new light on such issues in mammalian evolution as timing of divergences and routes of dispersal.

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References and Notes

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2. J. Krzywinski et al., *Syst. Biol.* **50**, 540 (2001).

Neuroscience of Stuttering

WE DISAGREE WITH WILLIAM H. PERKINS' comments (Letters, "Stuttering: a matter of bad timing," 26 Oct., p. 786) pertaining to the Random Samples item "The stammering brain" (3 Aug., p. 795). Perkins takes issue with the discovery by Anne Foundas at Tulane University and her colleagues that anatomical differences between stutterers and nonstutterers in the two brain regions

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NHLBI Mammalian Genotyping Service



The Mammalian Genotyping Service is funded by the National Heart, Lung, and Blood Institute to assist in linkage mapping of genes which cause or influence disease and other research purposes. Genotyping is carried out using whole genome polymorphism scans at Marshfield, Wisconsin under the direction of Dr. James Weber. Capacity of the Service is currently about 7,000,000 genotypes (DNA samples times polymorphic markers) per year and growing. Although the Service was initially established for genetic projects dealing with heart, lung, and blood diseases, the Mammalian Genotyping Service will now consider all meritorious applications. Genome scans for humans, mice, rats, dogs and zebrafish are available.

To ensure the most promising projects are undertaken, investigators must submit a brief application which will be evaluated by a scientific advisory panel. At this time, only projects with at least 10,000 genotypes will be considered. DNA samples must be in hand at the time of application. Most genotyping within the Service is currently done with multiallelic STRPs (microsatellites). However, genotyping with human diallelic polymorphisms has been initiated and will likely expand. **There are no genotyping fees for approved projects.** The Service is funded through September, 2006. Application deadlines are every six months.

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