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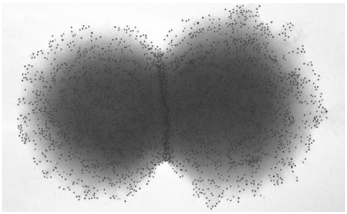
INAUGURAL ARTICLE, MEDICAL SCIENCES

Vaccine for group B meningitis

Neisseria meningitidis is the causative agent of bacterial meningitis and sepsis, diseases that affect ≈1.2 million people worldwide annually, particularly children. Almost all disease-causing bacterial strains fall into the A, B, C, Y, or W135 subtypes (serogroups). Of these, the currently available vaccine for serogroup B meningococcus, which is responsible for a majority of cases in developed countries, is ineffective (due to a self-antigen present in this bacterial subtype's capsular polysaccharide). Marzia Giuliani *et al.* report the development of a recombinant vaccine that protects mice against up to 95% of the bacterial strains principally responsible for serogroup B meningitis. Using the sequenced *N. meningitidis* genome as a guide, the authors screened numerous antigens in mice for antibody production and designed a vaccine combining the five best candidate antigens with aluminum hydroxide, a common human vaccine adjuvant. This vaccine protected mice against 78% of the serogroup B strains tested; other adjuvants increased the coverage to as much as 95%. Giuliani *et al.* believe that this study, which used human-safe adjuvants and a large pool of bacterial strains, could lead to clinical studies that may help eradicate this childhood disease. — N.Z.



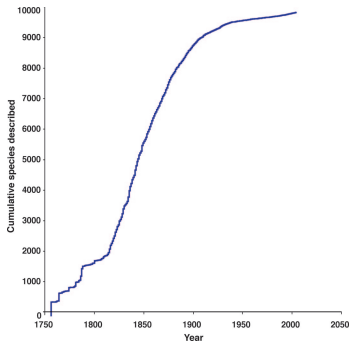
Serogroup B meningitis vaccine.

"A universal vaccine for serogroup B meningococcus" by Marzia M. Giuliani, Jeannette Adu-Bobie, Maurizio Comanducci, Beatrice Aricò, Silvana Savino, Laura Santini, Brunella Brunelli, Stefania Bambini, Alessia Biolchi, Barbara Capecchi, Elena Cartocci, Laura Ciucchi, Federica DiMarcello, Francesca Ferlicca, Barbara Galli, Enrico Luzzi, Vega Masignani, Davide Serruto, Daniele Veggi, Mario Contorni, Maurizio Morandi, Alessandro Bartalesi, Vanda Cinotti, Donatella Mannucci, Francesca Titta, Elisa Ovidi, JoAnne Welsch, Dan Granoff, Rino Rappuoli, and Mariagrazia Pizza (see pages 10834–10839)

ECOLOGY, SUSTAINABILITY SCIENCE

Reconsidering past, present, and future bird extinctions

At present, ≈130 of the 10,000 identified species of birds are known to have gone extinct since the year 1500, which results in an estimated bird extinction rate of 26 extinctions per million species per year (26 E/MSY). Stuart Pimm *et al.*, however, suggest that this estimate does not take into account certain key factors. According to the authors, the continual identification of new extinct species from skeletal remains, the consideration of missing bird species that have not yet been declared extinct, and the fact that most species of birds are known only after 1850 and not 1500 would all increase the actual extinction rate. When correcting for these factors, Pimm *et al.* present an updated estimate of 100 E/MSY since 1500, although in recent decades conservation efforts have lowered the value to 50 E/MSY. However, increased rates of habitat loss, as well as more modern threats such as invasive species and climate change, may cause a dramatic increase in extinction in the coming years. In fact, the authors predict a rate of 1,000 E/MSY in the 21st century, which could wipe out 12% of all bird species within 100 years. — N.Z.



Description dates of world's bird species.

"Human impacts on the rates of recent, present, and future bird extinctions" by Stuart Pimm, Peter Raven, Alan Peterson, Çağan H. Şekercioğlu, and Paul R. Ehrlich (see pages 10941–10946)

EVOLUTION

Tropical forests as "cradles" and "museums" of biodiversity

In regions of high species diversity like tropical forests, two evolutionary models are generally pitted against each other to explain the level of variation. The "cradle" model assumes that biodiversity primarily results from recent and rapid diversification, whereas the "museum" model suggests that biodiversity slowly accumulated over time, with tropical forests preserving ancient varieties of organisms. However, Duane McKenna and Brian Farrell report that the evolutionary histories of tropical organisms exhibit characteristics of both models. The authors surveyed the species-rich *Cephaloleia* genus of herbivorous Neotropical leaf beetles. Using molecular genetic, fossil, and biogeographic data, the authors found signatures of both "cradle" and "museum" models. They identified rapid diversification stemming from adaptive radiation beginning ≈55 million years ago, coinciding with massive climate changes. Ancient lineages originating from adaptive radiation events in the Oligocene era were found. Also, diversification during the relatively recent Miocene–Pliocene period coincident with the collision of the Panama arc with South America was observed. These highlights of *Cephaloleia* evolutionary history demonstrate that these organisms are products of both recent and ancient evolution. — B.T.

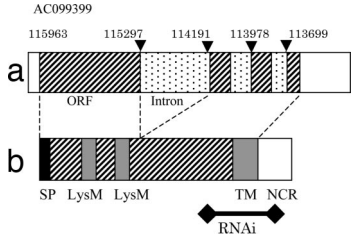
Beetle *Cephaloleia championi*.

"Tropical forests are both evolutionary cradles and museums of leaf beetle diversity" by Duane D. McKenna and Brian D. Farrell (see pages 10947–10951)

PLANT BIOLOGY

Glycoprotein helps rice fight infection

To defend against infection, plants initiate immune responses upon detection of macromolecules such as cell wall polysaccharides and proteins secreted by invading microorganisms. Derived from chitin, the major component of fungal cell walls, chitin oligosaccharides are known to induce defense responses in a wide range of monocots and dicots, but their receptors in these plants have remained elusive. Hanae Kaku *et al.* have identified a protein that aids rice in detecting potentially infectious microorganisms, the chitin oligosaccharide elicitor-binding protein (CEBiP). The researchers isolated and cloned the glycoprotein CEBiP from plasma membranes of cultured rice cells. In these cells, knockdown of the *CEBiP* gene by RNA interference suppressed responses typically elicited by invading pathogens, such as the production of reactive oxygen species. CEBiP contained amino acid motifs known to exist in receptors that are involved in signaling between legumes and nitrogen-fixing soil bacteria. This similarity, the authors say, indicates that homologous plasma membrane proteins are involved in both plant defense and symbiotic signaling. — F.A.



CEBiP schematic.

"Plant cells recognize chitin fragments for defense signaling through a plasma membrane receptor" by Hanae Kaku, Yoko Nishizawa, Naoko Ishii-Minami, Chiharu Akimoto-Tomiyama, Naoshi Dohmae, Koji Takio, Eiichi Minami, and Naoto Shibuya (see pages 11086–11091)