In Brief

No pain in marine waters

Beneath the sea surface lies a gold mine of chemicals that could have potential uses in the therapeutic treatment of human diseases. This treasure is found in marine organisms, which contain molecules with unique structures. The quest for these marine natural products has already brought positive results. One of these results was presented at the 2000 International Chemical Congress of Pacific Basin Societies (13–19 December 2000, Honolulu, HI, USA) by William Gerwick of Oregon State University (Corvallis, OR, USA). Gerwick reported the discovery of several new neurotoxic lipopeptides, isolated from marine cyanobacteria collected in the Caribbean Sea off Venezuela. Among the isolated compounds, one named kalkitoxin possesses intriguing pharmacological properties. Kalkitoxin appears to act by specifically blocking the Na^+ channels of neurons, thus preventing the nerve cells from firing off their electrical signals. Researchers hope to harness this property, not only to fight pain, but also to treat neurodegenerative diseases and nerve disorders such as epilepsy. (http://center.acs.org/applications/news)

A new phase for protein structures

Structural biologists determine the atomic structure of a protein by blasting the crystal with a beam of X-rays, followed by long weeks spent decoding the scattering pattern that results. However, physicist Veit Elser of Cornell University (Ithaca, NY, USA) is developing new computer algorithms that will significantly speed up the analysis of scattering data. The concept addresses the problem of measuring the *phases* of X-rays emerging from a sample: current X-ray diffraction methods measure the amplitude of the Fourier components of the electron density, but give no more information about the phases. Phase information would greatly help to decipher the pattern of the scattering data, and Elser hopes to find a way to identify, with the aid of computers, the phase pattern that corresponds correctly to the measured amplitudes. (http://www.news.cornell.edu/Chronicles)

EMBL increases technology transfer activities

Decisions were made at the last Council meeting of EMBL (European Molecular Biology Laboratory) that are strategically important to the development of biotechnology in the member states. The Council has planned the construction of an International Technology Transfer Centre (ITTC) on the EMBL campus in Heidelberg (Germany) (due to be completed by June 2002), to ensure that key research findings and technological innovations from the institution can move to industry in an efficient way. A commercial investment fund, named the Technology Transfer Fund, has also been established and is expected to provide funding mainly for EMBL-associated biotech start-up companies. (http://www.embl-heidelberg.de/ExternalInfo/oipa/presscon/PCengl.html)

A transatlantic bridge for bioinformatics

A new and powerful software package for simulating and analyzing biochemical pathways is currently under development. The project, named COPASI (Complex Pathway Simulator), involves bioinformatics experts at the Heidelberg-based European Media Laboratory (EML), a private research center for information technology; and the Virginia Bioinformatics Institute (VBI), a branch of Virginia Polytechnic Institute and State University (Blacksburg, VA, USA). Project leaders Ursula Kummer (EML) and Pedro Mendes (VBI) are confident that the new research program will significantly expand current possibilities for biochemists to simulate complex metabolic processes. When completed, the software package will be freely available for academic institutions. (http://www.vbi.vt.edu/archive/copasi_announce1.html)

A green light glows on copper disorders research

The complete genome of *Arabidopsis thaliana* – the first from the plant kingdom – is now in our hands. Expectations are that this discovery will also benefit fields not directly related to plant genetics and crop production. Human health could be one of these fields. This hope is fueled by the discovery that many of the *Arabidopsis* genes show a significant similarity to genes involved in human disease syndromes. In some cases, the human genes are more similar to the *Arabidopsis* homologues than to the genes of yeast, *Drosophila*, or *Caenorhabditis elegans*. Included in this group are the genes implicated in Wilson's and Menkes diseases, two disorders of copper homeostasis [Nature (2000) 408, 823–826]. The defective functioning of the membrane-bound copper-transporting P-type ATPases that are coded by these genes, leads to copper deficiency (Menkes) or copper accumulation (Wilson). Of the two conditions, Menkes is by far the worst, being usually fatal in childhood. Researchers at Deakin University (Burwood, Victoria, Australia) led by Julian Mercer, together with colleagues from Melbourne University (Melbourne, Victoria, Australia), are studying Menkes protein structure and function, and trying to understand why different mutations of the Menkes gene give rise to the diverse aspects of the disease. Experimental efforts are also directed at understanding how deleterious Menkes effects can be over-run on a genetic and molecular level. Study strategies include the transfection of cells from Menkes patients with healthy Menkes genes, and the manipulation of the Wilson's gene (which is normal in Menkes patients), to act as a surrogate for the defective Menkes gene. (http://www.research.deakin.edu.au/research_stories)

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