

# Genomics firm aims to fill Asian gene gap

David Cyranoski, Tokyo

A Taiwanese company last week turned the spotlight on Asian genetic variability when it opened its laboratories in Taipei.

Vita Genomics was formed last year to mine the mass of public and private genetic data in an effort to trace genes among the Asian population that are linked to specific diseases.

Researchers elsewhere in east Asia hope that the company's work will encourage the various governments to increase their efforts to use information on genetic variation to study diseases in the region.

Vita will focus on single nucleotide polymorphisms (SNPs), the single base variations in the genome that account for many genetic differences between individuals. SNPs can be used as markers in studies to identify the genes involved in a population's susceptibility to a given disease and its response to drugs.

By scouring databases of some 5 million SNPs, and comparing them with DNA taken from Taiwanese patient samples, Vita hopes to identify genes that are related to diseases, such as hepatitis, that are common in Asia. According to Vita's president, Ellson Chen, the databases to be used include those main-

tained by the international Human Genome Project and by the US-based company Celera Genomics. Celera, which owns a 5% stake in Vita, helped to set up the company after abandoning its original plan to establish a subsidiary in Taiwan.

"Western drug companies mostly concentrate on diseases common in the West," says Chen. "This has left a gap." As an example, he cites the difficulty of treating hepatitis B and C in Taiwan, where fewer than half of its victims respond to an interferon 'cocktail', the standard drug treatment.

"If we look at SNP patterns on 300 genes which seem to affect whether or not a patient responds to interferon, we could find out why the drug works when it does," says Chen. By July, he hopes to have a first draft of SNPs correlated to some 300 genes related to hepatitis C.

Vita already has a contract with the National Taiwan University Hospital to obtain samples from patients with hepatitis. It also plans to look at patients with breast cancer, liver cancer and asthma. "Even diseases common around the world could have different relevant SNPs in Asian populations," says Chen. Vita intends to cooperate with other institutes in Taiwan, especially the

Academia Sinica, which is greatly expanding its functional genomics capacity.

The question of how genetic diversity between different ethnic groups influences human health is a hotly contested one. But many researchers in east Asia believe that distinct sets of SNPs within a region can influence susceptibility to disease and response to drugs.

Similarities in disease susceptibility across Asian populations have encouraged Vita to mine extensive SNP data that are becoming publicly available in Japan. Yusuke Nakamura, director of the Human Genome Center at the University of Tokyo's Institute of Medical Science, has already found 200,000 SNPs, and has data on how often each variant exists in the population at some 23,000 of these sites (see *Nature* 410, 1013; 2001).

"These data should help any group studying Asian populations, because the SNPs will behave very similarly among the various Asians," says Pui-Yan Kwok, a geneticist at Washington University School of Medicine in St Louis, who is a scientific adviser to Vita.

♦ [snp.ims.u-tokyo.ac.jp](http://snp.ims.u-tokyo.ac.jp)

♦ [www.vitagenomix.com](http://www.vitagenomix.com)

# Formidable catalogue puts army of ants online

Tom Clarke, London

After four years of cooperation and tenacity worthy of their quarry, ant experts have completed Antbase, a centralized, online information resource cataloguing all 11,000 known species of ant.

Its creators hope that Antbase will one day become the ant equivalent of GenBank, the public database of genetic sequence data, and a boon not just for ant specialists, but for entomologists and ecologists of every kind.

Ant taxonomists Donat Agosti of the American Museum of Natural History in New York and Norman Johnson of Ohio State University in Columbus built Antbase using funds from general research budgets and small institutional grants. Having compiled a full list of ant names, they hope their homespun project will now win long-term funding and a permanent home. "It needs to be institutionalized," says Agosti.

The database's backbone is an updated list of species names. Compiling the list was anything but trivial, Agosti and Johnson say. Descriptions of new species published in obscure journals over the past century had led to heavy duplication. As the project progressed, Antbase shrank to its current size from an initial list of over 20,000 names. "We're trying to pick up the debris from



Ants galore: the foundation of Antbase provides an updated list of species names.

nineteenth-century taxonomy," says Johnson.

Records for each species are being linked to information on their geographical distribution and life history, plus pictures held by the Japanese Ant Color Image Database.

Antbase could emerge as a long-needed resource for ant taxonomists, says Ted Schultz, who works as one at the

Smithsonian Institution in Washington DC. "Before, you had to spend hours photocopying thousands of pages of primary literature," he says. The resource could also aid more general studies of ecosystems, where ants often have a prominent role. "Ants are an incredibly useful ecological indicator," Schultz adds.

♦ [www.antbase.org](http://www.antbase.org)