

In hierdie uitgawe:  
In this issue:

Redaksioneel	1
Genes behind common diseases	2
DOE Genome Institute	4
GM tomatoes	6
Promega Young Scientist of the Year Award	6
SAGS 2008	7
Smelly new orchid	8
Question of the year	8
Sci-doku	9

## Redaksioneel

Baie welkom terug in die tweede semester. Hopelik kon daar baie werk in die labs uitgerig word en is daar selfs so paar artikels ingestuur of aanvaar!!

I would like to remind you of two conferences in 2008 which might be of interest to most of the geneticists in the country. The first is the **20th Biannual South African Genetics Society (SAGS) Congress** which will be held at the University of Pretoria from **27 - 29 March 2008**. The abstract and early registration deadline for this is **30 January 2008**. Start preparing those abstracts and please encourage student participation specifically. Two international plenary speakers have already been confirmed:

**Prof. Rob Martienssen, Cold Spring Harbor Laboratory.** Prof Martienssen is a world-leader in the epigenetic mechanisms of

transposon silencing, gene regulation, stem cell fate and cell function in plants. **Dr Sergei Kosakovsky Pond, Antiviral Research Center, University of California San Diego.** Dr Pond's research focuses on developing methods, algorithms and software for statistical analysis, inference and hypothesis testing on molecular sequence data.

The second conference is **International Congress of Genetics**, to be held in Berlin, Germany, **July 12-17, 2008**. The abstract and early registration deadline for this is **15 January 2008**.

In hierdie uitgawe verskyn die amptelike persverklaring vir **DOE Joint Genome Institute** wat hulle nuutste **Community Sequencing Program (CSP)** portfolio bekendgestel het. Baie geluk aan ons ondervoorsitter Zander Myburgh en sy navorsingspan wat deel vorm van hierdie grootskaalse pro-

jek met hulle werk op die *Eucalyptus* genoom.

Remember we are on the web so for more info visit our homepage [sagene.co.za](http://sagene.co.za). If you want to see some specific info there please let us know.

Sterkte met die res van hierdie kwartaal en mag die res van hierdie jaar vir jou goeie navorsingsresultate, topgehalte publikasies en blink idees inhou!!!!

Navorsingsgroete  
[ROUVAY ROODT-WILDING](#)



It requires a very unusual mind to undertake the analysis of the obvious.

Alfred North Whitehead (1861-1947) English philosopher and mathematician

## Genes behind common diseases

In the largest ever study published to date, a consortium of UK scientists has discovered over 20 genes and regions of the human genome that contribute to diseases such as diabetes, rheumatoid arthritis and coronary heart disease.

The Wellcome Trust Control Consortium's 9 million pound study is a collaboration of 200 UK scientists from 50 teams at dozens of UK institutions. Between them they have analysed nearly 10 billion pieces of genetic information from 17,000 people throughout the UK in two years.

Their work comprises the largest ever study on the genetic origins of disease and was published in the journals *Nature* and *Nature Genetics* recently.

In the study they focused on single nucleotide polymorphic (SNPs) DNA markers.

People who share the same ethnic lineage often share the same SNPs. For instance, most Europeans share about 8 million of them. In this study, the scientists examined half a million SNPs and found more than 10 genes plus fragments of DNA that appear to be linked to elevated risk of some common diseases.

Chair of the Consortium, Professor Peter Donnelly from the University of Oxford said that: "Many of the most common diseases are very complex, part 'nature' and 'nurture', with genes interacting with our environment and lifestyles. He added that by identifying the genes underlying these conditions, their study should enable scientists to understand better how disease occurs, which people are most at

risk and, in time, to produce more effective, more personalised treatments.

Many of the discoveries were a surprise; scientists had not thought them to be related to disease. As more large scale studies complete their work, it is likely that more such surprises could be waiting to be discovered.

Dr Mark Walport, Director of the Wellcome Trust explained: "This research shows that it is possible to analyse human variation in health and disease on an enormous scale. It shows the importance of studies such as the UK Biobank, which is seeking half a million volunteers aged between 40 and 69, with the aim of understanding the links between health, the environment and genetic variation."

Of particular significance is the discovery of a link between the autoimmune diseases type 1 diabetes and Crohn's disease which causes inflammatory bowel. A gene called PTPN2 appears to link the two conditions.

Also, in the case of Crohn's, the study has confirmed the importance of the role of autophagy in the development of the disease. Autophagy (literally self-eating) is a cellular process for clearing cells of rubbish like unwanted bacteria. In Crohn's disease the immune system reacts to normal gut bacteria, and more understanding of autophagy and how it deals with bacteria could have clinical significance.

Professor John Todd from the University of Cambridge, who led this part of the study said: "The link between type 1 diabetes and Crohn's dis-

ease is one of the most exciting findings to come out of the Consortium." He added "It is a promising avenue for us to understand how the two diseases occur. The pathways that lead to Crohn's disease are increasingly well understood and we hope that progress in treating Crohn's disease may give us clues on how to treat type 1 diabetes in the future."

The Consortium scientists analysed DNA samples from 2,000 patients for each of seven major diseases (bipolar disorder, Crohn's disease, coronary heart disease, hypertension, rheumatoid arthritis and type 1 and type 2 diabetes) and 3,000 healthy controls. The next stage will be to get samples from larger populations to confirm the results.

Professor Donnelly summed up the contribution this study has made: "Human genetics has a chequered history of irreproducible results, but this landmark collaboration of scientists in Britain has shown conclusively that the new approach of analysing a large subset of genetic variants in large samples of patients and healthy individuals works." He concluded "We are now able to effectively scan most of the common variation in the human genome to look for variants associated with diseases. This approach will undoubtedly herald major advances in how we understand and tackle disease in the future."

However, the researchers are cautious when it comes to suggesting how soon genetic screening could be used to help individuals find out if whether they are going to develop a disease.

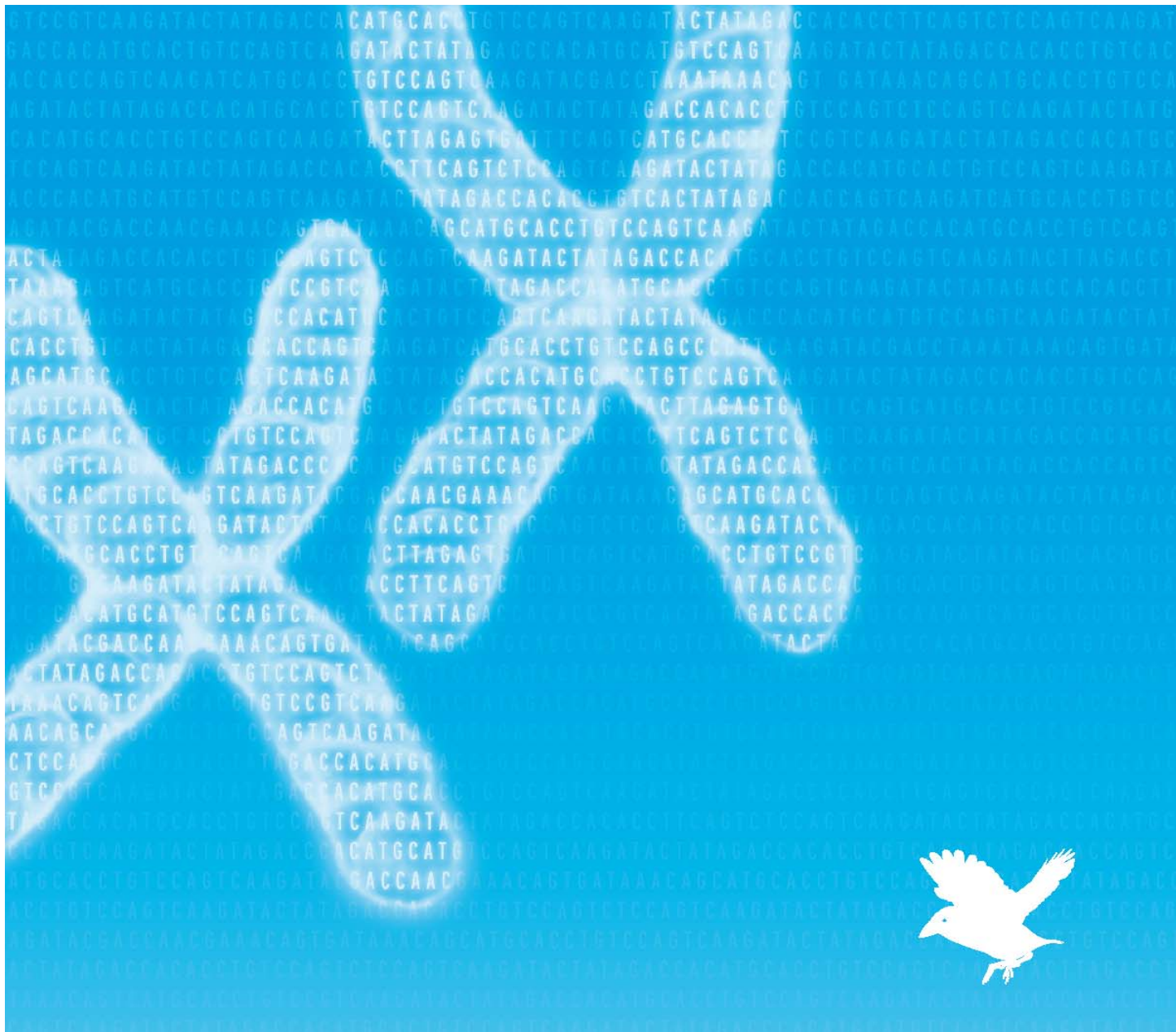
Having a predisposition is no longer seen as a matter of a particular gene. It could be a complex pattern of several genes acting together, and a tipping point that is decided by environment and lifestyle factors. However, the knowledge of whether they have one or both genes that predisposes an illness could help people make informed decisions about lifestyle and reduce the risk of that condition being triggered.

The Consortium is also looking into the genes behind tuberculosis (TB), breast cancer, autoimmune thyroid disease, multiple sclerosis and ankylosing spondylitis and will be publishing their findings later this year.

UK Biobank is a registered charity and major UK medical research project that aims to improve the prevention, diagnosis and treatment of a wide range of serious and life-threatening illnesses. These illnesses include cancer, heart diseases, diabetes, arthritis and forms of dementia.

The project is currently recruiting 500,000 people aged 40 to 69 from across the UK to be assessed and give blood samples.

The UK Biobank is funded by the Wellcome Trust, the Medical Research Council, the Department of Health, the Scottish Executive and the Northwest Regional Development Agency. It is also backed by the National Health Service and many of the UK's major medical research charities, including the British Heart Foundation and Cancer Research UK.



# GENETICS – UNDERSTANDING LIVING SYSTEMS

## XX INTERNATIONAL CONGRESS OF GENETICS

### BERLIN, GERMANY, JULY 12 – 17, 2008

A CONGRESS UNDER THE AUSPICES  
OF THE INTERNATIONAL GENETICS FEDERATION (IGF)

**CONGRESS PRESIDENT**

Prof. Dr. Rudi Balling  
Braunschweig · Germany

**SECRETARY GENERAL**

Prof. Dr. Alfred Nordheim  
Tübingen · Germany

**CONGRESS SECRETARIAT**

K.I.T. GmbH  
Association & Conference Management Group & Co. KG  
Kurfürstendamm 71 · 10709 Berlin · Germany  
Phone: ++49-30-246 03-0  
Fax: ++49-30-246 03-200  
E-Mail: [info@geneticsberlin2008.com](mailto:info@geneticsberlin2008.com)



German  
Genetics  
Society  
(IGF)

[WWW.GENETICSBERLIN2008.COM](http://WWW.GENETICSBERLIN2008.COM)

## DOE Genome Institute

### DOE Joint Genome Institute Announces 2008 Genome Sequencing Targets Eucalyptus, Foxtail Millet, Red Algae, and Novel Microbial Communities Added to Growing Bioenergy and Carbon Cycling Portfolio

WALNUT CREEK, CA—Toward the goal of harnessing the power of nature through DNA sequencing, the DOE Joint Genome Institute (DOE JGI) has announced the latest Community Sequencing Program (CSP) portfolio. These plant and microbial targets—most with implications for helping wean the nation's dependence on fossil fuel—total some 21 billion nucleotides of DNA sequence capacity allocated to public projects submitted through the CSP for fiscal year 2008.

"This year's selections are completely aligned with the CSP mission, that is, selecting DOE-relevant organisms with the large and diverse communities of investigators," said Jim Bristow, DOE JGI Deputy Director and manager of the CSP. "The response to this year's program, with over 120 submissions, demonstrates an increasing desire to fuel discovery with DNA sequence information—which DOE JGI makes freely available through its web portals and the public databases." Among the highest profile of these projects, and largest, with a 600-million-nucleotide genome, is the eucalyptus tree genome—geared to the generation of resources for renewable energy—led by Alexander Myburg of the University of

Pretoria, South Africa, with Gerald Tuskan of Oak Ridge National Laboratory (and DOE JGI), and Dario Grattapaglia, of EMBRAPA Genetic Resources and Biotechnology (Brazil).

"The biomass production and carbon sequestration capacities of eucalyptus trees match DOE's and the nation's interests in alternative energy production and global carbon cycling," said Bristow. "The consortium of eucalyptus draws upon the expertise from dozens of institutions and hundreds of researchers worldwide."

"A major challenge for the achievement of a sustainable energy future is our understanding of the molecular basis of superior growth and adaptation in woody plants suitable for biomass production," said CSP project proposer Myburg. Eucalyptus species are among the fastest growing woody plants in the world and, at approximately 18 million hectares in 90 countries, the most widely planted genus of plantation forest trees in the world. Eucalyptus is also listed as one of the U.S. Department of Energy's [candidate biomass energy crops](#).

"Genome sequencing is essential for understanding the basis of eucalyptus's superior properties and to compare and contrast them with other species," said Myburg. "The unique evolutionary history, keystone ecological status, and adaptation to marginal sites make eucalyptus an excellent focus for expanding our knowledge of the evolution and adaptive biology of perennial plants." The eucalyptus genome, the second tree to be sequenced, will also provide extraordinary oppor-

tunities for comparative genomic analysis with the poplar, the first tree sequenced, published in the journal *Science* by DOE JGI and collaborators in 2006.

The second largest CSP project selected for 2008 is foxtail millet (*Setaria italica*), led by researchers at the University of Georgia, the University of Florida, the University of Missouri, the U.S. Department of Agriculture Agricultural Research Service - Cold Spring Harbor Laboratory, and the University of Tennessee.

Foxtail millet, a forage crop, is a close relative of several prospective biofuel crops, including switchgrass, napiergrass, and pearl millet. In the U.S., pearl millet is grown on some 1.5 million acres. It is envisioned that pearl millet would be useful as a supplement or replacement for corn in ethanol plants in regions that suffer from drought and low-fertility soils.

The third largest genome project to be taken on by DOE JGI in 2008 is the marine red alga *Porphyra purpurea*. The ocean plays a key role in removing carbon dioxide from the atmosphere with the help of marine photosynthetic organisms like *Porphyra* consuming the carbon and releasing oxygen. *Porphyra* species are among the most common algae in the intertidal and subtidal zones of temperate rocky shores in both the northern and southern hemispheres. Understanding the effects of elevated climatic stresses on photosynthetic organisms would benefit from genome-enabled studies of carbon fixation in *Porphyra*, because of this organism's great diversity of light-

harvesting and photoprotective strategies.

The CSP will pursue eight smaller eukaryotic projects in 2008, using both traditional Sanger sequencing and next-generation pyrosequencing technology. These projects include the following:

- *Paxillus involutus*: Over 75 percent of the carbon in terrestrial ecosystems is stored in forests. More than half of this carbon is found in soil organic matter (SOM). Recent studies have indicated that ectomycorrhizal fungi like *Paxillus* provide the dominant pathway through which carbon enters the SOM. These fungi are also known to protect plants from toxic metals. Thus, the development of metal-tolerant fungal associations would provide a strategy for active remediation of metal-contaminated soils.
- Two species of *Phaeocystis* phytoplankton: The *Phaeocystis* genus contributes approximately 10 percent of annual global marine primary photosynthetic production, equivalent to four billion metric tons of carbon dioxide captured or "fixed" annually—reinforcing its importance for the study of the global carbon cycle and carbon sequestration.
- The leaf-degrading fungus *Agaricus bisporus*: Genomic studies of *A. bisporus* target enhanced understanding of the mechanisms employed for efficient conversion of lignocellulose—crucial for the production of fuels and products from renewable biomass.
- The first ciliated protozoan genome, *Tetrahymena thermophila*: A microbial model organism for discov-

## DOE Genome Institute

vering fundamental principles of eukaryotic biology, it will allow improved construction and stability of cell lines for the over-expression of proteins, including cellulase enzymes to overcome the limiting hurdle of biomass-to-biofuel production and metal-chelating proteins to enhance the already superior capacity of ciliates for bioremediation of toxic heavy metals in industrial effluents.

- **Pine and Conifer EST resource:** expressed sequence tags (ESTs) are fragments of DNA sequence that serve as a tool for the identification of genes and prediction of their protein products and their function. Conifer forests are among the most productive in terms of annual lignocellulosic biomass generation, and coniferous trees are the preferred feedstock for much of the forest products industry. Climate change and exotic forest pests are threatening conifer populations. Breeding programs to improve conifers will benefit from access to this genomic resource.

- **The soybean pathogen *Heterodera glycines*:** Soybean is a major oil, feed, and export crop, with \$17 billion annually in unprocessed crop value in the U.S. alone. Soy biodiesel is a leading contender for a renewable, alternative vehicle fuel with a high energy density. Soybean has the environmental and energy advantage of not requiring the use of nitrogen fertilizer. *H. glycines* is the most significant pathogen of soybean in the U.S.; thus, sequencing its genome would aid in the development of control strategies and directly con-

tribute to soybean yield enhancement.

The liverwort, *Marchantia polymorpha*: The origin of land plants is acknowledged as one of the major evolutionary events in the earth's history. Experimental, paleontological, morphological, and molecular systematic data all point to the liverworts as being among the first plants to evolve and colonize the landscape. Thus, liverworts are a key group to include in any comparative study aimed at understanding the origin and evolution of organisms that now cover much of terrestrial earth.

DOE JGI and its collaborators have pioneered the emerging discipline of metagenomics—isolating, sequencing, and characterizing DNA extracted directly from environmental samples—to obtain a genomic and metabolic profile of the microbial community residing in a particular environment. In addition to adding 54 different microbial isolate genomes to the production sequencing queue in 2008, DOE JGI will work with large communities of collaborators to take on four important metagenomic projects.

- **Anammox bacteria:** Anammox bacteria are able to synthesize the rocket fuel hydrazine from ammonia and hydroxylamine. Insight into the genes and proteins involved in this reaction may be the basis for further optimization of the production of this potent fuel in a suitable biological system. Also, anammox bacteria are responsible for about 50 percent of the processing of ammonia to nitrogen gas in the ocean. In marine ecosystems, the carbon and nitro-

gen cycles are closely connected. More information about the regulation and mechanism of CO<sub>2</sub> sequestration by anammox bacteria in the ocean will contribute to our understanding of the global biogeochemical cycles and their impact on climate change.

- **Biogas-degrading community:** It is estimated that 236 million tons of municipal solid waste is produced annually in the U.S., 50 percent of which is biomass. Converting organic waste to renewable biofuel represents an appealing option to exploit this potential resource. In California alone, it is estimated that 22 million tons of organic waste is generated annually, which if converted by microbial digestion, could produce biogas equivalent to 1.3 million gallons of gasoline per day. Yet little is known about the microorganisms involved and their biology. This study aims to optimize the anaerobic digestion process and promote conversion of biomass into biofuel.

- ***Accumulibacter* population genomics:** Enhanced biological phosphorus removal (EBPR) is a wastewater treatment process used throughout the world to protect surface waters from accelerated stagnation and depletion of oxygen. EBPR can be unreliable and often requires expensive backup chemical treatments to protect sensitive receiving waters. This project will shed light on the microbial population dynamics leading to better use and management of these important environmental systems. Genomics of Yellowstone geothermal environments: The hot pools of Yellow-

stone National Park harbor a mostly unexplored treasure-trove of extremeophiles, microbes that thrive in extreme conditions. These communities represent a rich opportunity to identify enzymes or processes that promise to advance biofuels and nanomaterial science applications.

Established in 2005, the Community Sequencing Program (CSP) provides the scientific community at large with access to high-throughput sequencing by DOE JGI for projects of relevance to DOE missions. Sequencing projects are chosen based on scientific merit—judged through independent peer review—and relevance to issues in bio-energy, global carbon cycling, and bioremediation.

For a full list of the CSP 2008 sequencing projects, see <http://www.jgi.doe.gov/sequencing/cspseqplans2008.html>

The DOE Joint Genome Institute, supported by the DOE Office of Science, unites the expertise of five national laboratories, Lawrence Berkeley, Lawrence Livermore, Los Alamos, Oak Ridge, and Pacific Northwest, along with the Stanford Human Genome Center to advance genomics in support of the DOE mission related to clean energy generation and environmental characterization and cleanup. DOE JGI's Walnut Creek, Calif. Production Genomics Facility provides integrated high-throughput sequencing and computational analysis that enable systems-based scientific approaches to these challenges.

**Source: University of Bath, Press release—29/03/07**

## GM tomatoes

Shoppers who miss the taste of farm-grown tomatoes may find solace in a new technology that puts back what generations of breeding for hardiness and shelf life have taken out. A new variety of tomato has been genetically modified (GM) to produce geraniol, a rose-smelling compound found in fruits and flowers. In a blind taste test, 60 percent of 37 testers preferred the flavor of the GM tomato, according to a study published online in *Nature Biotechnology*.

The result proves that genetic modification can potentially restore some of the flavor and aroma lost as breeders have created more durable strains of tomatoes and other crops, says biotechnologist

Efraim Lewinsohn of the Neve Ya'ar Research Center in Ramat Yishay, Israel, who led the research. "You often sit down in living rooms and people complain tomatoes don't taste like they used to," he says.

In an effort to banish such idle supper time chatter forever, Lewinsohn and colleagues gave extra-large cherry tomatoes a geraniol-synthesizing gene from the lemon basil plant. The modified tomato does not taste exactly like a traditional tomato, but it does noticeably change and enhance the flavor—something that GM technology has not achieved before, Lewinsohn says. Tomatoes contain more than 400 vola-

tiles, or potentially fragrant compounds, and researchers have yet to identify the most important contributors to the classic tomato taste.

The team found that tomatoes broke down geraniol into at least ten other lemon- and rose-smelling compounds. Taste testers described the fruit as smelling like rose, geranium and lemongrass. One side effect of the change was a reduction in lycopene, a red carotenoid pigment, which gave the tomatoes a more orange hue.

Lewinsohn says the commercial acceptance of this or any other flavor-enhanced tomato would depend on consumer

tastes and attitudes. He adds that, in principle, flavor improvement could come from more traditional breeding instead of GM technology, which is unpopular in European countries.

Another possible source of better-tasting tomatoes is the local farmers' market—or even the backyard garden—but Lewinsohn notes that locally grown tomatoes are not available year-round. "If you want commercial production of good quality tomatoes," he says, "that's more difficult."

**Scientific American**  
June 25, 2007

## Promega Young Geneticist of the Year Award

The International Genetics Society is seeking nominations for the 2008 Promega Young Geneticist of the Year Award. The competition is open to PhD student/recent post-doctoral graduate members of the Society.

This year we have decided to open up the competition to all student members of the Society and also those who have recently submitted their PhD thesis (after 1st January 2006). The competition is open to those working in any area of genetics and only previous

Promega YGYA prize winners are excluded from entering the 2008 competition.

Applications should consist of the thesis abstract, details of any publications arising from the work, the submission date of the thesis and a letter of recommendation from your supervisor and/or Head of Department (the supporting letter should be a signed copy sent in a sealed envelope or an electronic copy sent directly from the author's email address). Applications should be sent to the

Honorary Secretary of the Genetics Society, Prof. John Armour (john.armour@nottingham.ac.uk), and must be received by Friday 26th October 2007.

Up to 6 short-listed finalists will be invited to present their work at the Mammalian Genetics and Development Workshop, to be held at the Institute for Child Health in London on 29-30th November 2007.

Following this, three prizes will be awarded:

1st prize £600 and Promega Young Geneticist of the Year Award Trophy  
2nd prize £400  
3rd prize £200

In addition, the three prize winners will each receive a 1 year subscription to Science magazine, the media sponsors of this award.

The first prize winner will be invited to accept the award and to give a short presentation at a Genetics Society meeting during 2008.

[http://www.genetics.org.uk/promega\\_young\\_geneticist\\_of\\_the\\_year\\_award\\_2008](http://www.genetics.org.uk/promega_young_geneticist_of_the_year_award_2008)

## SAGS 2008

The first official notice of the **20th Biannual South African Genetics Society (SAGS) Congress** to be held in the Sanlam Conference Centre at University of Pretoria from **27 - 29 March 2008** has been sent out recently.

The SAGS 2008 Congress will be hosted by the Department of Genetics at UP. The theme of the conference will be "*The Next Century of Genetics*" and will form part of the University of Pretoria Centenary Programme in 2008.

The conference website can now be accessed at [www.sags2008.co.za](http://www.sags2008.co.za).

Early registration will open on 1 Oct 2007. Other major deadlines are listed on the website. Further registration details will soon be made available on the website.



Persons interested in participating in the SAGS 2008 Congress are encouraged to complete our pre registration survey: [SAGS 2008 Survey](#).

The organising committee also asks your kind assistance in updating the SAGS email database. Please distribute this information to all new students and colleagues that

may not be in the SAGS email database. Also please forward this to students or colleagues that may have relocated within the past two years.

If you want to receive further notices of the SAGS 2008 Conference, please send your email address to [mail@sags2008.co.za](mailto:mail@sags2008.co.za)

We look forward to hearing from you and hope that you will be able to participate in the 20th South African Genetics Society (SAGS) Congress.

Kind regards

**SAGS 2008 Organizing Committee**

For further questions, please contact the Conference Secretariat at [info@sags2008.co.za](mailto:info@sags2008.co.za)

## GE & Science Price for Young Life Scientists

Time's running out to submit your entry - Submission deadline is 1 August 2007.

The prize is open to all molecular biologists that have been awarded a Ph.D. during 2006. To enter, a student has to submit a 1,000 word synopsis of the doctoral work by August 1, 2007.

One Grand Prize winner and four regional winners will be selected.

Each winner will be flown to Stockholm, where they will meet some of the Nobel Prize laureates and visit GE Healthcare and Uppsala University. While in Stockholm they will also attend a prize ceremony.

The Grand Prize winner will receive \$25,000 and have the prize essay published in the journal *Science*. Regional winners will receive \$5,000 and have their essays published in the online version of *Science*.

Please feel free to forward this to any and all exceptional student

Ph.D.s you may know.

For further information visit:

[www.sciencemag.org/feature/data/prizes/ge/index.dtl](http://www.sciencemag.org/feature/data/prizes/ge/index.dtl)

or

[www.gehealthcare.com/science](http://www.gehealthcare.com/science)

## Smelly new orchid

A foul-smelling orchid that flourishes only in Yosemite National Park and was first collected in 1923 is a distinct species, scientists have announced after re-evaluating the flower.

Botanist Alison Colwell said the smell of sweaty feet that the Yosemite bog-orchid emits to attract pollinators was what first led her to it.

"I was out surveying clovers one afternoon, and I started smelling something," said Colwell, who works for the U.S. Geological Survey in El Portal. "It smelled like a horse corral on a hot afternoon."

The plant, which is the only known orchid species endemic to California's Sierra Nevada range, grows in spring-fed areas between 6,000 and 9,000 feet, Colwell said. All nine sites where the orchid has been spotted are in the park, some adjacent to areas popular among visitors, according to an article announcing the species' discovery published in *Madrono*, a journal of the California Botanical Society.

The species isn't likely to have any commercial value since its flowers are less than a quarter of an inch wide, but some orchid lovers

were so enthused by the news they began planning cross-country trips to see its delicate summer blooms.

Wild orchid expert Paul Martin Brown plans to include the orchid in his latest book.

Colwell, one of three scientists credited with the discovery, said the bog-orchid is thought to have persisted in the upland meadows south of Yosemite Valley, which nourished unique plant species because the area never froze under glacial cover.

At least seven other rare plant species have been found there, including the Yosemite onion, Yosemite woolly sunflower and Bolander's clover.

Park officials said they would not release details about where the plant was found because they were concerned visitors might love it to death.

"There's concern that it will get trampled," said ranger Adrienne Freeman. "It's a rare and precious resource that we want to protect."

A botanist named George Henry Grinnell first collected the Yosemite bog-orchid in 1923 and sent the dried, pressed flower to an herbarium that later gave its collec-

tions to Rancho Santa Ana Botanic Garden, Colwell said.

Ron Coleman, a visiting scientist at the garden, was combing through the collection one Friday morning in July 1993 when he found the original specimen on a herbarium sheet ringed with notes handwritten by Grinnell, who believed the flower was related to the green bog-orchid.

"It was just a little dry brown thing, but right away I saw several things about it didn't fit the pattern of any other orchid in California," Coleman said. "This discovery is not only personally satisfying but scientifically satisfying."

Coleman and his colleague Leon Glicenstein drove up to Yosemite the next day and rejoiced when they spotted the flowers in the fading light. They snapped a photograph and sent it to orchid expert Charles Sheviak, hoping he would confirm their suspicion that the plant was a unique species.

Sheviak, curator of Botany at the New York State Museum, concluded the orchid was related to an existent variety that grows in the Rocky Mountains, but botanists familiar with Yosemite remained curious.

After Colwell — in her first year on the job — caught a whiff of the flower and was drawn to it in 2003, she called her boss Peggy Moore. Together, they dug a plant from the meadow and sent it to Sheviak, who later revised his opinion.

The trio's publication on July 3 announcing the *Platanthera yosemitensis*, the Yosemite bog-orchid's official name, made its status as a separate species official.

Lovers of orchids, the largest plant family in nature with some 30,000 species worldwide, prized the new specimen for its rarity.

"I am a total student of orchids and I am thrilled to hear about that," said Paul Gripp, an organizer of the Santa Barbara Orchid Estate's fair, which was held over the weekend of 14 and 15 July.

Taken from: <http://www.cnn.com/2007/TECH/science/07/17/orchid.discovery.ap/index.html>

## Nature Genetics: Question of the year

The sequencing of the equivalent of an entire human genome for \$1,000 has been announced as a goal for the genetics community, and new technologies suggest that reaching this goal is a matter of when, rather than if. What then?

In celebration of its upcoming 15th anniversary, *Nature Genetics* is asking prominent geneticists to weigh in on this question: what would you do if this sequencing capacity were available immediately?

This new *Nature Genetics* 'Question of the Year' website, sponsored by Applied Biosystems, will reveal their answers. The website will be updated monthly, so check back regularly to get a glimpse of the future of genetics.

**NG: What would you do if it became possible to sequence the equivalent of a full human genome for only \$1,000?**

<http://www.nature.com/ng/qoty/index.html>

## Interesting websites

<http://www.nsf.gov>

<http://www.aaas.org>

<http://www.conferencealerts.com>

<http://www.medicalnewstoday.com>

SAGV/ SAGS is on the web  
<http://www.sagene.co.za>

## KONGRESSE

### The Mammalian Genetics and Development Workshop

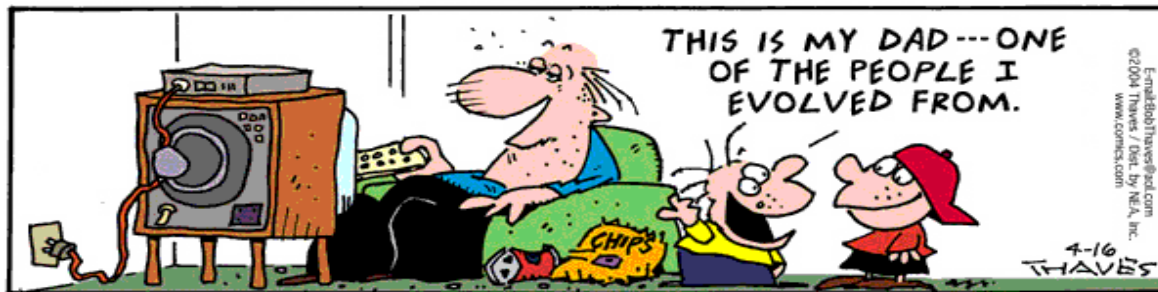
A meeting of the Genetics Society  
 29 to 30 Nov 2007

Institute of Child Health, UCL, London

[http://www.genetics.org.uk/the\\_mammalian\\_genetics\\_and\\_development\\_workshop](http://www.genetics.org.uk/the_mammalian_genetics_and_development_workshop)

### International Conference on Biotechnology and Bioinformatics

18 to 20 September 2009  
 Balaclava, Mauritius



## Sci-doku

	P		L	S	M			O
							S	
O		A					Y	
			C	O				T
	T		S		P			O
M				L	Y			
		L					O	C
		T						
P			M	A	C			L

SCI-DOKU is a sudoku puzzle that uses letters instead of numbers, with an added twist: a science-related clue accompanies each puzzle and the answer is spelled out in one row or column of the puzzle. Nine different letters are used to fill the grid. Each letter must appear once in each row, once in each column and once in every 3x3 square

**CLUE:** Cell substance

## M&Ms and genetics

Whenever I get a package of plain M&Ms, I make it my duty to continue the strength and robustness of the candy as a species.

To this end, I hold M&M duels. Taking two candies between my thumb and forefinger, I apply pressure, squeezing them together until one of them cracks and splinters. That is the "loser," and I eat the inferior one immediately.

The winner gets to go another round. I have found that, in general, the brown and red M&Ms are tougher, and the newer blue ones are genetically inferior. I have hypothesized that the blue M&Ms as a race cannot survive long in the intense theatre of competition that is the modern candy and snack-food world.

Occasionally I will get a mutation, a candy that is misshapen, or pointier, or flatter

than the rest. Almost invariably this proves to be a weakness, but on very rare occasions it gives the candy extra strength. In this way, the species continues to adapt to its environment.

When I reach the end of the pack, I am left with one M&M, the strongest of the herd. Since it would make no sense to eat this one as well, I pack it neatly in an envelope and send it to M&M Mars, along with a 3x5 card reading, "Please use this M&M for breeding purposes."

This week they wrote back to thank me, and sent me a coupon for a free 1/2 pound bag of plain M&Ms. I consider this "grant money." I have set aside the weekend for a grand tournament. From a field of hundreds, we will discover the True Champion. There can be only one

**Author unknown**  
<http://www.netfunny.com/rhf/jokes/97/Jan/mnms.html>