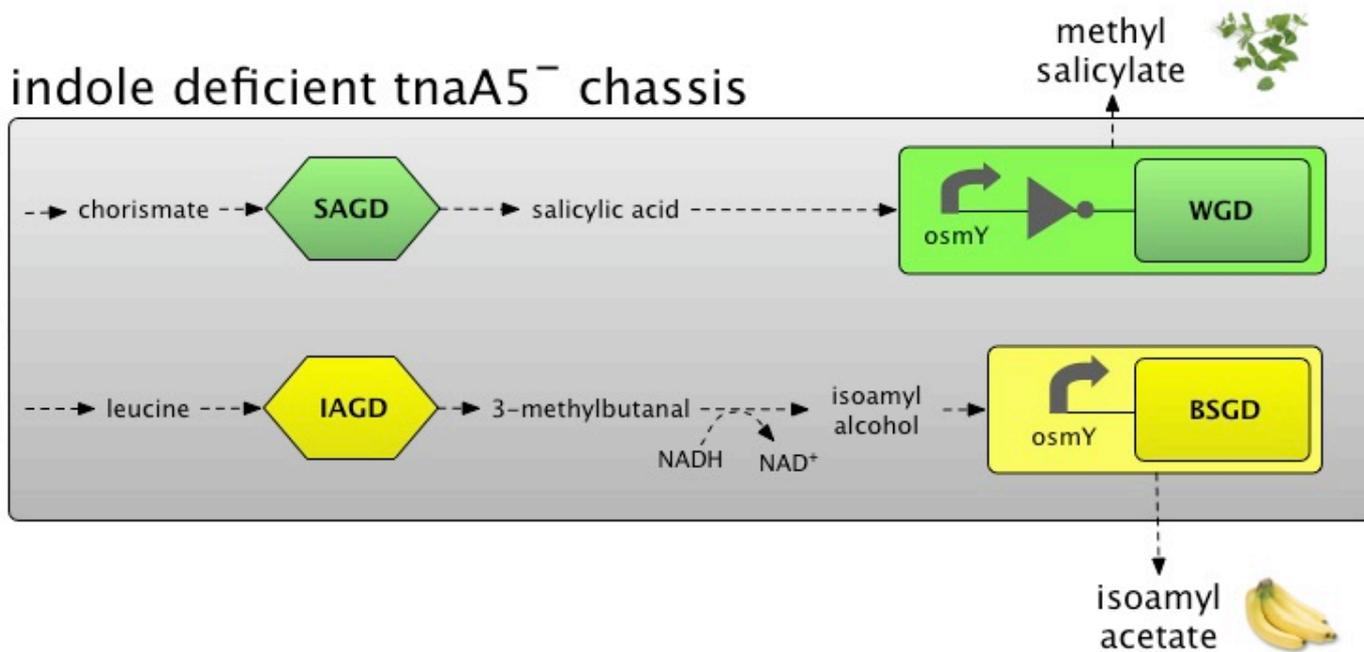




indole deficient *tnaA5⁻* chassis















































Unknown
Our Lord's Candle (*Yucca whipplei*), Lakeview Mountains, 22 Apr 2006
Smugmug.com



Unknown

<http://www.rootsweb.com/~usgenweb/mn/stearns/postcards/quarry.jpg>



Stone Bridge over Bull Run

<http://www.virginiaplaces.org/vagupnova/mnbp.html>

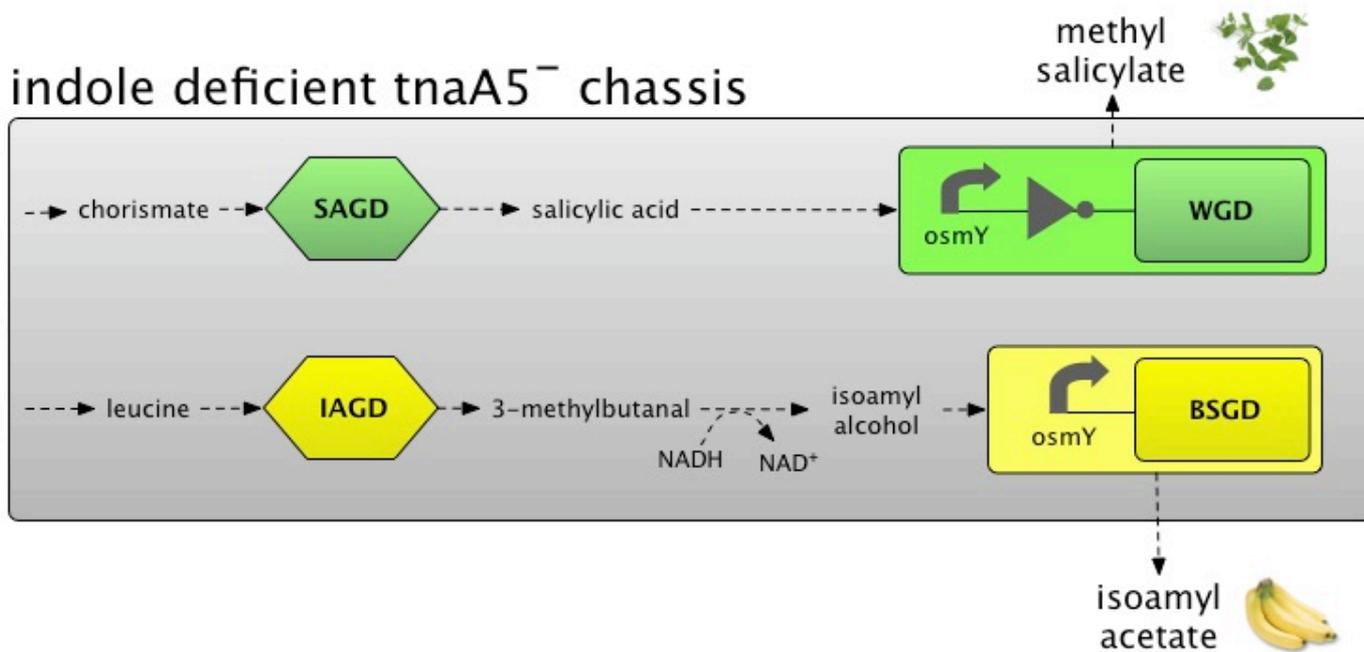


Millau Viaduct, France

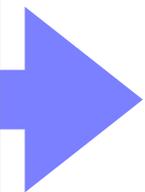
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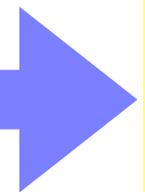
indole deficient *tnaA5⁻* chassis



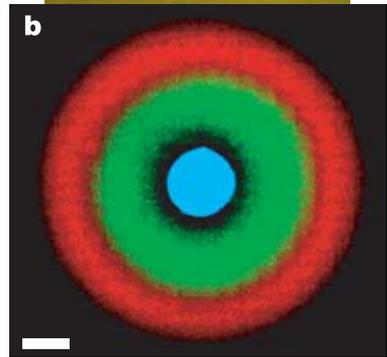
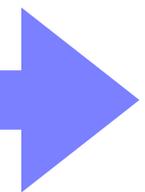
Design & Construction



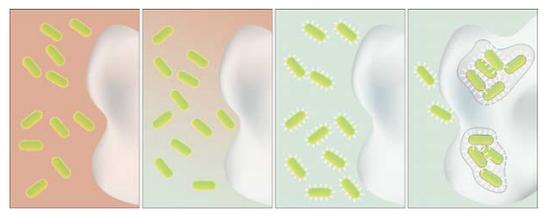
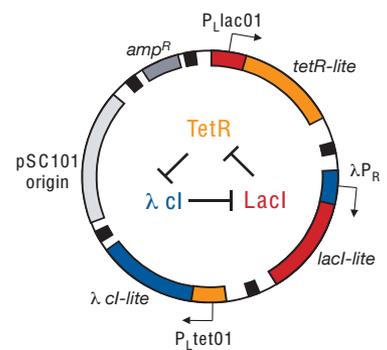
Devices???



Systems???



a Repressitor



Aerobic Conditions
Low Cell Density
OFF

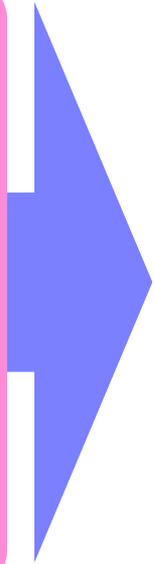
Hypoxia
High Cell Density
ON

\longrightarrow *inv* Induction \longrightarrow Invasion

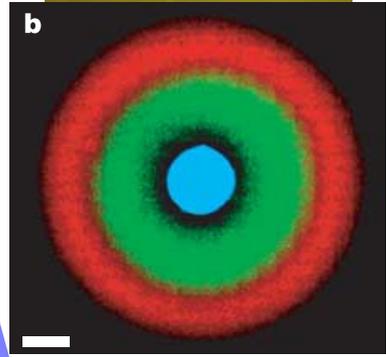
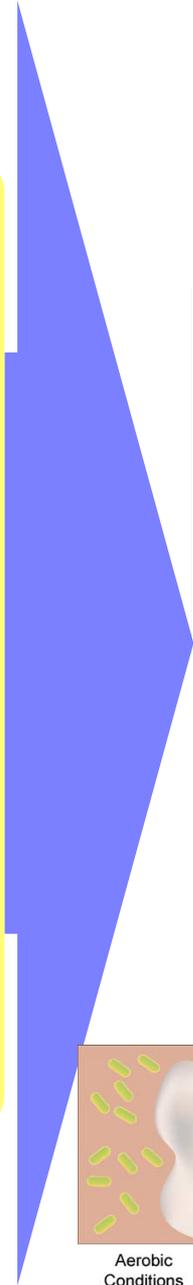
Design



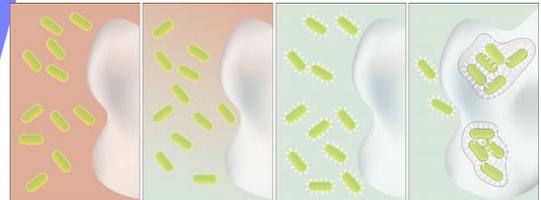
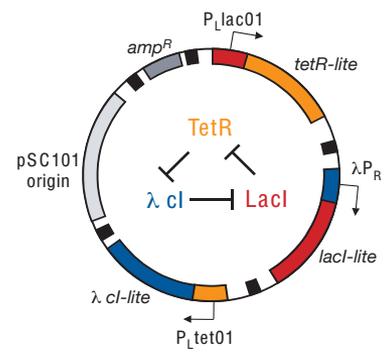
Parts
&
Devices



Construction



a Repressator



Aerobic Conditions
Low Cell Density
OFF

Hypoxia
High Cell Density
ON

inv Induction

Invasion

6. Abstraction

5. Standardization

4. Automated construction

3. Automated sequencing

2. Polymerase chain reaction

1. Recombinant DNA

FAB TREE HAB

Massachusetts Institute of Technology
Team H.E.D. [Human Ecology Design]

Mitchell Joachim, Ph.D.

Lara Greden, Ph.D.

Javier Arbona, SMArchS.



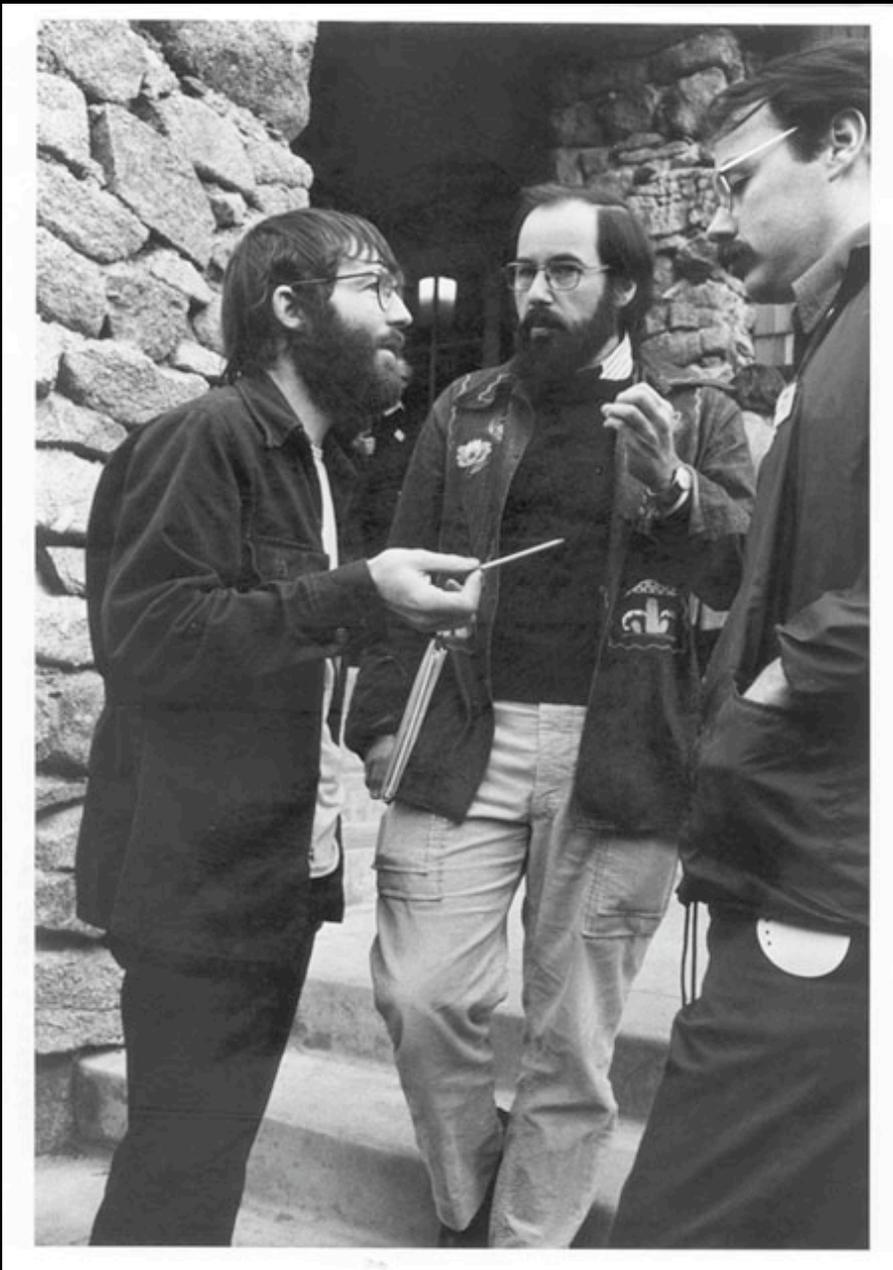
1. Safety
2. Security
3. Ownership, Sharing, Innovation
4. Understanding & Perception
5. Ethics (Religion)
6. Community

Biosafety Level 1 practices, safety equipment, and facility design and construction are appropriate for undergraduate and secondary educational training and teaching laboratories, and for other laboratories in which work is done with defined and characterized strains of viable microorganisms not known to consistently cause disease in healthy adult humans. Biosafety Level 1 represents a basic level of containment that relies on standard microbiological practices with no special primary or secondary barriers recommended, other than a sink for handwashing.

Biosafety Level 2 practices, equipment, and facility design and construction are applicable to clinical, diagnostic, teaching, and other laboratories in which work is done with the broad spectrum of indigenous moderate-risk agents that are present in the community and associated with human disease of varying severity. With good microbiological techniques, these agents can be used safely in activities conducted on the open bench, provided the potential for producing splashes or aerosols is low. Hepatitis B virus, HIV, the salmonellae, and *Toxoplasma* spp. are representative of microorganisms assigned to this containment level.

Biosafety Level 3 practices, safety equipment, and facility design and construction are applicable to clinical, diagnostic, teaching, research, or production facilities in which work is done with indigenous or exotic agents with a potential for respiratory transmission, and which may cause serious and potentially lethal infection. *Mycobacterium tuberculosis*, St. Louis encephalitis virus, and *Coxiella burnetii* are representative of the microorganisms assigned to this level. Primary hazards to personnel working with these agents relate to autoinoculation, ingestion, and exposure to infectious aerosols. At Biosafety Level 3, more emphasis is placed on primary and secondary barriers to protect personnel in contiguous areas, the community, and the environment from exposure to potentially infectious aerosols.

Biosafety Level 4 practices, safety equipment, and facility design and construction are applicable for work with dangerous and exotic agents that pose a high individual risk of life-threatening disease, which may be transmitted via the aerosol route and for which there is no available vaccine or therapy. Agents with a close or identical antigenic relationship to Biosafety Level 4 agents also should be handled at this level. When sufficient data are obtained, work with these agents may continue at this level or at a lower level. Viruses such as Marburg or Congo-Crimean hemorrhagic fever are manipulated at Biosafety Level 4. The primary hazards to personnel working with Biosafety Level 4 agents are respiratory exposure to infectious aerosols, mucous membrane or broken skin exposure to infectious droplets, and autoinoculation. All manipulations of potentially infectious diagnostic materials, isolates, and naturally or experimentally infected animals, pose a high risk of exposure and infection to laboratory personnel, the community, and the environment.



(c/o US NAS Archives)

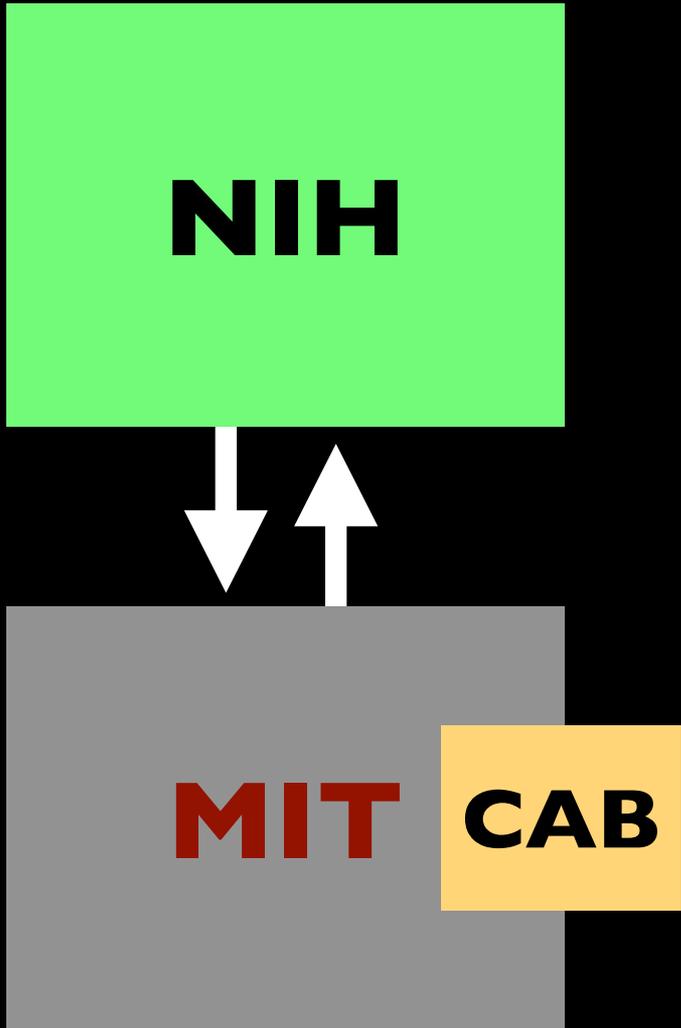
The Real Paper

ly newspaper July 16, 1977 35¢

**DOING DNA
AT HOME:
A RECIPE FOR
BOTULISM**



**PAT
CADELL:
CARTER'S
GREASY
POLLSTER
SHAPIRO:
THEY'RE
BANNING
ABORTIONS
AGAIN**



<http://mit.edu/cab/>



Published online before print October 31, 2006

Genome Research, DOI: 10.1101/gr.5565706

Letter

Identification of an infectious progenitor for the multiple-copy HERV-K human endogenous retroelements

Marie Dewannieux^{1,3}, Francis Harper^{2,4}, Aurélien Richaud^{1,4}, Claire Letzelter¹, David Ribet¹, Gérard Pierron², and Thierry Heidmann^{1,5}

¹ *Unité des Rétrovirus Endogènes et Eléments Rétroïdes des Eucaryotes Supérieurs, UMR 8122 CNRS, Institut Gustave Roussy, 94805 Villejuif Cedex, France;* ² *Laboratoire de Réplication de l'ADN et Ultrastructure du Noyau, UPR1983 Institut André Lwoff, 94801 Villejuif Cedex, France*

Human Endogenous Retroviruses are expected to be the remnants of ancestral infections of primates by active retroviruses that have thereafter been transmitted in a Mendelian fashion. Here, we derived in silico the sequence of the putative ancestral "progenitor" element of one of the most recently amplified family—the HERV-K family—and constructed it. This element, *Phoenix*, produces viral particles that disclose all of the structural and functional properties of a bona-fide retrovirus, can infect mammalian, including human, cells, and integrate with the exact signature of the presently found endogenous HERV-K progeny. We also show that this element amplifies via an extracellular pathway involving reinfection, at variance with the non-LTR-retrotransposons (LINEs SINEs) or LTR-retrotransposons, thus recapitulating ex vivo the molecular events responsible for its dissemination in the host genomes. We also show that in vitro recombinations among present-day human HERV-K loci can similarly generate functional HERV-K elements, indicating that human cells still have the potential to produce infectious retroviruses.

³ Present address:

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Safety precautions

All manipulations involving the reconstructed HERV-K were carried out in our lab according to the rules established by the "Commission de Génie Génétique" from the "Ministère délégué à l'Enseignement supérieur et à la Recherche" French authority that regulates handling of genetically modified organisms in all research institutions in France.

Albeit the HERV-K virus has a very low infectivity and does not sustain multiple-cycle infection, at least in all the cells tested, *Phoenix* is a retrovirus, and as such, is a priori eligible to BL3 conditions for manipulation. Accordingly, the material will only be sent to other labs in appropriate sealed containers in the form of small amounts of plasmid DNA that will require it to be amplified before use as a transfection vector to produce viral particles. At the present time and as a precautionary principle, it will only be distributed under a material transfer agreement specifying the commitment of the recipient labs to carry out every experiment using the material under BL3 conditions and accompanied by a duly signed authorization form from the Biosafety Committee responsible for genetic manipulations in their country of origin.

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What's changed since the 1970s?

1. Databases populated with sequence information.
2. The internet.
3. Early improvements in automated DNA construction technology.
4. Overnight shipping.
5. Expanded concern re: active misapplication of biotech.

What's the difference between
safety & security?

Information (DNA Sequence)

The diagram features two large horizontal arrows pointing to the right. The top arrow is blue with a red-to-blue gradient and contains the text 'Information (DNA Sequence)'. The bottom arrow is red with a blue-to-red gradient and contains the text 'Material (Physical DNA)'. A white arrow labeled 'Sequencing' points upwards from the bottom arrow to the top arrow. A white arrow labeled 'Synthesis' points downwards from the top arrow to the bottom arrow.

Sequencing

Synthesis

Material (Physical DNA)

Unknown
reservoir →

- 1: [NC_001608](#)
Lake Victoria marburgvirus, complete genome
ssRNA; linear; Length: 19,112 nt
Created: 1994/01/26
- 2: [NC_006432](#)
Sudan ebolavirus, complete genome
ssRNA; linear; Length: 18,875 nt
Created: 2004/11/15
- 3: [NC_004161](#)
Reston Ebola virus, complete genome
ssRNA; linear; Length: 18,891 nt
Created: 2002/09/04
- 4: [NC_002549](#)
Zaire ebolavirus, complete genome
ssRNA; linear; Length: 18,959 nt
Created: 1999/02/10

Locked-up
↓

- [NC_008291](#)
Taterapox virus, complete genome
dsDNA; linear; Length: 198,050 nt
Created: 2006/08/24
- [NC_001611](#)
Variola virus, complete genome
dsDNA; linear; Length: 185,578 nt
Created: 1993/05/04
- [NC_006966](#)
Mule deer poxvirus, complete genome
dsDNA; linear; Length: 166,259 nt
Created: 2005/04/08

Don't exist →

- 1: [DQ208309](#) Reports
Influenza A virus (A/Brevig Mission/1/1918(H1N1)) polymerase PB2 (PB2) mRNA, complete cds
gil76786704|gb|DQ208309.1|[76786704]
- 1: [DQ208310](#) Reports
Influenza A virus (A/Brevig Mission/1/1918(H1N1)) polymerase PB1 (PB1) mRNA, complete cds
gil76786706|gb|DQ208310.1|[76786706]

Should the DNA sequence
encoding human pathogens be
freely available online?

1918 Flu and Responsible Science

The influenza pandemic of 1918 is estimated to have caused 50 million deaths worldwide; 675,000 in the United States. The reconstruction of the 1918 virus by the synthesis of all eight subunits and the generation of infectious virus are described on p. 77 of this issue,* and the sequences of the final three gene segments of the virus are described in a concurrent *Nature* paper.† Predictably, but alarmingly, this virus is more lethal to mice than are other influenza strains, suggesting that this property of the 1918 virus has been recovered in the published sequence. The good news is that we now have the sequence of this virus, perhaps permitting the development of new therapies and vaccines to protect against another such pandemic. The concern is that a terrorist group or a careless investigator could convert this new knowledge into another pandemic.

Should the sequence of the 1918 virus have been published, given its potential use by terrorists? The dual-use nature of biological information has been debated widely since September 11, 2001. In 2003, a committee of the U.S. National Academies chaired by Gerald Fink considered this issue, weighing the benefits against the risks of restricting the publication of such biological information. They outlined the tradeoff between erring on the side of prudence, thus potentially hindering the progress of critical science, and erring on the side of disclosure, thus potentially aiding terrorists. The U.S. National Science Advisory Board for Biosecurity (NSABB) was established to advise governmental agencies and the scientific community on policies relative to public disclosure. This board has begun to deliberate, but the questions are complex, as typified by these papers on the 1918 virus. It is reassuring that the NSABB was asked to consider these papers before publication and concluded that the scientific benefit of the future use of this information far outweighs the potential risk of misuse. People may be reassured that the system is working, because agencies representing the public, the scientific community, and the publishing journals were involved in the decision.

I firmly believe that allowing the publication of this information was the correct decision in terms of both national security and public health. It is impossible to forecast how scientific observations might stimulate others to create new treatments or procedures to control future pandemics. For example, in the *Nature* article, sequence comparisons suggest that the 1918 virus was generated not by incremental changes in the polymerase genes, but by the movement of these genes, in total, from an avian source into a human influenza virus. The availability of these sequences will permit identification of their avian origin and should show why this particular set of genes was selected. Similarly, the results in the *Science* article suggest that the cleavage of a protein on the surface of the 1918 virus, a step critical for virulent infection, may occur by a previously unknown mechanism—a hint that could lead to new drugs for inhibiting this step and thus preventing future pandemic eruptions.

Influenza is highly infectious, and a new strain could spread around the world in a matter of months, if not weeks. The public needs confidence that the 1918 virus will not escape from research labs. All of the described experiments were done in a Biosafety Level 3 laboratory, a high-containment environment recommended by the U.S. Centers for Disease Control and Prevention and the National Institutes of Health on an interim basis, whose use should become a permanent requirement for such experiments. Current evidence suggests that some available drugs and possible future vaccines could suppress infections by the 1918 virus. Given the prospect of another natural influenza pandemic, the recent decision by the U.S. administration to stockpile antivirals for influenza treatment seems wise. Finally, although a sequence of the 1918 virus has been determined and is highly virulent in mice, this may not be the specific form of the virus that caused the pandemic of 1918. An article in the same issue of *Nature*‡ reports the existence of sequence variation in a natural population of influenza virus; yet we have only one sequence for the 1918 pandemic strain, and the reconstructed virus described in the *Science* article was built into the backbone of a laboratory strain. Because a pandemic infection is dependent on many unknown properties, there is no certainty that the reconstructed 1918 virus is capable of causing a pandemic.



Phillip A. Sharp

Phillip A. Sharp is Institute Professor at the Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA.

10.1126/science.1120820

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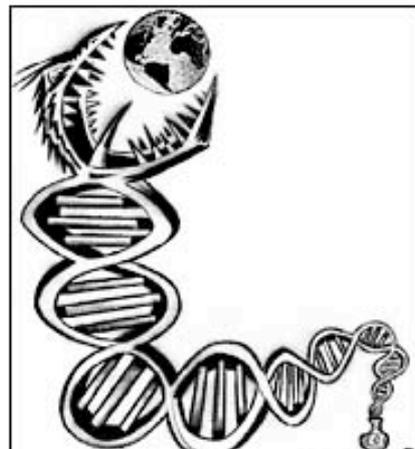
OP-ED CONTRIBUTORS

Recipe for Destruction

By RAY KURZWEIL and BILL JOY

Published: October 17, 2005

AFTER a decade of painstaking research, federal and university scientists have reconstructed the 1918 influenza virus that killed 50 million people worldwide. Like the flu viruses now raising alarm bells in Asia, the 1918 virus was a bird flu that jumped directly to humans, the scientists reported. To shed light on how the virus evolved, the United States Department of Health and Human Services published the full genome of the 1918 influenza virus on the Internet in the GenBank database.



This is extremely foolish. The genome is essentially the design of a weapon of mass destruction. No responsible scientist would advocate publishing precise designs for an atomic bomb, and in two ways revealing the sequence for the flu virus is even more dangerous.

First, it would be easier to create and release this highly destructive virus from the genetic data than it would be to build and detonate an atomic bomb given only its design, as you don't need rare raw materials like plutonium or enriched

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DNA synthesis and biological security

Hans Bügl, John P Danner, Robert J Molinari, John T Mulligan, Han-Oh Park, Bas Reichert, David A Roth, Ralf Wagner, Bruce Budowle, Robert M Scripp, Jenifer A L Smith, Scott J Steele, George Church & Drew Endy

A group of academics, industry executives and security experts propose an oversight framework to address concerns over the security of research involving commercial DNA synthesis.

DNA synthesis allows the direct construction of genetic material starting from information and raw chemicals¹. Improvements in synthesis technology are accelerating innovation across many areas of research, from the development of renewable energy to the production of fine chemicals, from information processing to environmental monitoring, and from agricultural productivity to breakthroughs in human health and medicine. Like any powerful technology, DNA synthesis has the potential to be purposefully misapplied. Misuse of DNA-synthesis technology could give rise to both known and unforeseeable threats to our biological safety and security. Current government oversight of the DNA-synthesis industry falls short of addressing this unfortunate reality.

Here, we outline a practical plan for developing an effective oversight framework for

Hans Bügl, John P. Danner, Robert J. Molinari, John T. Mulligan, David A. Roth & Ralf Wagner are members of the International Consortium for Polynucleotide Synthesis; Hans Bügl and Ralf Wagner are at GENEART; John P. Danner, George Church & Drew Endy are at Codon Devices; Robert J. Molinari & David A. Roth are at CODA Genomics; John T. Mulligan is at Blue Heron Biotechnology; Han-Oh Park is at Bioneer; Bas Reichert is at BaseClear B.V.; Ralf Wagner is at the University of Regensburg Molecular Virology & Gene Therapy Unit, Institute of Medical Microbiology and Hygiene; Bruce Budowle, Robert M. Scripp, Jenifer A. L. Smith & Scott J. Steele are at the US FBI; George Church is in the Department of Genetics, Harvard Medical School; Drew Endy is in the Department of Biological Engineering, MIT; George Church & Drew Endy are at the multi-institution US National Science Foundation Synthetic Biology Engineering Research Center. e-mail: endy@mit.edu

the DNA-synthesis industry². The resulting framework serves three purposes. First, it promotes biological safety and security. Second, it encourages the further responsible development of synthetic biology technologies and their continued, overwhelmingly construc-

tive application. And third, it is designed to be international in scope. Our plan is informed by past and ongoing discussions of biological security issues associated with DNA-synthesis technology³⁻⁵ and represents the collective views of all founding members of the

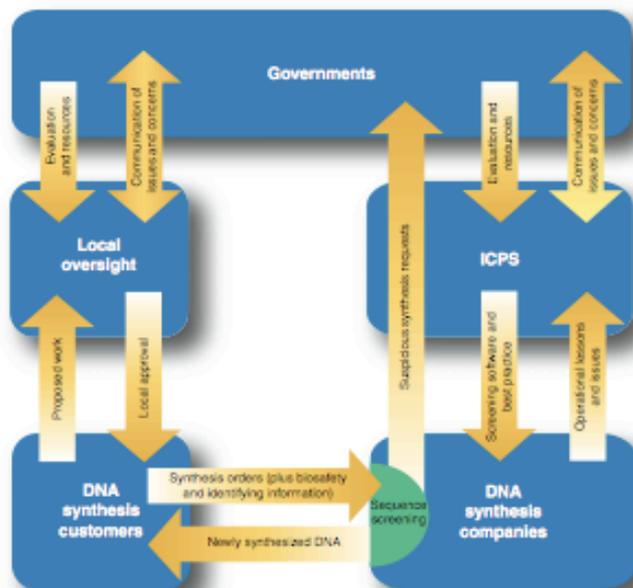


Figure 1 Our framework calls for the immediate and systematic implementation of a tiered DNA synthesis order screening process. To promote and establish accountability, individuals who place orders for DNA synthesis would be required to identify themselves, their home organization and all relevant biosafety information. Next, individual companies would use validated software tools to check synthesis orders against a set of select agents or sequences to help ensure regulatory compliance and flag synthesis orders for further review. Finally, DNA synthesis and synthetic biology companies would work together through the ICPS, and interface with appropriate government agencies (worldwide), to rapidly and continually improve the underlying technologies used to screen orders and identify potentially dangerous sequences, as well as develop a clearly defined process to report behavior that falls outside of agreed-upon guidelines. ICPS, International Consortium for Polynucleotide Synthesis.



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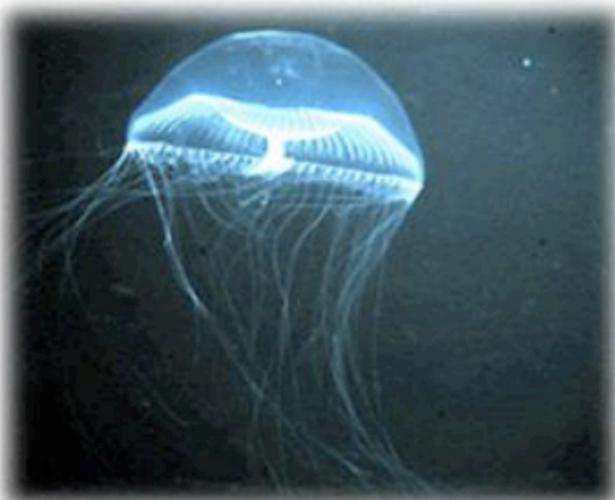
National Biodefense Analysis and Countermeasures Center

From Wikipedia, the free encyclopedia

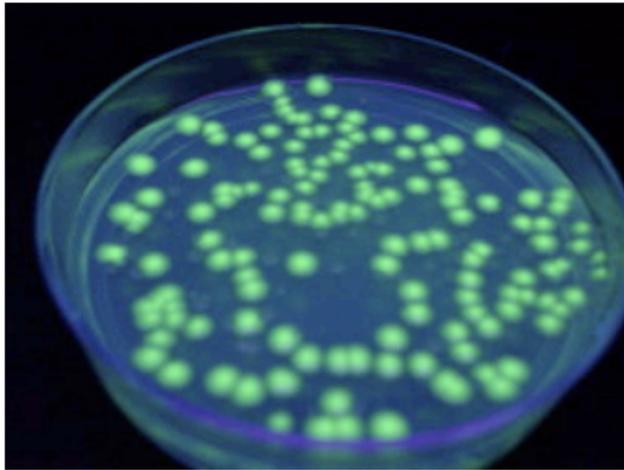
The **National Biodefense Analysis and Countermeasures Center** (NBACC) is a highly classified government [biodefense](#) research laboratory created by the [U.S. Department of Homeland Security](#) (DHS) and located at the government's sprawling biodefense campus at [Fort Detrick](#) in [Frederick, MD](#), USA. Created quietly a few months after the [2001 anthrax attacks](#), the NBACC (pronounced *EN-back*) is intended to be the principal U.S. [biological warfare](#) research institution engaged in "science-based threat assessment."



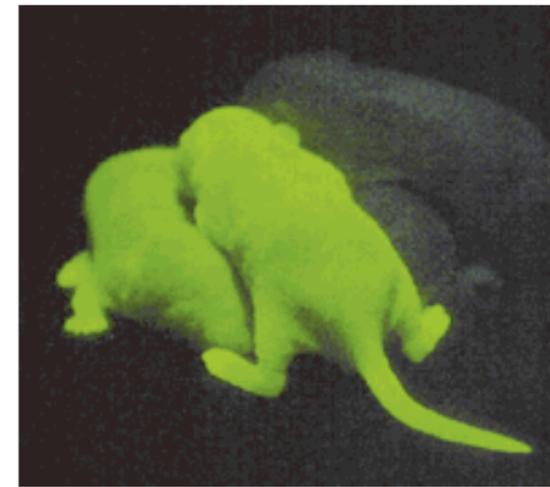




<http://www.yildizindunyasi.net/bilim%20dunyasi/gfp.htm>



http://homepage3.nifty.com/nature_of_minami



http://www.brown.edu/Courses/BI0105_Miller/read/optical.html

United States Patent
Chalfie , et al.

5,491,084
February 13, 1996

Uses of green-fluorescent protein

Abstract

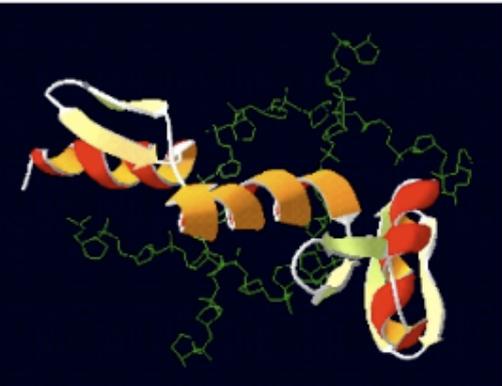
This invention provides a cell comprising a DNA molecule having a regulatory element from a gene, other than a gene encoding a green-fluorescent protein operatively linked to a DNA sequence encoding the green-fluorescent protein. This invention also provides a method for selecting cells expressing a protein of interest which comprises: a. introducing into the cells a DNA I molecule having DNA sequence encoding the protein of interest and DNA II molecule having DNA sequence encoding a green-fluorescent protein; b. culturing the introduced cells in conditions permitting expression of the green-fluorescent protein and the protein of interest; and c. selecting the cultured cells which express green-fluorescent protein, thereby selecting cells expressing the protein of interest. Finally, this invention provides various uses of a green-fluorescent protein.

Inventors: **Chalfie; Martin** (New York, NY); **Prasher; Douglas** (East Falmouth, MA)

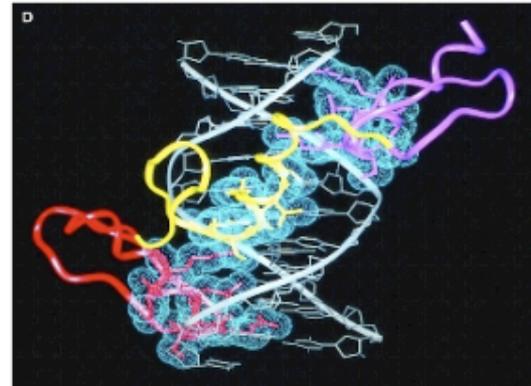
Assignee: **The Trustees of Columbia University in the City of New York** (New York, NY); **Woods Hole Oceanographic Institution** (Woods Hole, MA)

Appl. No.: **119678**

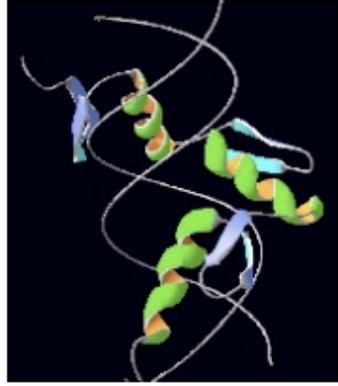
Filed: **September 10, 1993**



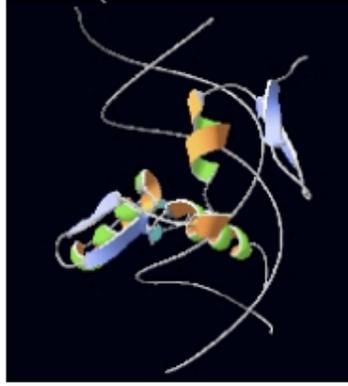
Zif268, Paveltich & Pabo c. 1991



Random Zif268s, Greisman & Pabo c. 1997



TATA_{ZF-6} & TATA_{ZF-7}



Wolfe et al. c. 2001

United States Patent
Kim, et al.

6,903,185
June 7, 2005

Poly *zinc* finger proteins with improved linkers

Abstract

Chimeric proteins, and methods for their production and use are disclosed. The chimeric proteins comprise a flexible linker between two *zinc* finger DNA-binding domains, wherein the linker comprises eight or more amino acids between the second conserved histidine residue of the carboxy-terminal *zinc* finger of the first domain and the first conserved cysteine residue of the amino-terminal *zinc* finger of the second domain.

Inventors: **Kim; Jin-Soo** (Inchon, KR); **Pabo; Carl O.** (Newton, MA)
 Assignee: **Massachusetts Institute of Technology** (Cambridge, MA)
 Appl. No.: **146221**
 Filed: **May 13, 2002**

United States Patent Application

20050112615

Kind Code

A1

Davies, Stephen William ; et al.

May 26, 2005

Genetic circuit inverting amplifier

Abstract

We describe methods and compositions for setting the level of gene expression in a cell. The instant invention is of an amplifier, an analog circuit. It is directly analogous to the inverting amplifier commonly used in electronics. This circuit produces an output wherein an increase in the input signal leads to a proportional decrease in the output. Similarly, a decrease in the input leads to an increase in the output signal. Here the

if
w
ir

United States Patent Application

20040235101

Kind Code

A1

Maclsaac, Kenzie D. ; et al.

November 25, 2004

Genetic circuit clocked latch

Abstract

We describe methods and compositions for setting and maintaining the state of gene expression in a cell. The genetic circuit clocked latch has two states with each state corresponding to a different pattern of gene expression. The genetic circuit clocked latch allows one to set the state of

United States Patent

6,774,222

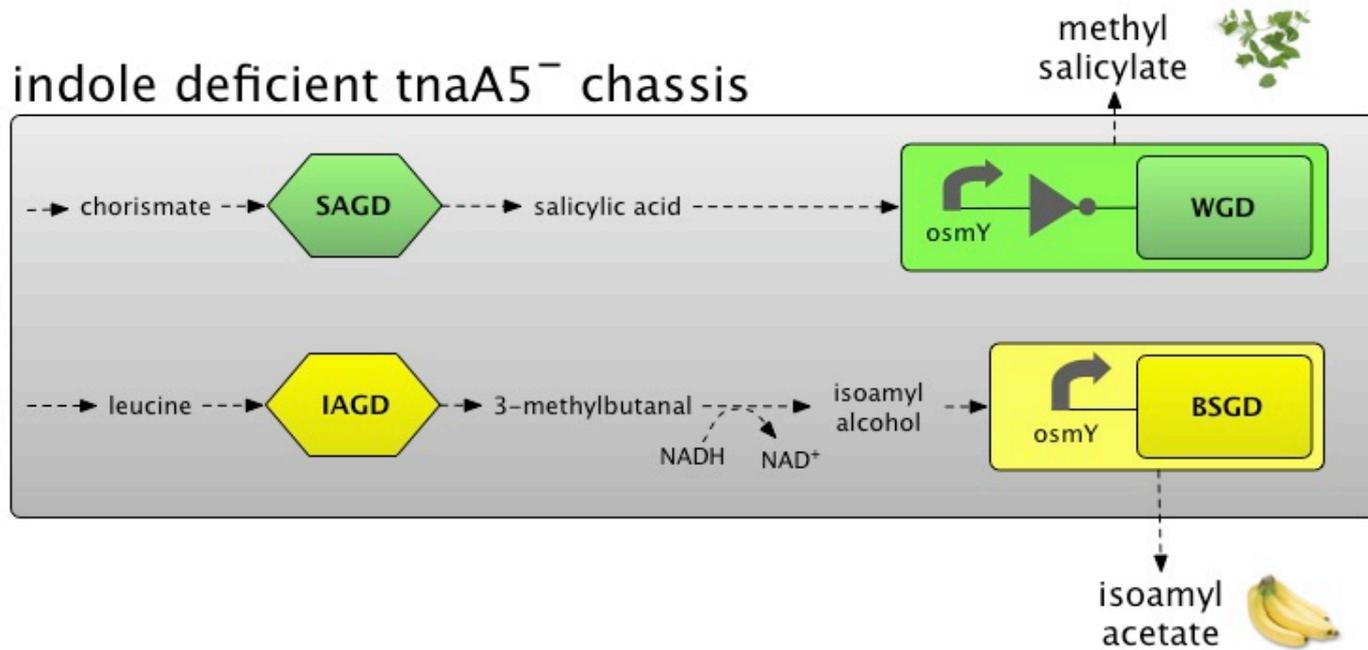
Schneider , et al.

August 10, 2004

Molecular computing elements, gates and flip-flops

Abstract

This invention relates to novel molecular constructs that act as various logic elements, i.e., gates and flip-flops. The constructs are useful in a wide variety of contexts including, but not limited to, computation and control systems. The basic functional unit of the construct comprises a nucleic acid having at least two protein binding sites that cannot be simultaneously occupied by their cognate binding protein. This basic unit can be assembled in any number of formats providing molecular constructs that act like traditional digital logic elements (flips-flops, gates, inverters, etc.).



Ms. iGEM:

I have received a request from you for plasmids developed by Dr. Postdoc when he was at the University of Somewhere. I have these plasmids that I received from Dr. Postdoc; however, I am not allowed to give them out. You must obtain these from Dr. Postdoc.

As part of your educational experience at <Your School>, I would have thought that you would know how to do a PUBMED search on the NCBI website. If you search <Postdoc's Name> you will find Dr. Postdoc's latest publications and his current contact information.

Further, I seriously doubt that Dr. Postdoc will send the plasmids to a university sophomore. You should have a faculty member request these plasmids. Additionally a materials transfer agreement will likely have to be completed for the plasmids to be transferred.

Best wishes in your work.

--

Muckety Muck, Ph.D.
Big Time Professor
Somewhere in North America

Thank you Professor Muckety Muck.

I am sorry that I contacted you.

In <My School's> defense, yes I do know how to do a PUBMED search, and I had already emailed and faxed Dr. Postdoc at his current contact information before I tried contacting you.

Also, in response to your serious doubts that Dr. Postdoc would send plasmids to a university sophomore -- he has already sent them to me (with no faculty member involvement).

My team is very appreciative of Dr. Postdoc's generosity and support, and I hope that you can also come to understand that iGEM is about student initiative, learning, and sharing of information.

To conclude, I was in the wrong to have bothered you. This has been a learning experience for me. I thank you for responding to my fax request.

Sincerely, Ms. iGEM

Patents:

Standard practice

Slow & expensive

Copyright:

Cheap, easy to Use

Could be too strong.
Not used today

Contracts:

Defined agreements

Leaky

Public Domain:

Cheap, fast

May not offer protection.
Hard to build community

Sui Generis:

Could be exactly right

Expensive & political

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The BioBricks Foundation (BBF) is a not-for-profit organization founded by engineers and scientists from MIT, Harvard, and UCSF with significant experience in both non-profit and commercial biotechnology research. BBF encourages the development and responsible use of technologies based on BioBrick™ standard DNA parts that encode basic biological functions.

Using BioBrick™ standard biological parts, a synthetic biologist or biological engineer can already, to some extent, program living organisms in the same way a computer scientist can program a computer. The DNA sequence information and other characteristics of BioBrick™ standard biological parts are made available to the public free of charge currently via MIT's [Registry of Standard Biological Parts](#).

Any individual or organization is welcome to design, improve, and contribute BioBrick™ standard biological parts to the Registry. For example, in the summer of 2007, over 600 students and instructors at 60+ universities around the world are making, sharing, and using BioBrick™ standard biological parts as part of the [International Genetically Engineered Machine \(iGEM\)](#) competition.

News

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PROJECT 2: Build a Thermal Cycler and Run PCR

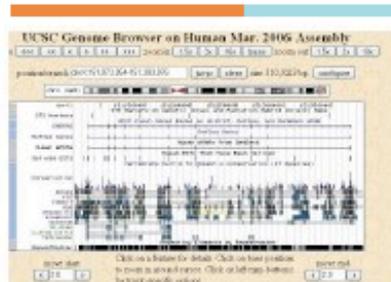
Real DNA “fingerprinting” is usually done using a procedure called *polymerase chain reaction*, or PCR. This process replicates DNA, making a much larger sample that produces more detail in electrophoresis and is therefore easier to match. To perform PCR, you need some specialized chemicals and equipment.

The chemicals are small, predesigned pieces of DNA known as primers, plus a heat-stable DNA polymerase reagent such as Taq. The primers combine into new copies of the sample DNA strand, and the polymerase enzyme catalyzes this assembly process. Both of these materials are readily available from biotech supply companies such as Takara (takaramirusbio.com) for less than \$100, which buys enough for about 100 reactions.

For the hardware, you need some small plastic tubes and a thermal cycler, which applies programmable temperature changes to the tubes. Commercial thermal cyclers for laboratories range from \$2,500 to more than \$7,000, but you can make your own MacGyver version using a Handy Board microcontroller (handyboard.com, around \$225) and about 50 dollars’ worth of additional components. Here’s a metalevel description of the different pieces and how to put them together. (You can find the schematic and full parts list online at makezine.com/07/fingerprinting/.)

How It Works

The component that performs the thermal heavy lifting for our thermal cycler is a Peltier device, aka thermoelectric cooler. This is a flat, solid-state device that “pumps” heat from one plate to the other when you apply a DC current. Inside, current zigzags through alternating sections of P-type and N-type semiconductor material sandwiched between the two plates. Heat is drawn away along



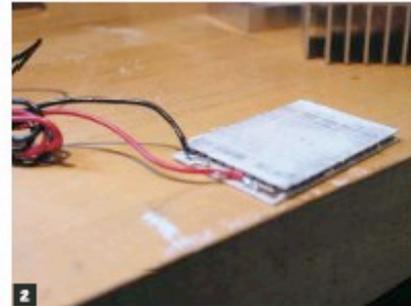
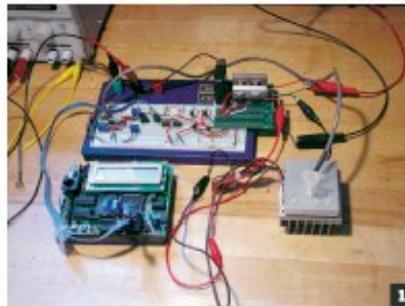
THE GENOME BROWSER

Our genome represents all of the DNA in our cells’ nuclei. This DNA is the “genetic blueprint” that determines how we’re put together on a molecular level, what we look like, and how healthy we are. It contains over 3 billion letters, called nucleotides, which the Human Genome Project has mapped using DNA sequencing technologies built from the same basic principles outlined in the projects presented here. Now that we have the sequences, the next step is figuring out what they do, which parts of the sequence aren’t “junk” and actually produce proteins, and what these proteins’ functions are in the body.

Anyone can read this blueprint and browse the latest discoveries online using the Genome Browser at the UCSC Genome Bioinformatics Site (genome.ucsc.edu/cgi-bin/hgGateway). This breakthrough tool is like a Google Maps for genomes, and it’s being updated continuously as researchers decipher different parts of the genome.

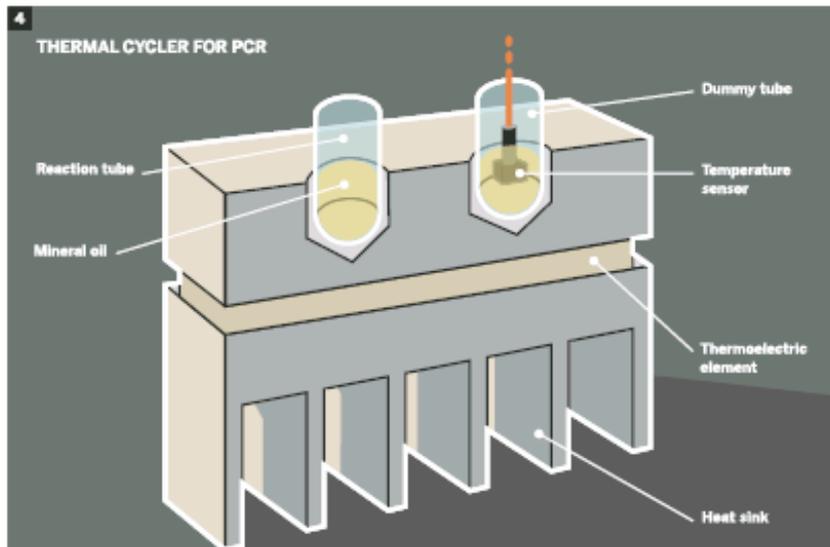
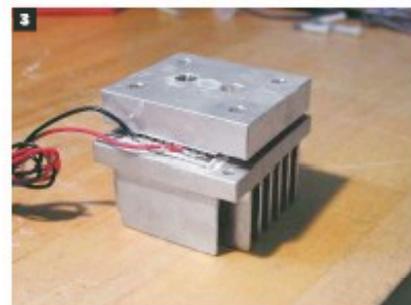
You can use the Genome Browser to search the entire genome sequence and navigate around any part of it. You can see the detailed features of any particular location by searching for an address; instead of a street address, you enter the numerical position of the nucleotide in the entire sequence. Researchers routinely use the Genome Browser when they need raw data from the human blueprint.

current, you reverse the heat flow. Peltier devices are used to cool microprocessors and photoelectric devices. By themselves (without a power supply and controller), you can get them for less than \$15 from surplus companies; check peltier-info.com/surplus.html. We used a 1.5”x2” device rated at 5V and 8 amps (Marlow Industries item #SP2083). For the device’s power supply, we



How to make a thermal cycler for DNA replication:

1. Instead of paying \$5,000 for a commercial thermal cycler (which you’ll need to replicate DNA samples), you can make the one shown here for less than \$300.
2. This Peltier device pumps heat from one plate to another when a current is applied.
3. Here, the Peltier device has been outfitted with 2 aluminum blocks. The top block has holes to hold the reaction tubes. The bottom block is a heat sink.
4. The top block of the thermal cycler contains holes for a tube where the reaction takes place, and a dummy tube that contains a temperature sensor. The data from the sensor provides feedback to the microcontroller, which controls the Peltier device.



MAKE IT.



BUILD AND USE YOUR CLEAN BOX

START » Time: 1 hour to build; 2 weeks to grow Complexity: Easy

1. CUT THE HOLE

1a. Find the output side of the air purifier, and trace it on the bottom of the plastic box.

1b. Drill pilot holes at the corners of the traced outline.

1c. Use a keyhole saw or jigsaw at the highest speed to cut out the entire hole.



2. INSTALL THE PURIFIER

2a. Fit the air purifier into the hole, with the intake side facing out and the output side blowing into the box. You might want to prop it up on some books to keep it in place.



2b. Use silicone sealer to generously caulk around the air filter, securing it in place. Let it sit overnight so that the caulk can dry. That's it — now you have your hood! Move it onto a good work surface with its opening facing you, and let's start using it.



Photography by Philip Reiss

3. CLEAN THE HOOD

This isn't just Step 3; it's something you'll need to do every time you work inside your laminar flow hood. The hood is crucial for mushroom growing, but it's only one part of the larger regimen of cleanliness required for successful lab work.

3a. Clean all of the hood's surfaces with warm, soapy water.

3b. Disinfect all surfaces of the hood with a bleach-and-water solution.

3c. Finally, turn the fan on and disinfect the hood with isopropyl alcohol. You can never be too clean!

4. MAKE THE AGAR PLATE

We'll begin growing our mushroom tissue in agar (seaweed gelatin), a standard laboratory growth medium. Petri dishes are traditionally used, but you can use any shallow, washable container with a lid. As long as you're cooking a batch of agar, you'll find it handy to make several of these plates at once and store them in airtight bags for later use.

4a. Drill or cut a ½" hole in the lid of a washable plastic container.

4b. Wash the container and lid with soap and water, and then sterilize by immersing them in simmering water for 3 minutes. Switch on your hood's fan, and move the container and lid inside for drying.

4c. Make a filter by soaking a piece of cotton or sponge in isopropyl alcohol and then wringing it out. Place the filter in the hole in the container lid. It should fit snugly.



The sponge-piece filter keeps the mushroom tissue protected while letting it exchange gases with the surrounding air.

4d. Mix 1 tablespoon of agar in 1 cup of water. Bring to a low boil and slowly simmer for about 15 minutes, stirring occasionally. Add a large pinch of the growing substrate you'll be using later (sawdust, cat litter, barley, etc.) to the simmering agar as a source of nutrition.

4e. Inside your hood, pour the hot agar into the newly sterilized container until it is about as thick as a pencil. Let the gelatin cool and congeal.



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NO PHOTOS



NO VIDEOS

STRICTLY ENFORCED



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by Professor L

The creation of genetically modified organisms (GMOs) is now within the ability of a knowledgeable and dedicated hacker. The most common genetic modification is the insertion of genes from one organism into another. The recipient is called a "transgenic organism" and this article will give you enough information so that anyone who could pass a high school biology lab can create one.

The usual 2600 article starts off with a disclaimer about how the article is for informational purposes only, and should the reader do anything illegal or dangerous, that's the reader's fault. The disclaimer in this article has to be stronger. Creating transgenic organisms has the potential to do great, possibly even catastrophic harm to the entire biosphere. Although the specific manipulations I describe in this article are safe (and often done in biology teaching labs), knowledge of the methods of genetic engineering have the potential to unleash enormous forces for good or for evil.

The most likely harmful consequence of hackers making a mistake with genetic engineering is for the hackers to get sick or to make the people around them sick. Maybe really, really sick. If you are going to try these techniques, learn about safe laboratory practices and follow them. The consequences of screwing up with genetic engineering are much worse than a mere jail sentence, so treat it seriously. No kidding.

If these techniques are so dangerous, why on earth would I want to tell hackers how to use them? I've thought about this long and hard before writing this article, and I have three reasons for writing. First, none of the information in this article is all that hard to find these days. Good high school biology classes teach the ideas (although they often figure out how to make it seem boring), and pretty much every community college will have a molecular biology lab class that teaches all of this information and good lab technique, too. If you think this article is

cool, I would strongly encourage you to take a real lab mol bio course and get at the good stuff.

My second reason is that I believe in the hacker mentality. When as a teenager I got tired of stacking tandems with my 8038-based blue box, I built an Imsai 8008, one of the first computer kits. Twenty-five years later, looking at my lab and all the scientific publications and prizes I have, even the straight world would have to admit that some hackers have made positive contributions to society. The hackers in the Homebrew Computer Club in the 70's spawned much of what would become Silicon Valley. The technologies that fascinate us have the power to create a radically different world; that is, they have the potential to be used for both awesome creation and awesome destruction. Hackers, who these days I think of as kids with a thirst for knowledge and the urge to try things for themselves, can be the ones with the powerfully creative ideas about how to use new technologies.

And my third reason for writing is that corporate powers are already using these technologies very broadly, and in ways that I don't feel are doing justice to their potential. With this article, I hope to inspire people to learn about what genetic engineering can do, and to come up with superior alternatives to the profit-seeking corporate approach. How do corporations use genetically modified organisms? Chances are, you are eating them! Pretty much all processed food in America contains GMOs. Monsanto's Roundup Ready crops dominate worldwide commercial agriculture, including soybeans, corn, cotton, canola oil, and sugar. The particular genetic modification in these foods makes it possible to dump the weedkiller Roundup on the crops without killing them. It's convenient for industrial farmers and it helps keep Monsanto the world's largest seller of herbicides. Surely there must be a better use for transgenic organisms than that! I hope someone reading this article will one day invent it.

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2600 Magazine



International Genetically Engineered Machine Competition

Global Distribution of Competing Teams

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