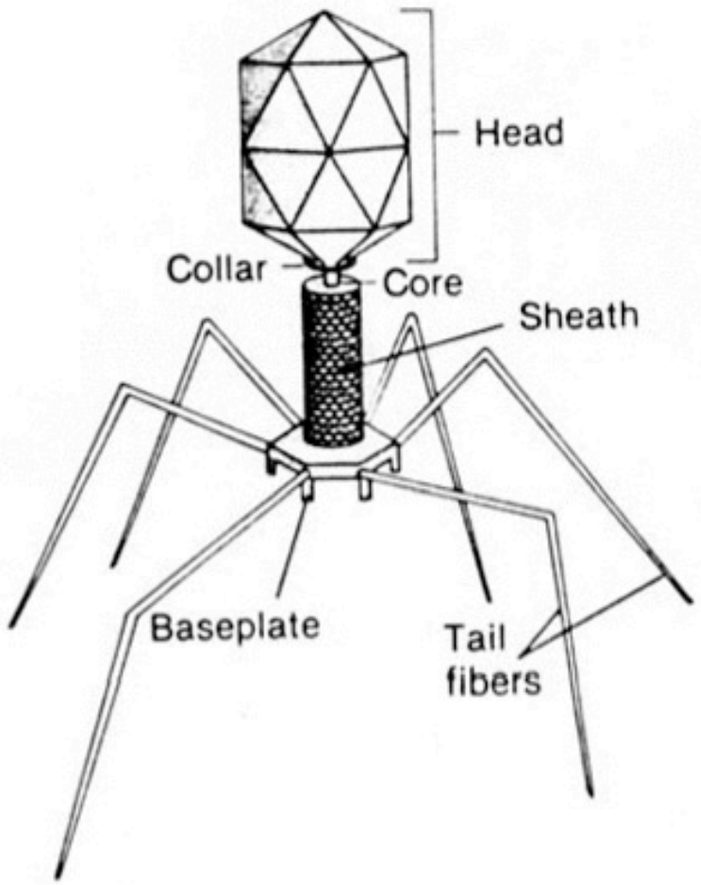
20.020

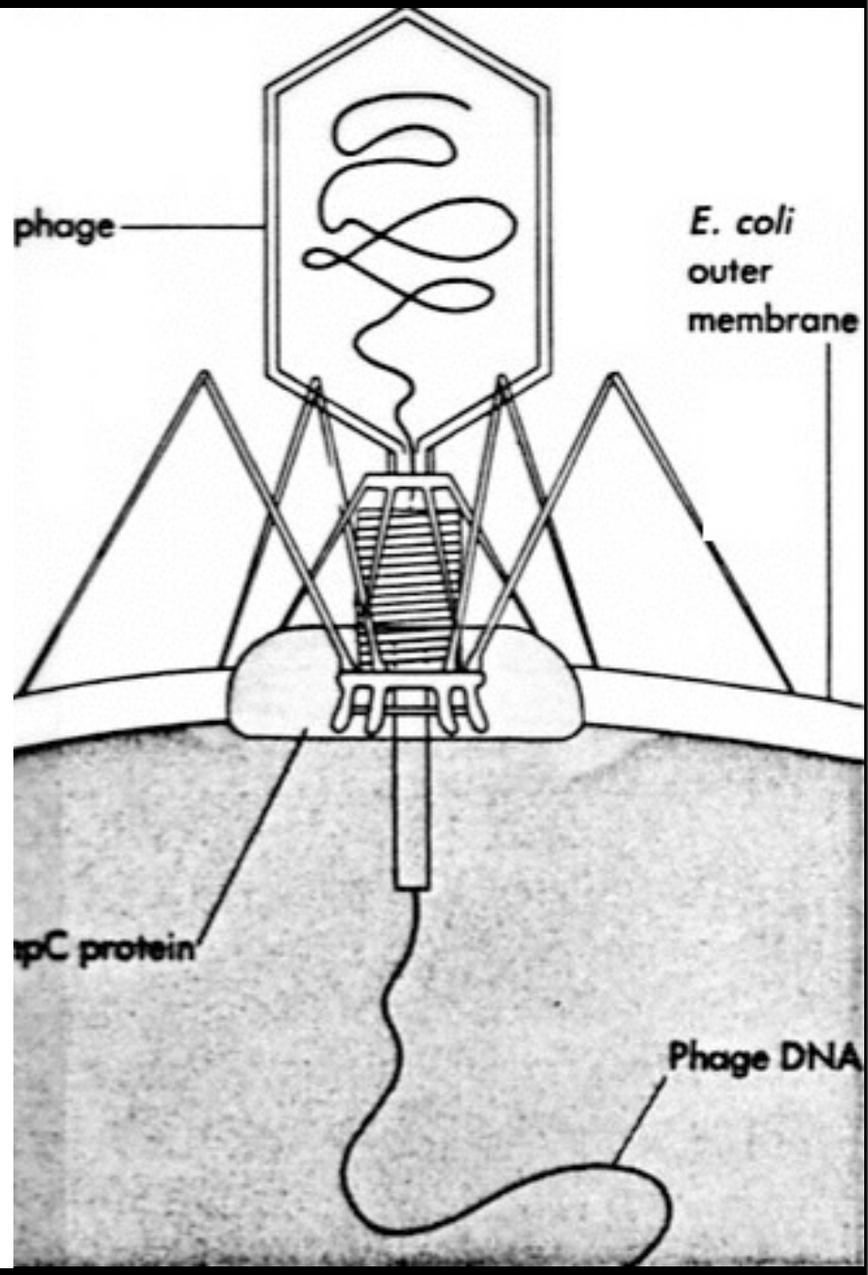
Introduction to Biological Engineering Design

5 February 2008

Biology Engineering

Biological virus



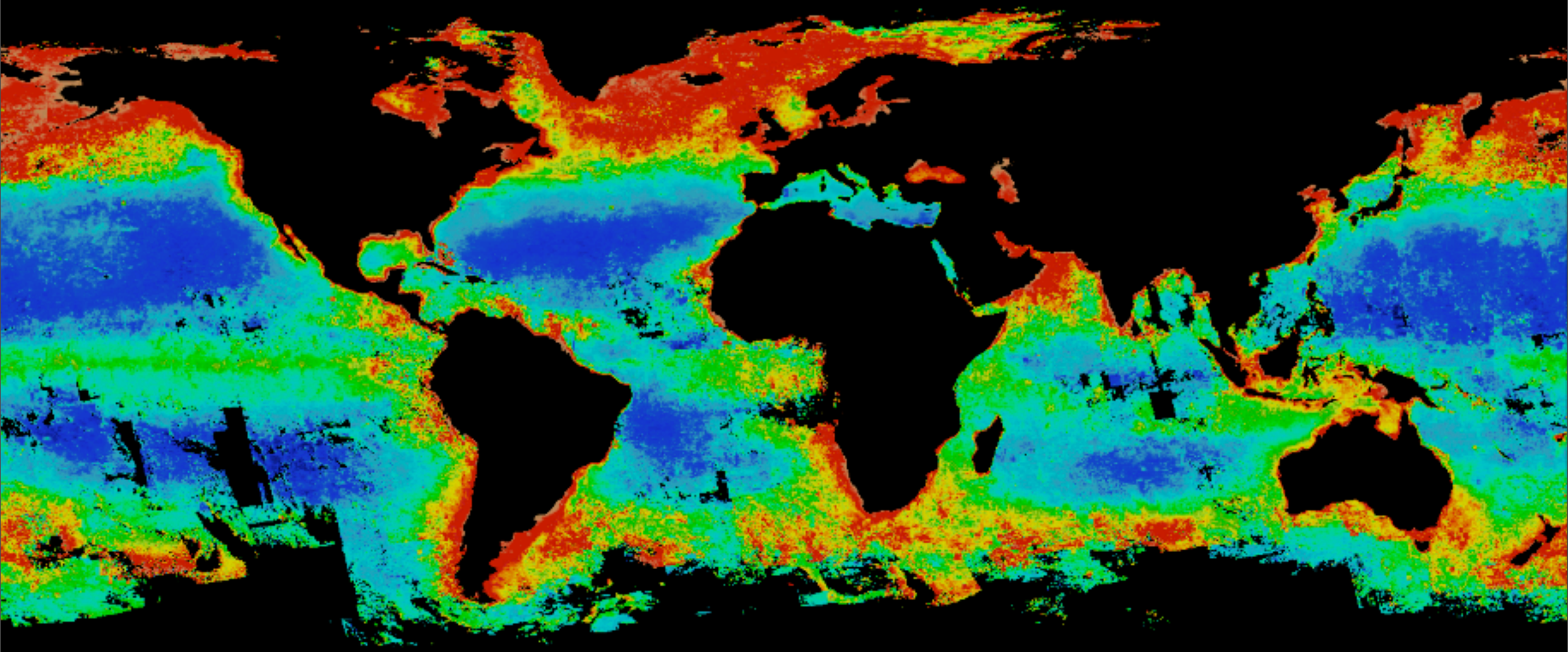


http://www.bact.wisc.edu/themicrobialworld/Phage.html

Key Features

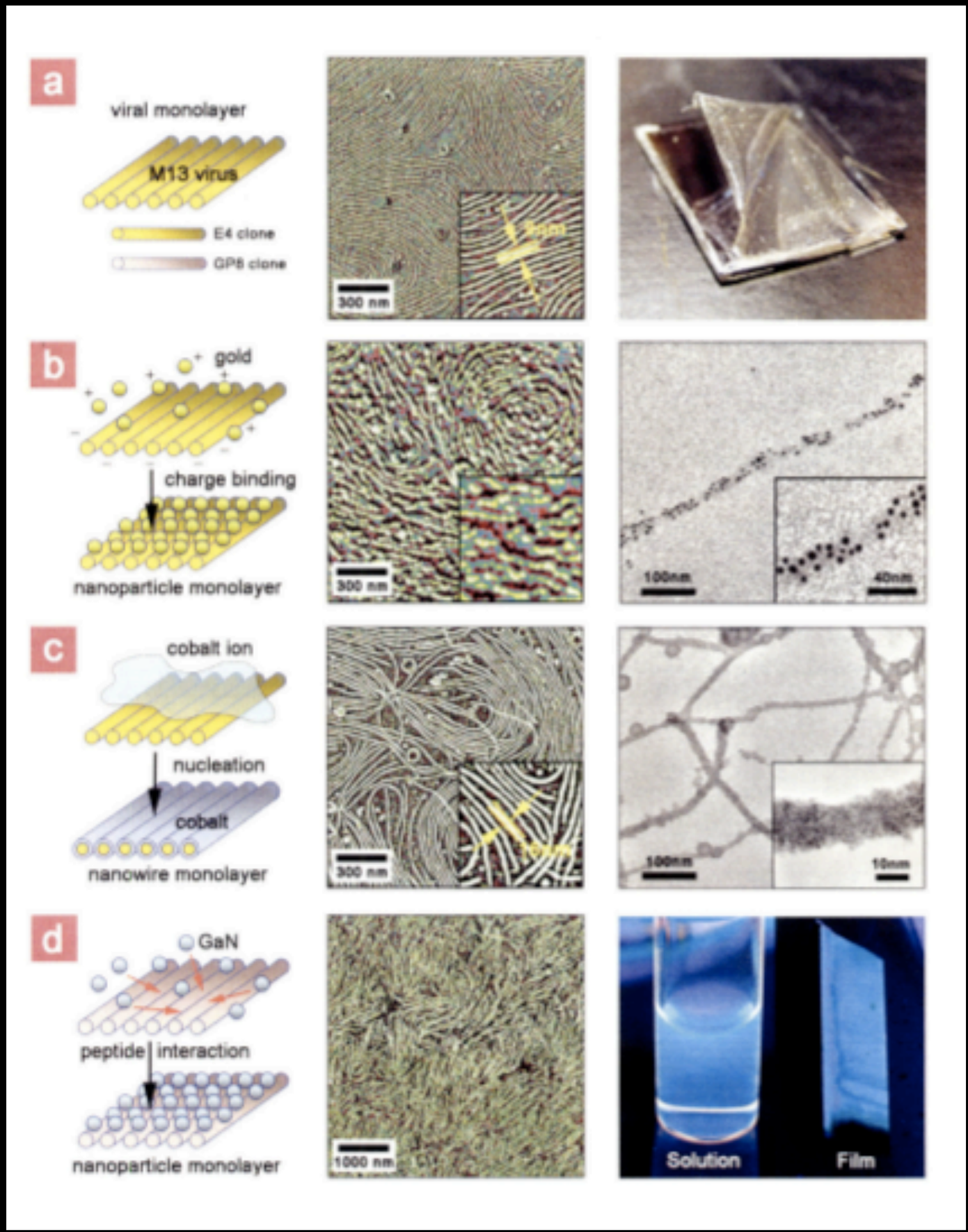
- *self assembling*
- *nanoscale*
- *reproducing machine*
- *programmed via DNA*

Ecological importance



http://svs.gsfc.nasa.gov/vis/a000000/a002400/a002497/index.html

Technical importance



http://dspace.mit.edu/handle/1721.1/39677

http://www.thegreenhead.com/imgs/california-redwood-2.jpg

http://www.firpointfarms.com/images/giantpumpkins.jpg

Combining two genomes in one cell: Stable cloning of the *Synechocystis* PCC6803 genome in the *Bacillus subtilis* 168 genome

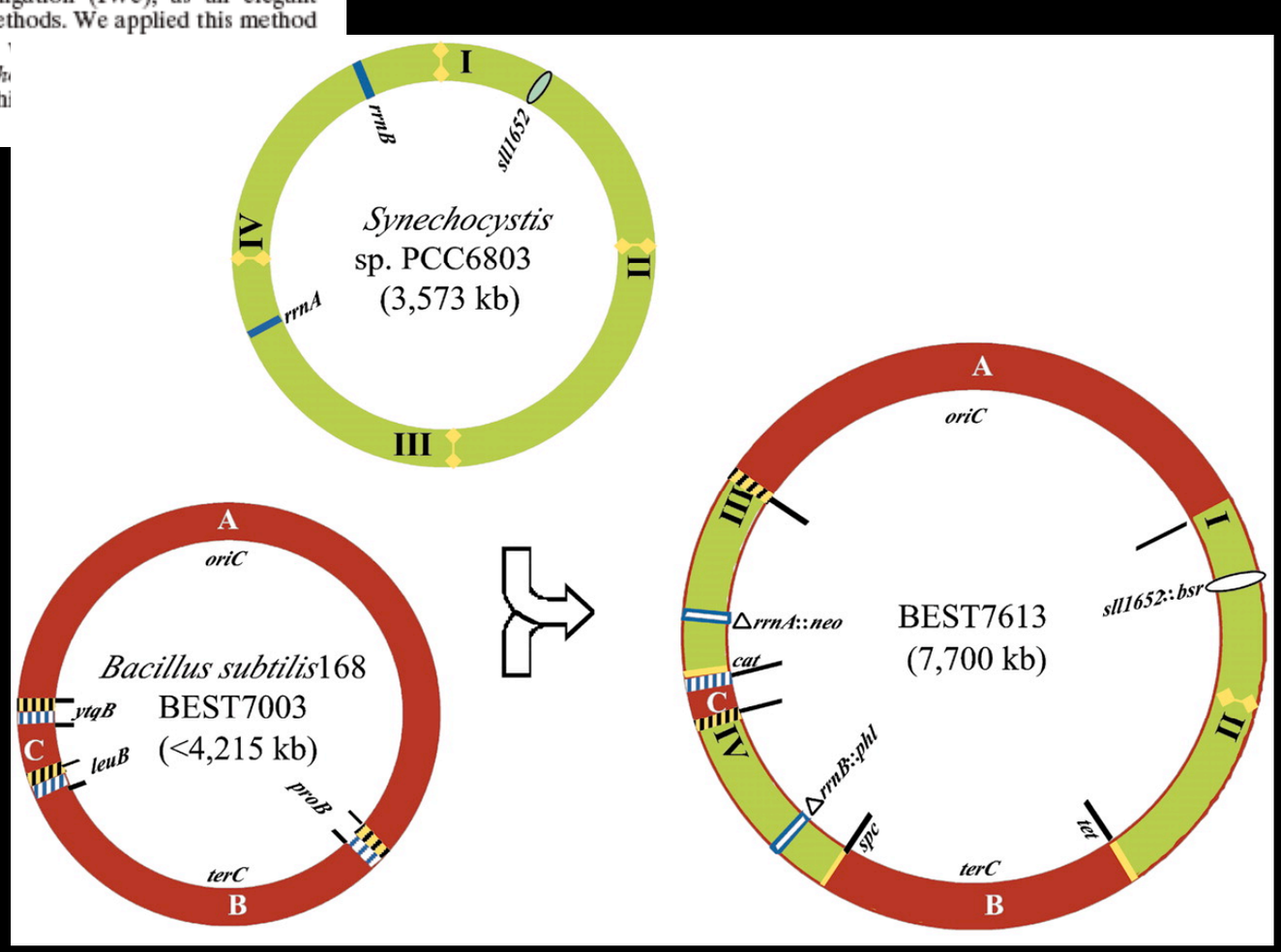
Mitsuhiro Itaya*, Kenji Tsuge, Maki Koizumi, and Kyoko Fujita

Mitsubishi Kagaku Institute of Life Sciences, 11 Minamiooya, Machida-shi, Tokyo 194-8511, Japan

Edited by J. Craig Venter, The J. Craig Venter Institute, Rockville, MD, and approved September 16, 2005 (received for review May 10, 2005)

Cloning the whole 3.5-megabase (Mb) genome of the photosynthetic bacterium *Synechocystis* PCC6803 into the 4.2-Mb genome of the mesophilic bacterium *Bacillus subtilis* 168 resulted in a 7.7-Mb composite genome. We succeeded in such unprecedented large-size cloning by progressively assembling and editing contiguous DNA regions that cover the entire *Synechocystis* genome. The strain containing the two sets of genome grew only in the *B. subtilis* culture medium where all of the cloning procedures were carried out. The high structural stability of the cloned *Synechocystis* genome was closely associated with the symmetry of the bacterial genome structure of the DNA replication origin (*oriC*) and its termination (*terC*) and the exclusivity of *Synechocystis* ribosomal RNA operon genes (*rrnA* and *rrnB*). Given the significant diversity in genome structure observed upon horizontal DNA transfer in nature, our stable laboratory-generated composite genome raised fundamental questions concerning two complete genomes in one cell. Our megasize DNA cloning method, designated megacloning, may be generally applicable to other genomes or genome loci of free-living organisms.

and demonstrated the successful reconstruction of long contiguous DNAs (12–14). Our cloning principle took advantage of features inherent to this bacterium, i.e., the development of natural competence and the subsequent homologous recombination activity in the cytoplasm. Both features are induced because of their association with growth-phase transition (15, 16). The target DNA is guided in the BGM vector by simultaneous homologous recombination at two small flanking DNAs called landing pad sequences (LPS), integrated at the BGM cloning locus before cloning. The two LPS, ordered and oriented correctly, are termed the LPS array (LPA) (13, 14). Sliding the LPA results in elongation of the adjacent target DNA (Fig. 1). We offer such elongation-coupled cloning in the BGM vector, hereafter called inchworm elongation (IWe), as an elegant alternative to current cloning methods. We applied this method in the complete cloning of the
photosynthetic bacterium *Synech*
4.2-Mb genome of the mesophi
(Fig. 2).



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 Letzelter[1], David Ribet[1], Gérard Pierron[2], 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:

doi:10.1016/j.jmb.2005.10.076 J. Mol. Biol. (2006) 355, 619–627

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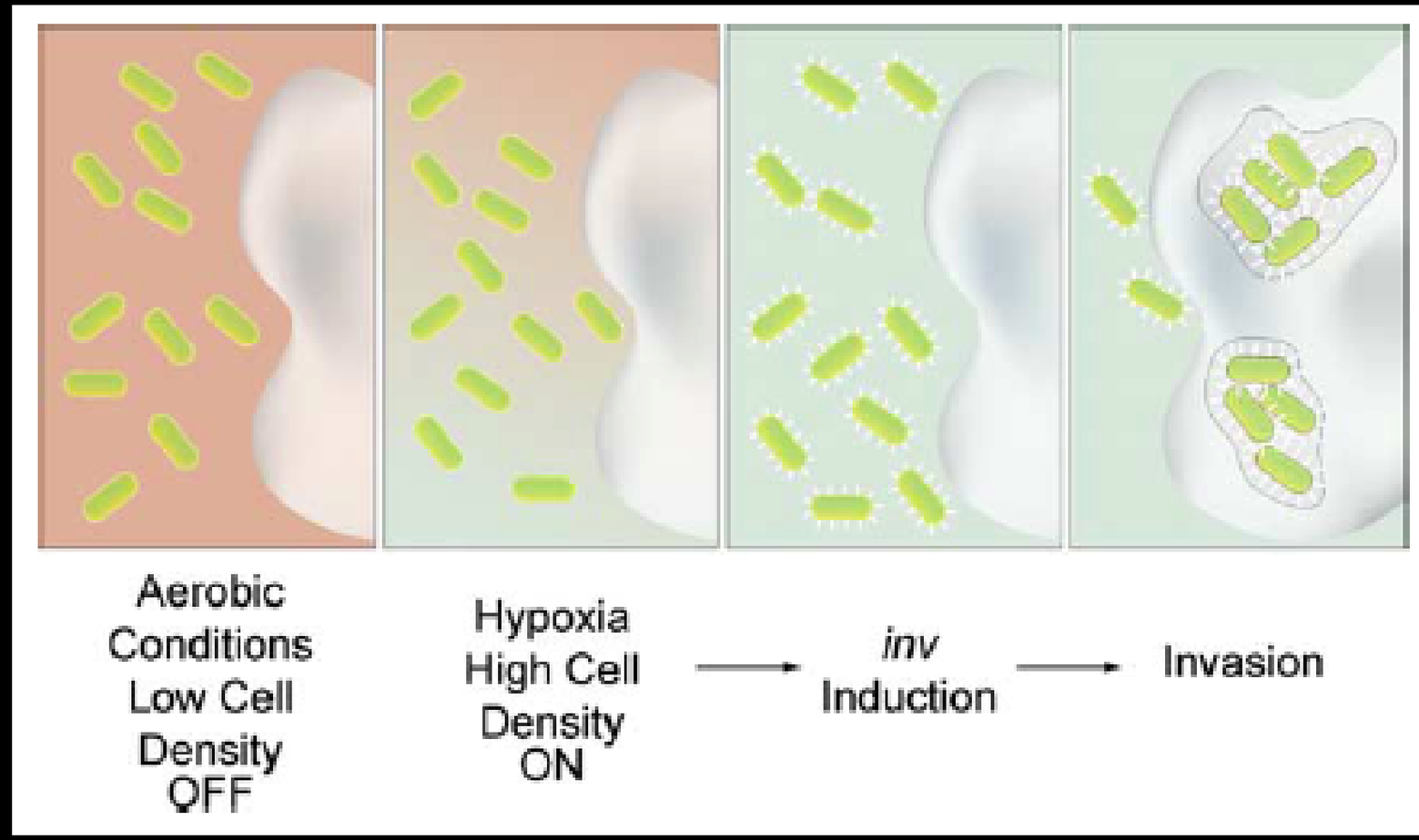
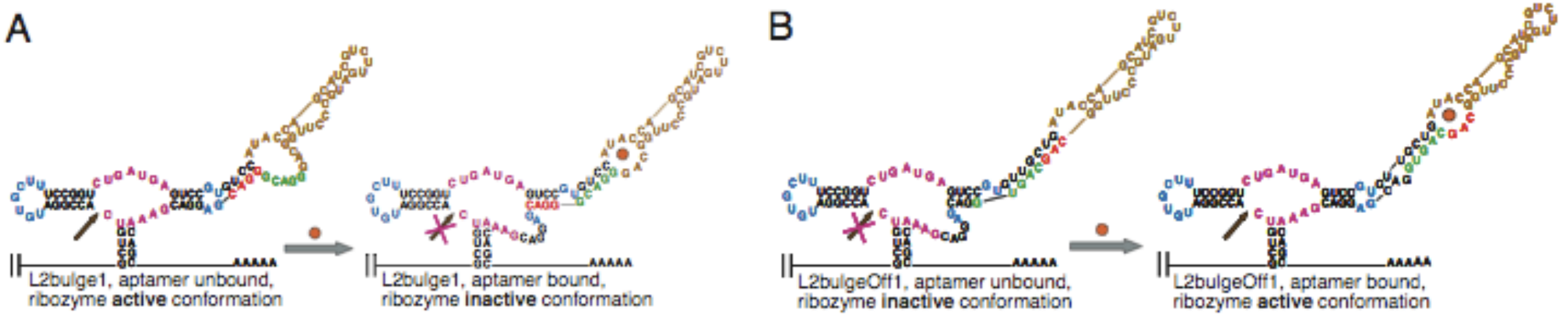
Environmentally Controlled Invasion of Cancer Cells by Engineered Bacteria

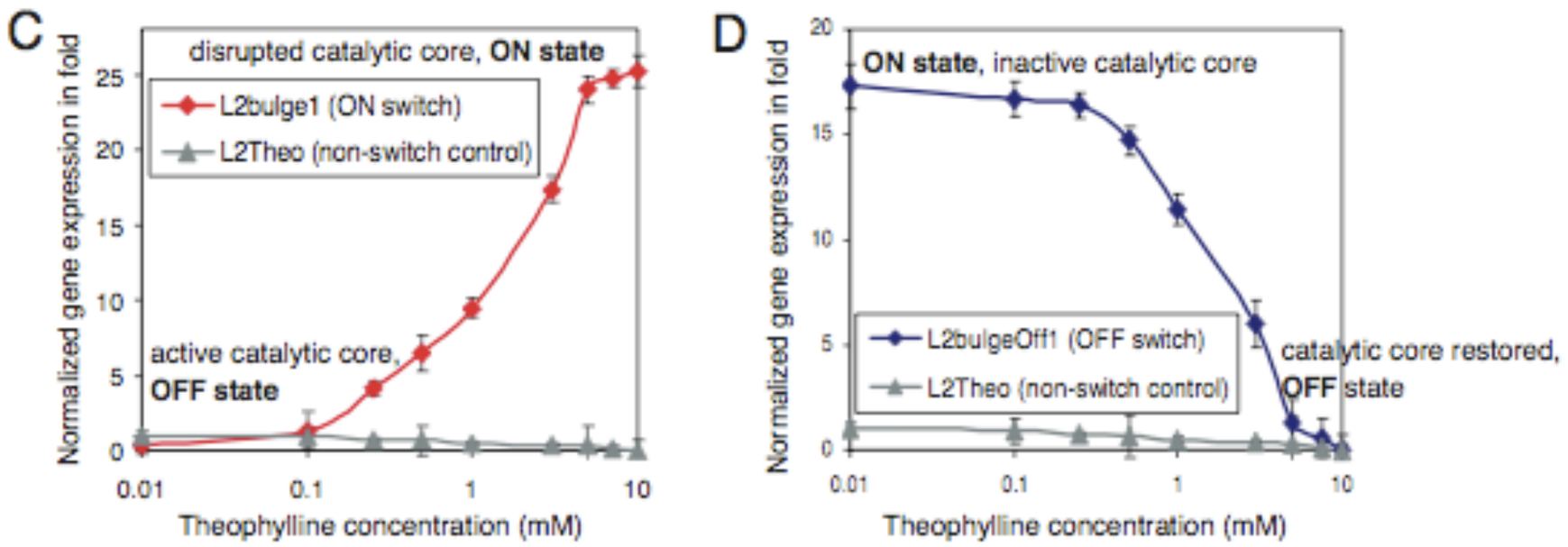
J. Christopher Anderson[1,3], Elizabeth J. Clarke[3], Adam P. Arkin[1,2*] and Christopher A. Voigt[2,3]



A modular and extensible RNA-based gene-regulatory platform for engineering cellular function

Maung Nyan Win and Christina D. Smolke*





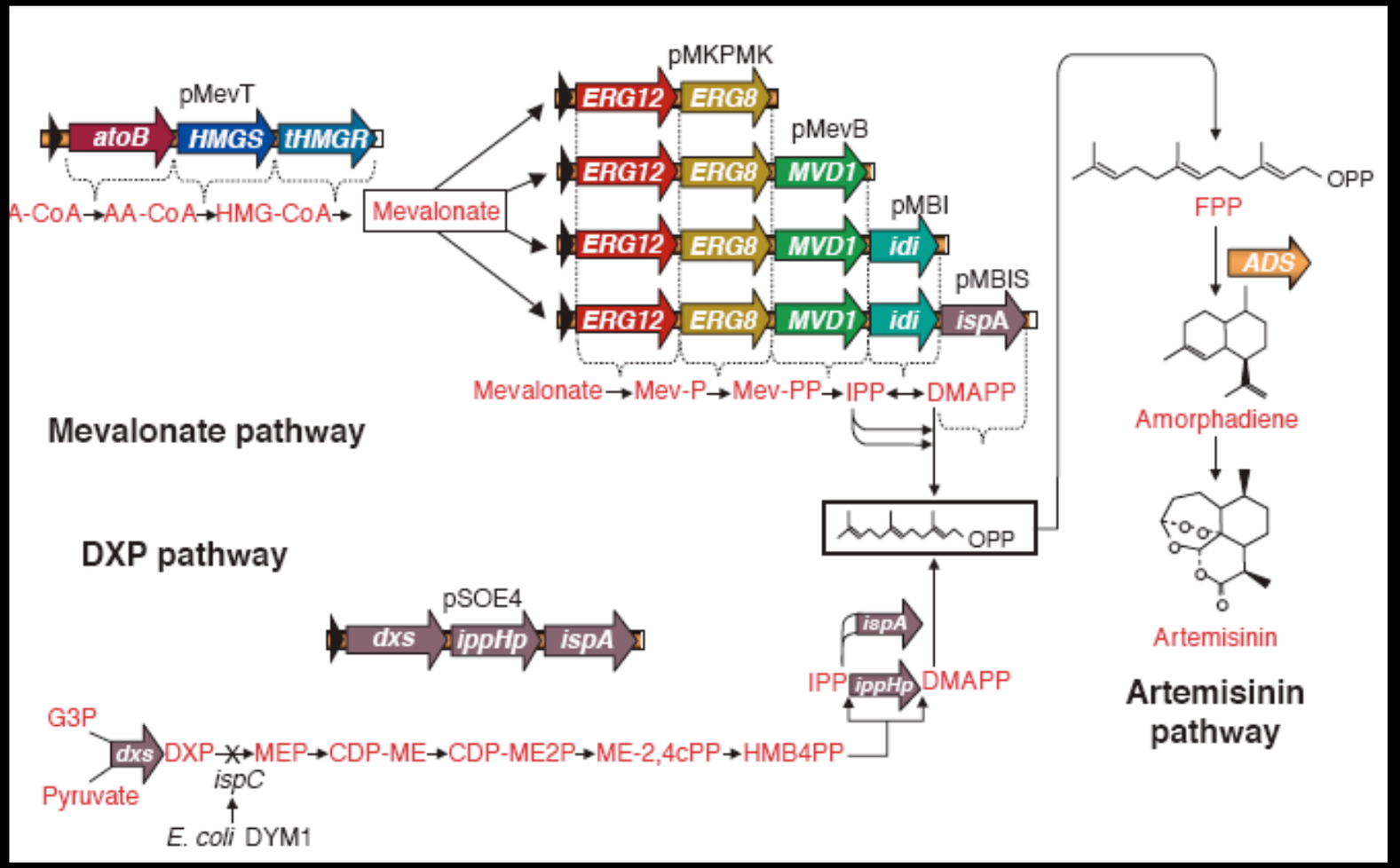
A synthetic oscillatory network of transcriptional regulators

Michael B. Elowitz & Stanislas Leibler

Engineering a mevalonate pathway in *Escherichia coli* for production of terpenoids

Vincent JJ Martin[1,2,3], Douglas J Pitera[1,3], Sydnor T Withers[1], Jack D Newman[1] & Jay D Keasling[1]

Isoprenoids are the most numerous and structurally diverse family of natural products. Terpenoids, a class of isoprenoids often isolated from plants, are used as commercial flavor and fragrance compounds and antimalarial or anticancer drugs. Because plant tissue extractions typically yield low terpenoid concentrations, we sought an alternative method to produce high-value terpenoid compounds, such as the antimalarial drug artemisinin, in a microbial host. We engineered the expression of a synthetic amorpha-4,11-diene synthase gene and the mevalonate isoprenoid pathway from *Saccharomyces cerevisiae* in *Escherichia coli*. Concentrations of amorphadiene, the sesquiterpene olefin precursor to artemisinin, reached 24 μg caryophyllene equivalent/ml. Because isopentenyl and dimethylallyl pyrophosphates are the universal precursors to all isoprenoids, the strains developed in this study can serve as platform hosts for the production of any terpenoid compound for which a terpene synthase gene is available.



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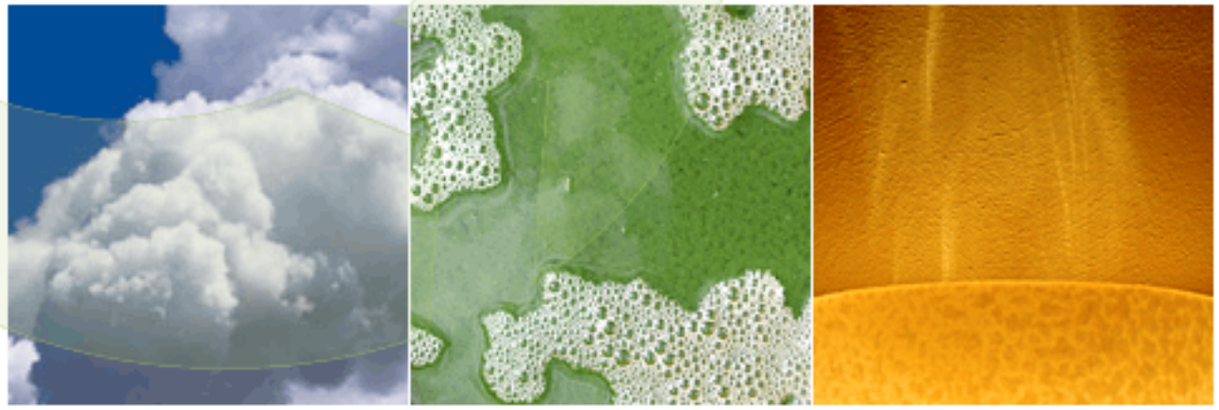

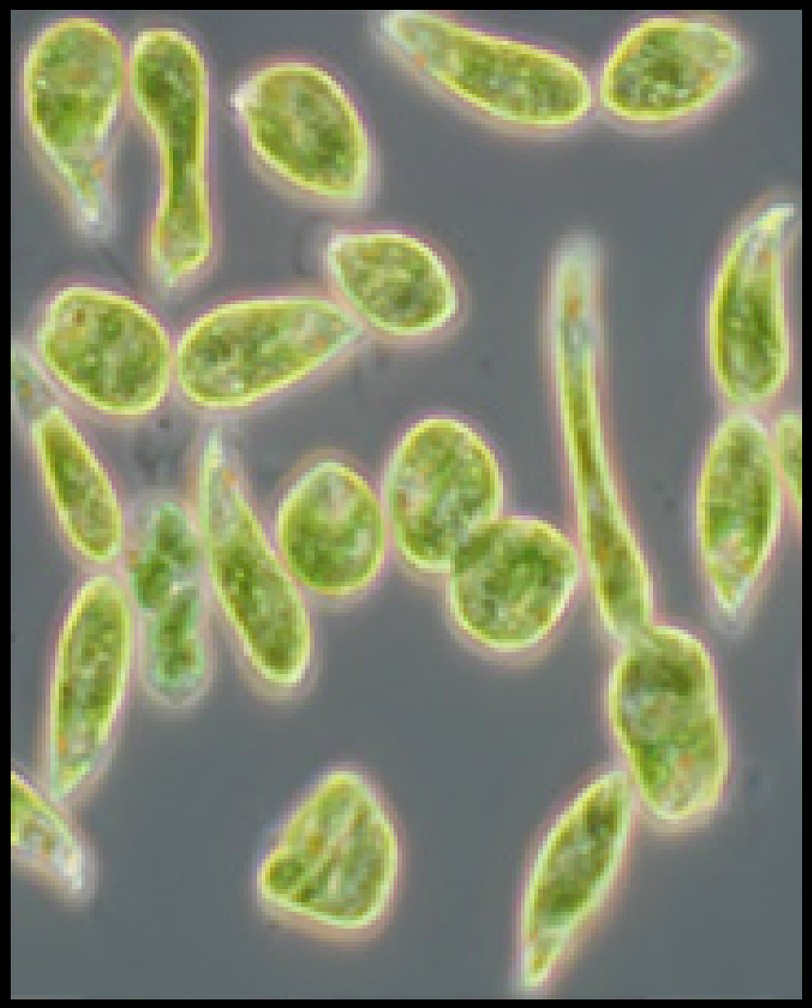

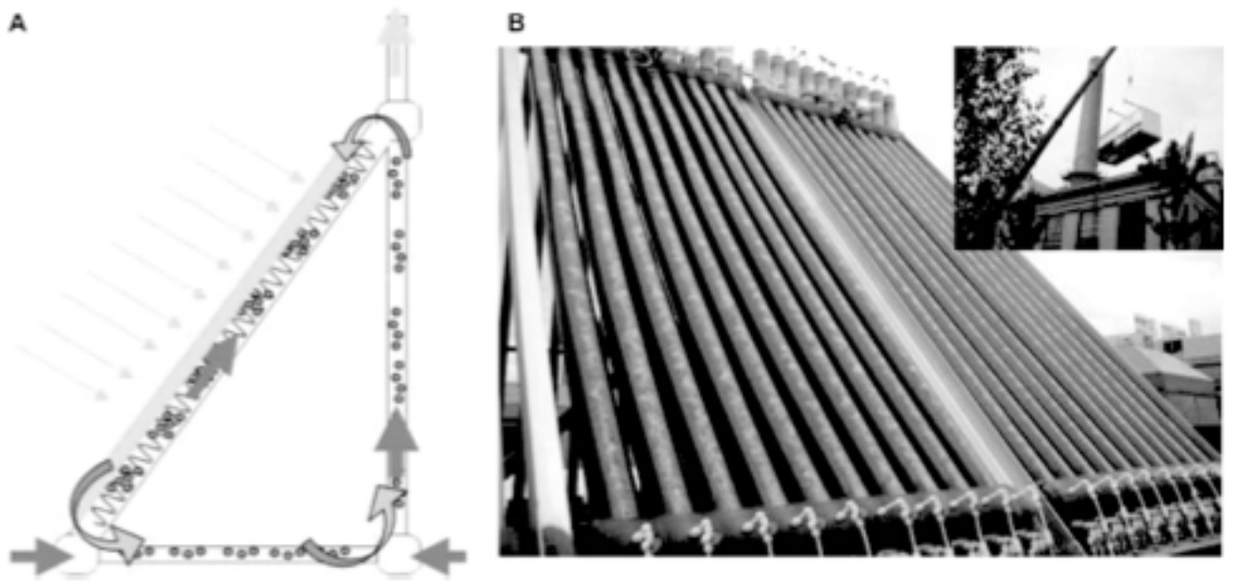

Figure 8. Inclined-tube ALR configuration: (A) schematic presentation of one ALR "triangle". Solid arrows indicate the direction of the gas flow, and open arrows indicate the direction of the liquid flow (B). An array of 30 ALRs, each with a volume of 30 L, with an algal culture grown on a flue gas. Inset: installation of the array of ALRs on the roof of MIT's Cogeneration Power Plant.

Science 23 March 2007:
Vol. 315. no. 5819, pp. 1723 – 1725
DOI: 10.1126/science.1138838

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REPORTS

Emergence of Novel Color Vision in Mice Engineered to Express a Human Cone Photopigment

Gerald H. Jacobs,[1*] Gary A. Williams,[1] Hugh Cahill,[2,3,4] Jeremy Nathans[2,3,4,5]

Changes in the genes encoding sensory receptor proteins are an essential step in the evolution of new sensory capacities. In primates, trichromatic color vision evolved after changes in X chromosome–linked photopigment genes. To model this process, we studied knock-in mice that expressed a human long-wavelength-sensitive (L) cone photopigment in the form of an X-linked polymorphism. Behavioral tests demonstrated that heterozygous females, whose retinas contained both native mouse pigments and human L pigment, showed enhanced long-wavelength sensitivity and acquired a new capacity for chromatic discrimination. An inherent plasticity in the mammalian visual system thus permits the emergence of a new dimension of sensory experience based solely on gene-driven changes in receptor organization.

[1] Neuroscience Research Institute and Department of Psychology, University of California, Santa Barbara, CA 93106, USA.
[2] Department of Neuroscience, Johns Hopkins Medical School, Baltimore, MD 21205, USA.
[3] Department of Ophthalmology, Johns Hopkins Medical School, Baltimore, MD 21205, USA

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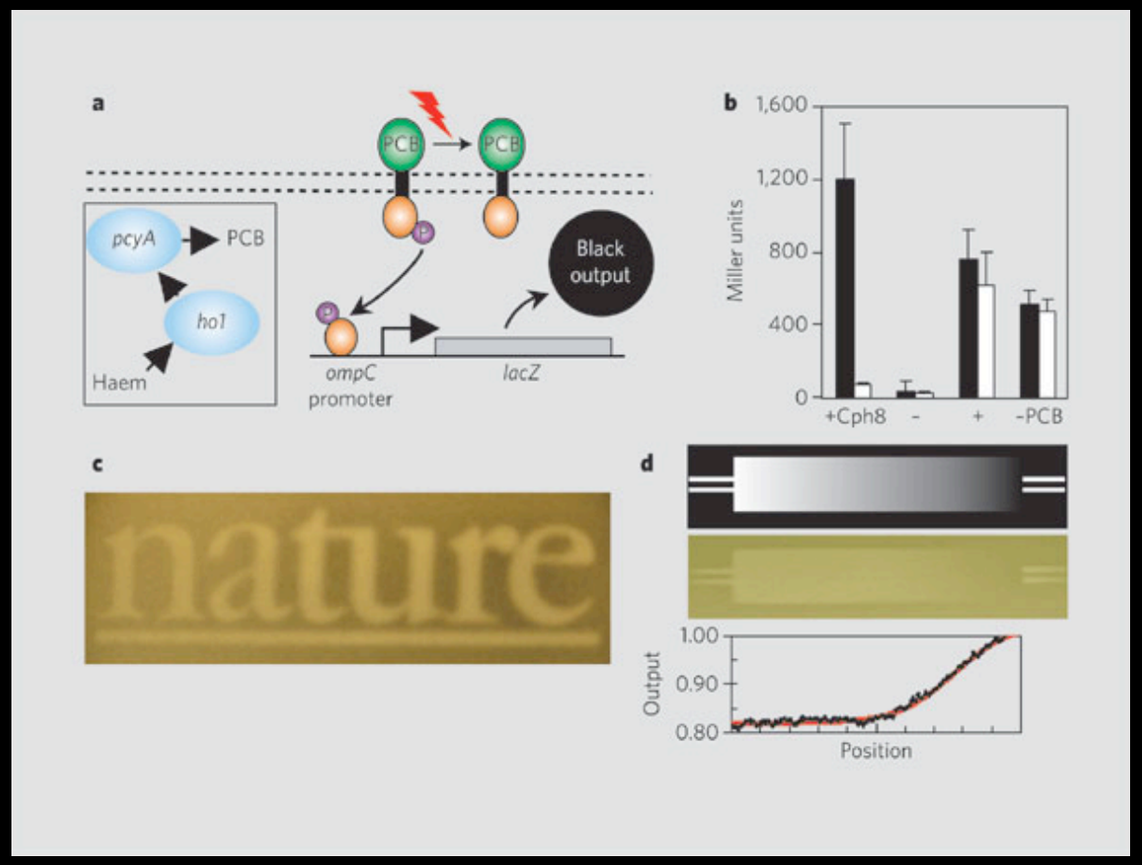
Vol 438 | 24 November 2005 nature

BRIEF COMMUNICATIONS

Engineering *Escherichia coli* to see light

These smart bacteria 'photograph' a light pattern as a high-definition chemical image.

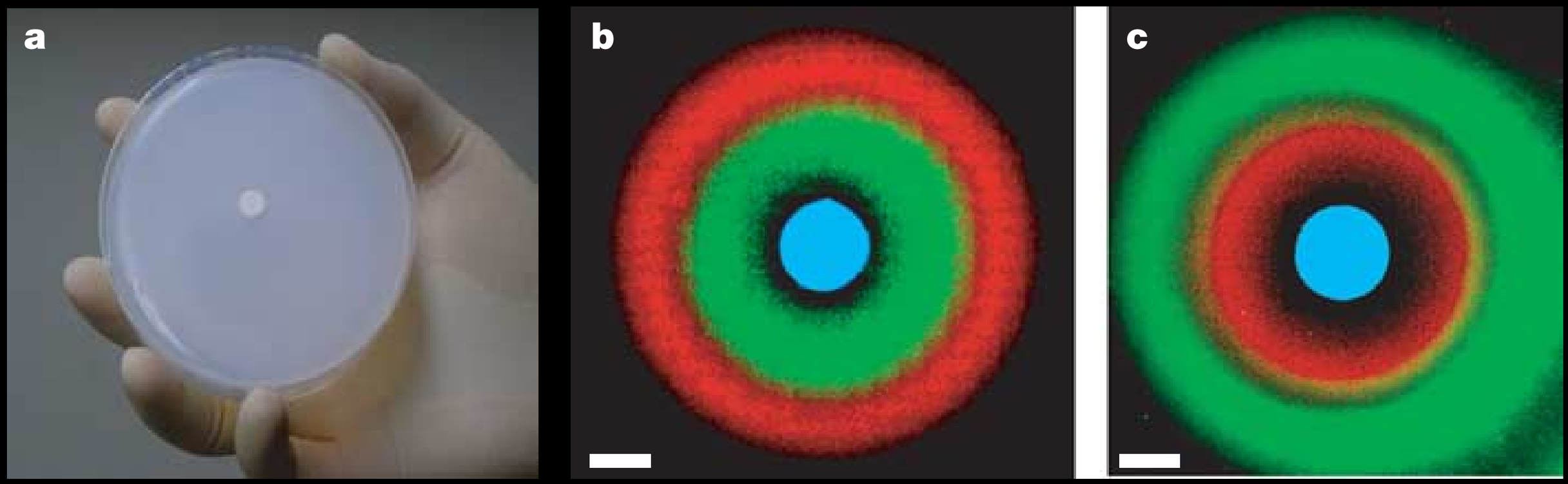
Anselm Levskaya*, Aaron A. Chevalier†, Jeffrey J. Tabor†, Zachary Booth Simpson†, Laura A. Lavery†, Matthew Levy†, Eric A. Davidson†, Alexander Scouras†, Andrew D. Ellington†‡, Edward M. Marcotte†‡, Christopher A. Voigt*§||



A synthetic multicellular system for programmed pattern formation

Subhayu Basu[1], **Yoram Gerchman**[1], **Cynthia H. Collins**[3], **Frances H. Arnold**[3] **& Ron Weiss**[1,2]

[1]*Department of Electrical Engineering and* [2]*Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544, USA*
[3]*Division of Chemistry and Chemical Engineering, California Institute of Technology 210-41, Pasadena, California 91125, USA*



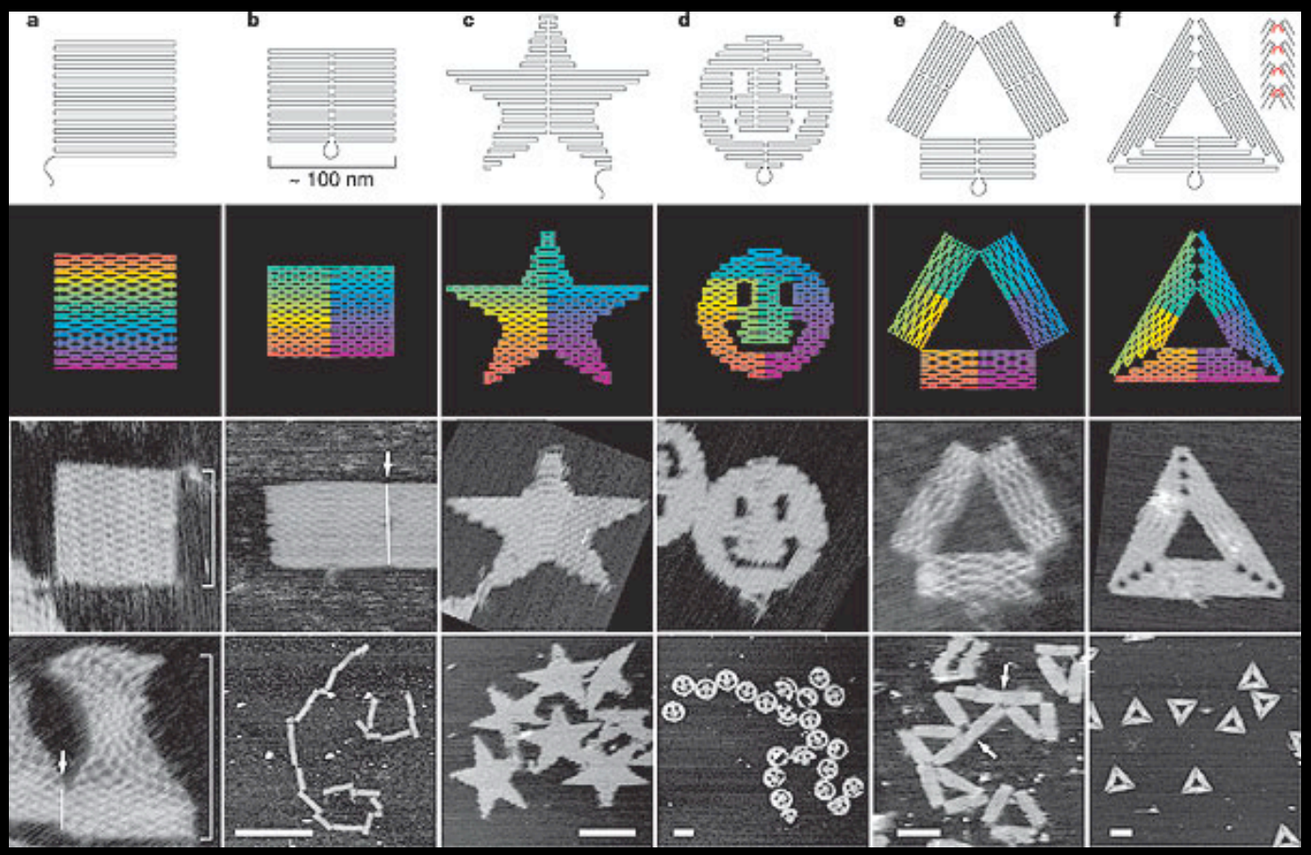
Vol 440|16 March 2006|doi:10.1038/nature04586

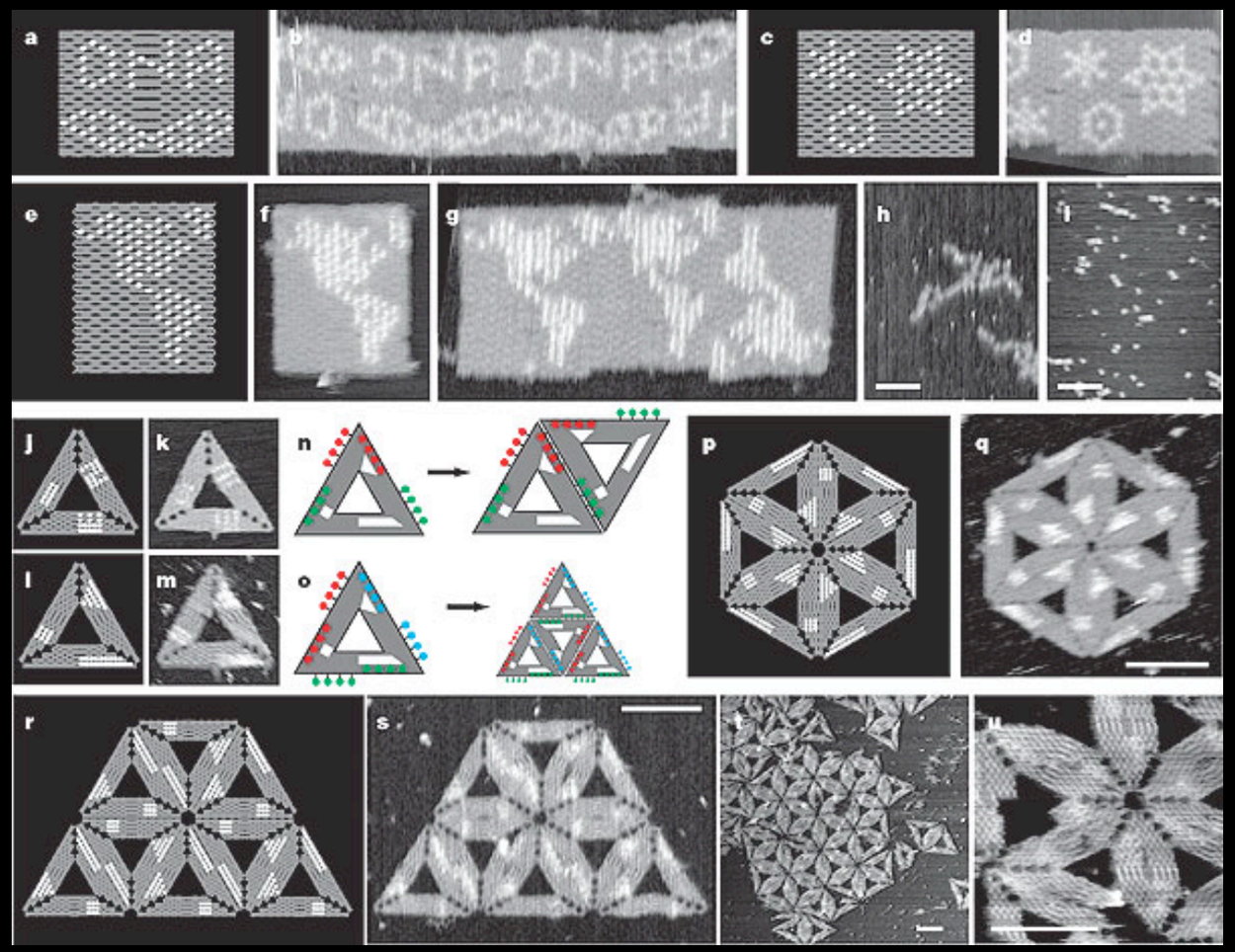
nature

ARTICLES

Folding DNA to create nanoscale shapes and patterns

Paul W. K. Rothemund[1]





JOURNAL OF BACTERIOLOGY, May 1998, p. 2450–2458
0021-9193/98/$04.00+0

Vol. 180, No. 9

Gas Vesicle Genes Identified in *Bacillus megaterium* and Functional Expression in *Escherichia coli*

NING LI AND MAURA C. CANNON*

Department of Microbiology, University of Massachusetts, Amherst, Massachusetts 01003

Received 4 December 1997/Accepted 4 March 1998

Gas vesicles are intracellular, protein-coated, and hollow organelles found in cyanobacteria and halophilic archaea. They are permeable to ambient gases by diffusion and provide buoyancy, enabling cells to move upwards in liquid to access oxygen and/or light. In halobacteria, gas vesicle production is encoded in a 9-kb cluster of 14 genes (4 of known function). In cyanobacteria, the number of genes involved has not been determined. We now report the cloning and sequence analysis of an 8,142-bp cluster of 15 putative gas vesicle genes (*gvp*) from *Bacillus megaterium* VT1660 and their functional expression in *Escherichia coli*. Evidence

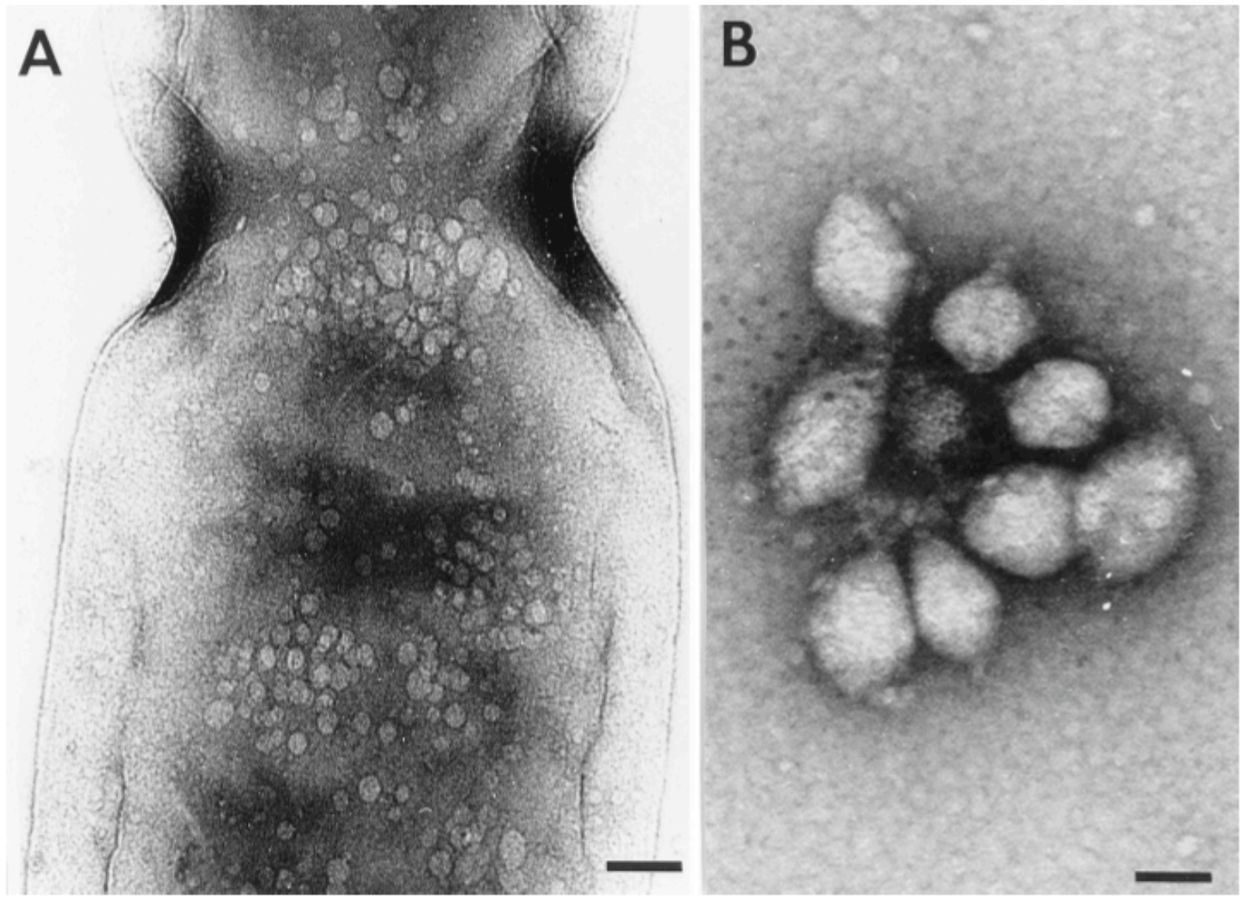


FIG. 6. Electron micrographs of *E. coli*(pNL26). (A) Protoplast of a dividing cell shows gas vesicles within the cell. Bar, 123 nm. (B) Gas vesicles from cell lysate. Bar, 44 nm.

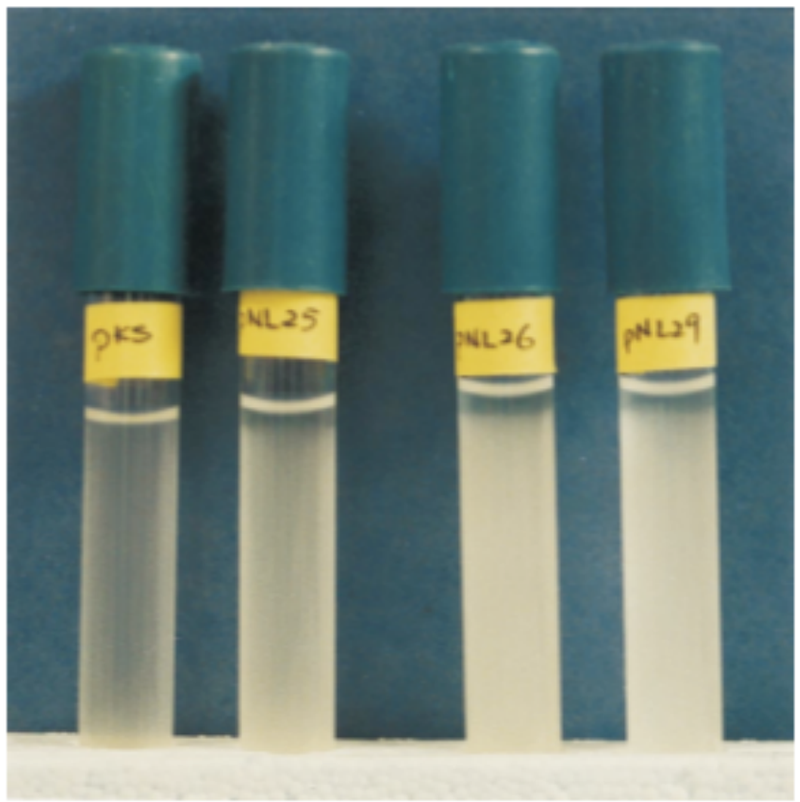
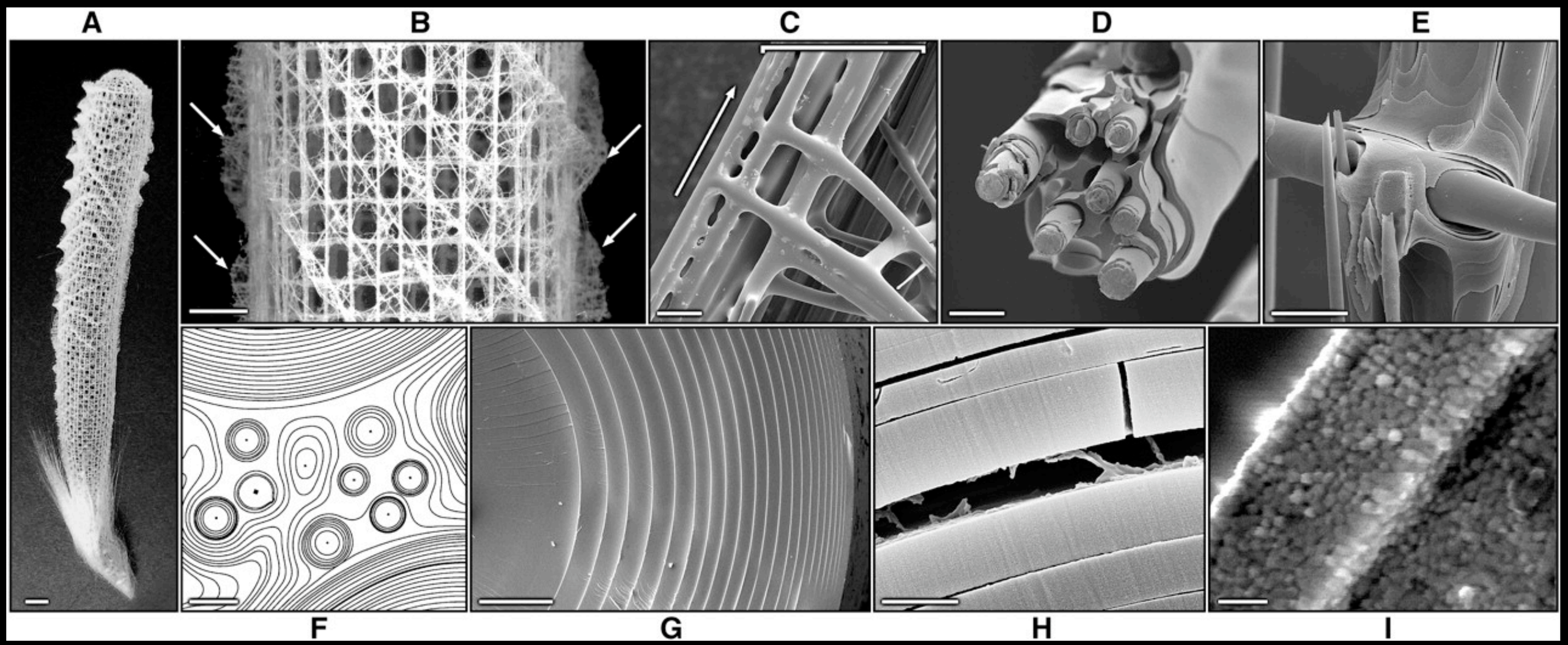


FIG. 3. Buoyancy of *E. coli* strains carrying plasmids with cloned *B. megaterium gvp* genes as labeled: pNL25, pNL26, pNL29, and the control, pKS (pBluescriptIIKS).

Skeleton of *Euplectella* sp.: Structural Hierarchy from the Nanoscale to the Macroscale

Joanna Aizenberg,[1*] James C. Weaver,[2] Monica S. Thanawala,[1] Vikram C. Sundar,[1] Daniel E. Morse,[2] Peter Fratzl[3]



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.


10-1030-5S
GLEN RESEARCH
5912014
5.0g
10-1010-1S
GLEN RESEARCH
5909030
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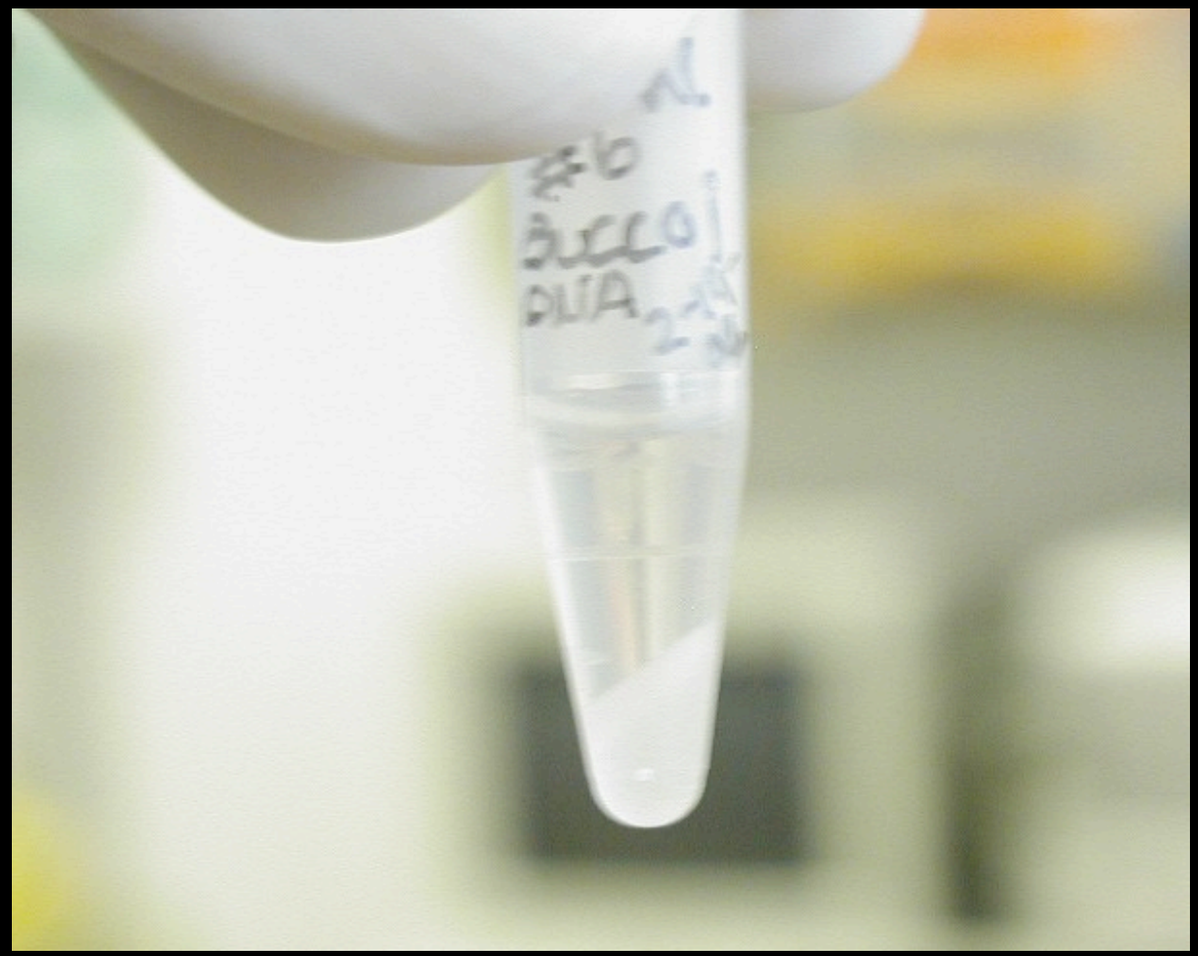
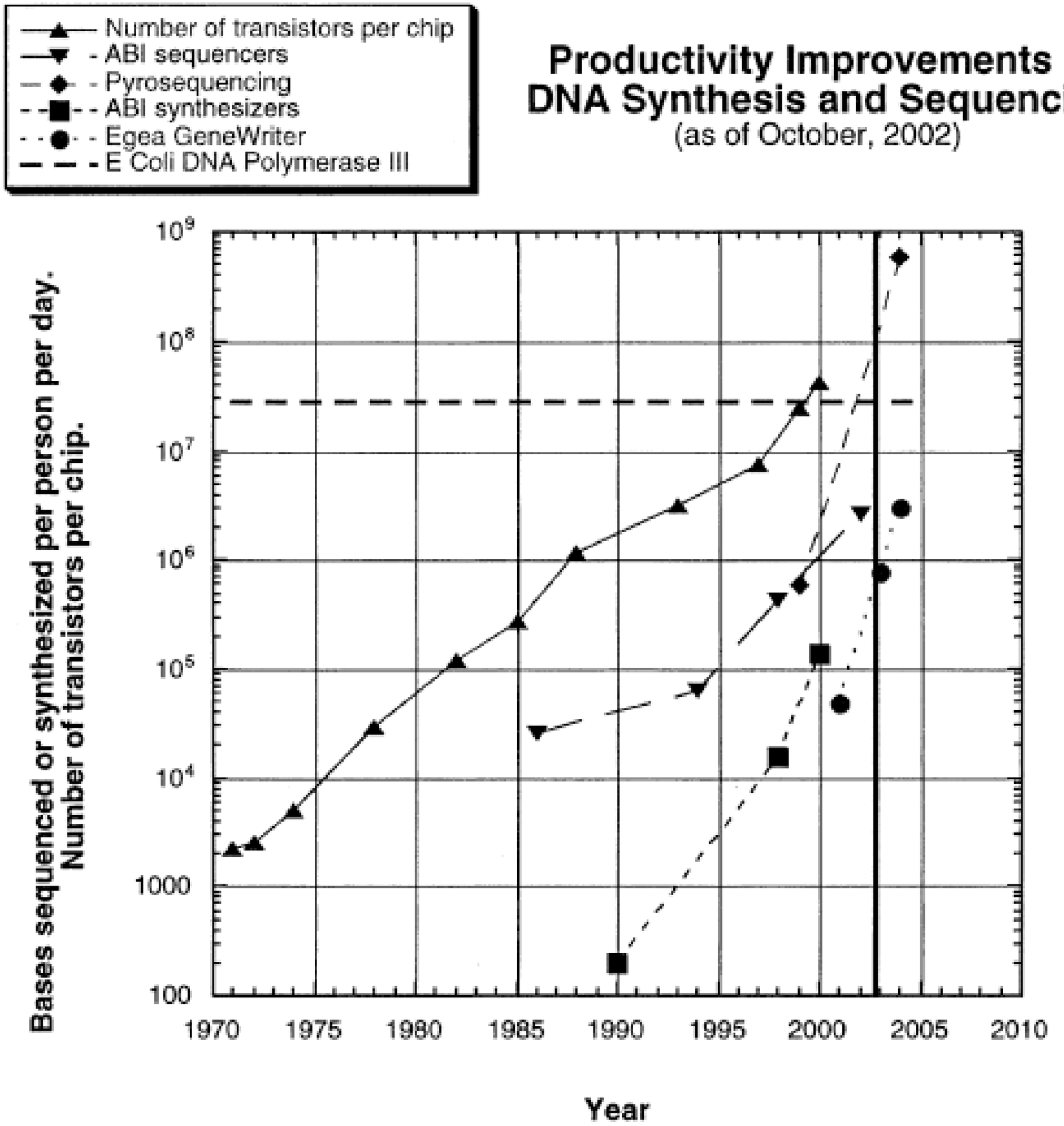


Productivity Improvements in DNA Synthesis and Sequencing

(as of October, 2002)



Carlson, Pace & Proliferation of Biological Technologies, Biosec. & Bioterror. 1(3):1 (2003)

Sciencexpress Research Article

Complete Chemical Synthesis, Assembly, and Cloning of a *Mycoplasma genitalium* Genome

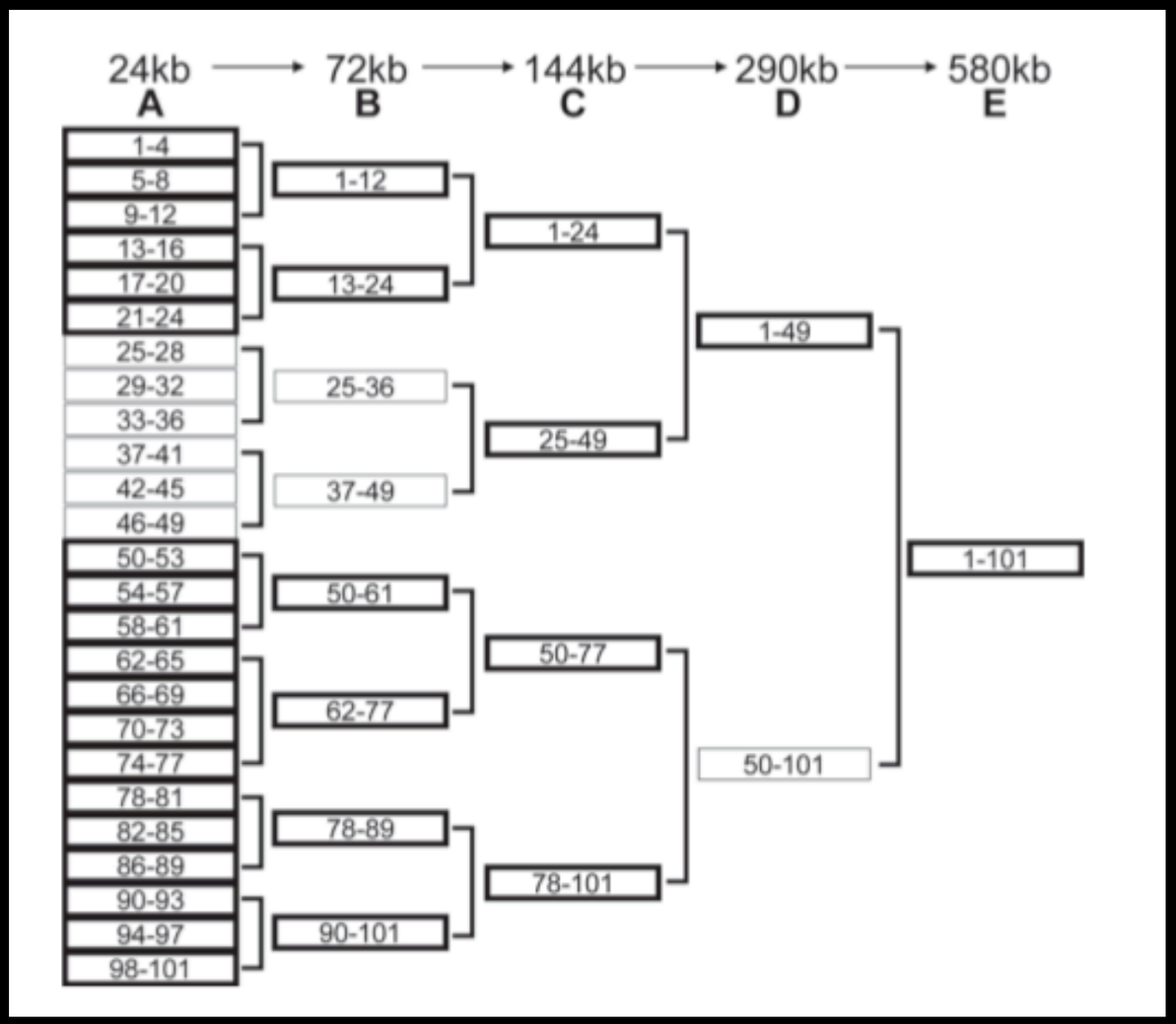
Daniel G. Gibson, Gwynedd A. Benders, Cynthia Andrews-Pfannkoch, Evgeniya A. Denisova, Holly Baden-Tillson, Jayshree Zaveri, Timothy B. Stockwell, Anushka Brownley, David W. Thomas, Mikkel A. Algire, Chuck Merryman, Lei Young, Vladimir N. Noskov, John I. Glass, J. Craig Venter, Clyde A. Hutchison III, Hamilton O. Smith*

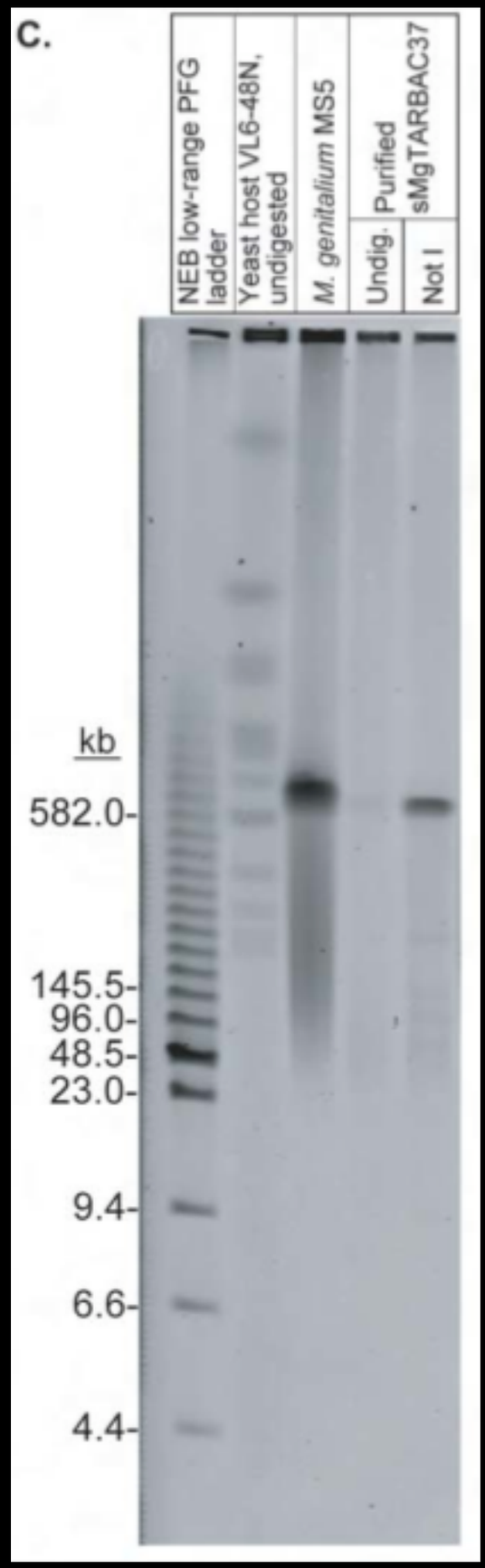
The J. Craig Venter Institute, Rockville, MD 20850, USA.

*To whom correspondence should be addressed. E-mail: hsmith@jcvi.org

We have synthesized a 582,970 bp *Mycoplasma genitalium* genome. This synthetic genome, named *M. genitalium*

The actual synthesis and assembly of this genome presented a formidable technical challenge. Although





What do you think are important problems?

Can we help solve any with biological technologies?

Do you think that humans can
contribute directly to the living world?

Can you make something beautiful?

How can we get better at engineering biology?

Should we be engineering biology?

What might we hope to learn from nature?