

NSABB July 1, 2005

Synthetic Genomics

From Reading to Writing the Genetic Code

Genes are the design
components of the future

J. Craig Venter

I N S T I T U T E

First Genome Sequenced 1995

Ten years ago this month



J. Craig Venter

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Microbial Abundance

- Microbes make up roughly $\frac{1}{2}$ of the Earth's biomass
- 6×10^{30} microbes over entire Earth
- Animals make up 1/1000th of Earth's total biomass
- Each ml of sea water has one million bacteria and 10 million viruses

www.sorcerer2expedition.org

SORCERER II Expedition | EXPEDITION INFO | VOYAGE TRACKER | MULTIMEDIA GALLERY | SCIENTIFIC DATA | GLOSSARY

38°58.33' N

Expedition Overview

▲ The Sorcerer II Expedition is the brainchild of The Institute for Biological Energy Alternatives (IBER) president, J. Craig Venter, Ph.D. Dr. Venter is well known as the scientist who pioneered methods of rapid gene analysis used to decode the human genome. He and his teams developed revolutionary techniques and used of state of the art technology and mathematical algorithms that also led to the sequencing of nearly 88 genomes including model organisms such as the fruit fly and the mouse. As

▼

Latest News

▲ 03/04/04 [14:00 EST]
IBER researchers publish results from environmental shotgun sequencing of Sargasso Sea in Science; discover 1,800 new species and 1.2 million new genes, including nearly 800 new photoreceptor

▼

Mailing List

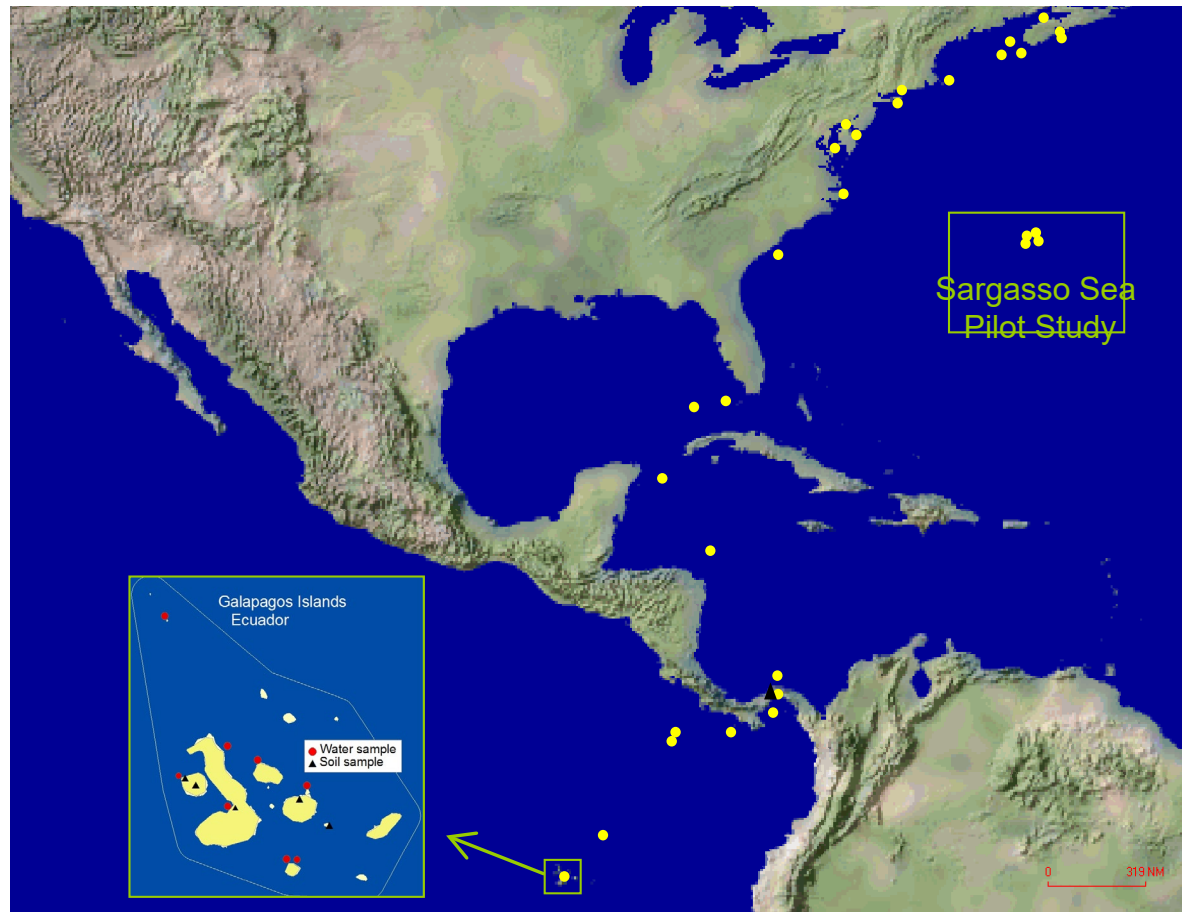
Receive expedition updates and news! [Join!](#)

*"In one drop of water are found all the secrets of the oceans."
- Kahlil Gibran*

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Sorcerer II Global Ocean Survey: Nova Scotia through Galapagos Islands



J. Craig Venter

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**100 Million letters of genetic code
every 24 hours**



454 Genome Sequencing System

- Up to 100x throughput over Fluorescent Sequencing:
 - 20 megabases/4 hr instrument run (20-32 high Q)

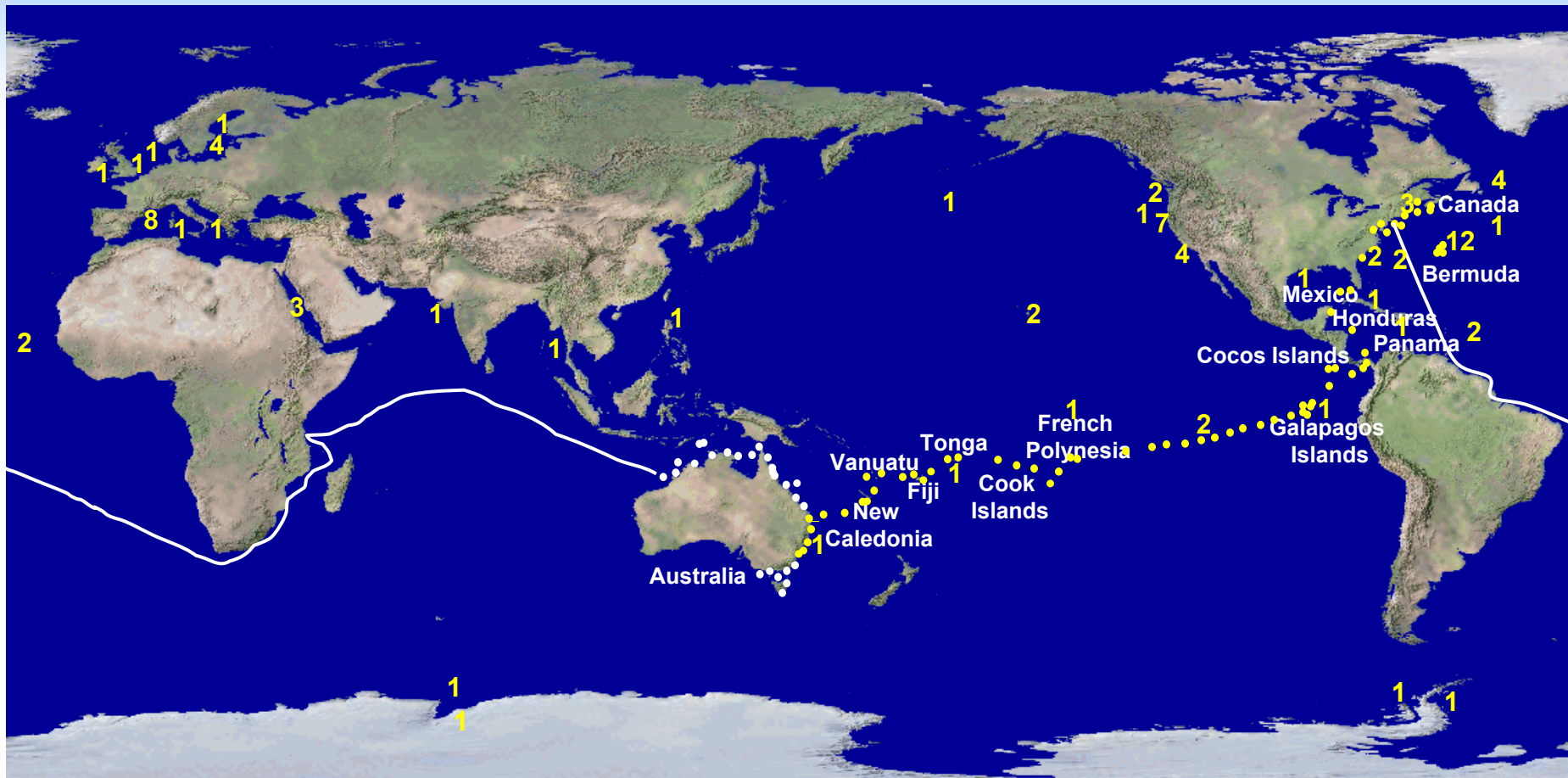
Current vs 454

<i>Platform</i>	<u>3730</u>	<u>454</u>
<i>Bases per day</i>	945K	100-200 million
<i>Runs per day</i>	12	5
<i>Bases per run</i>	78.7K	20-40 million
<i>Average RL</i>	820bp	125bp
<i>Cost</i>	~\$0.0012/base (\$1.20/Kb)	\$0.00025/base (\$0.25/Kb)

Marine Microbe Sequencing Project

- **\$9M Funded by Gordon and Betty Moore Foundation**
 - **Sequence, Assemble and Auto-Annotate up to 130 Marine Microbes**
 - **Add to the current (10-20) set of sequenced Marine Microbes**
 - **1000% increase**
 - **Synergy with Sorcerer Expedition**

Sorcerer II Expedition and Moore Foundation Isolated Organisms



● Sampled stations

○ Planned stations

Number of organisms isolated from each region for the Moore Foundation Program

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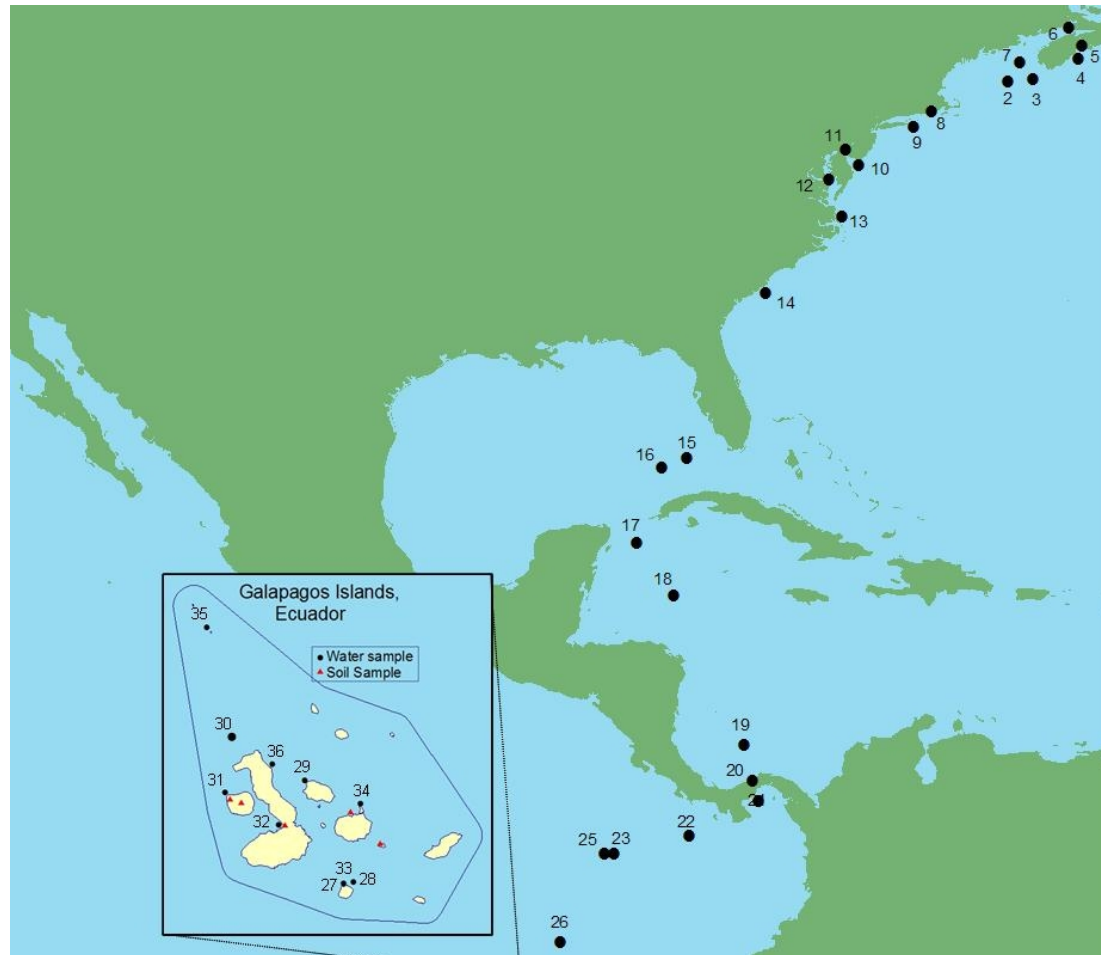
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Aerosol sample collection

- Samples 1360 m³ air in 24 hrs (58 m³/hr)
- Average 1 X 10⁹ bacteria/filter/day
- Multi-day sample averages known diurnal variation in microbial composition



Preliminary Analysis: Nova Scotia through Galapagos



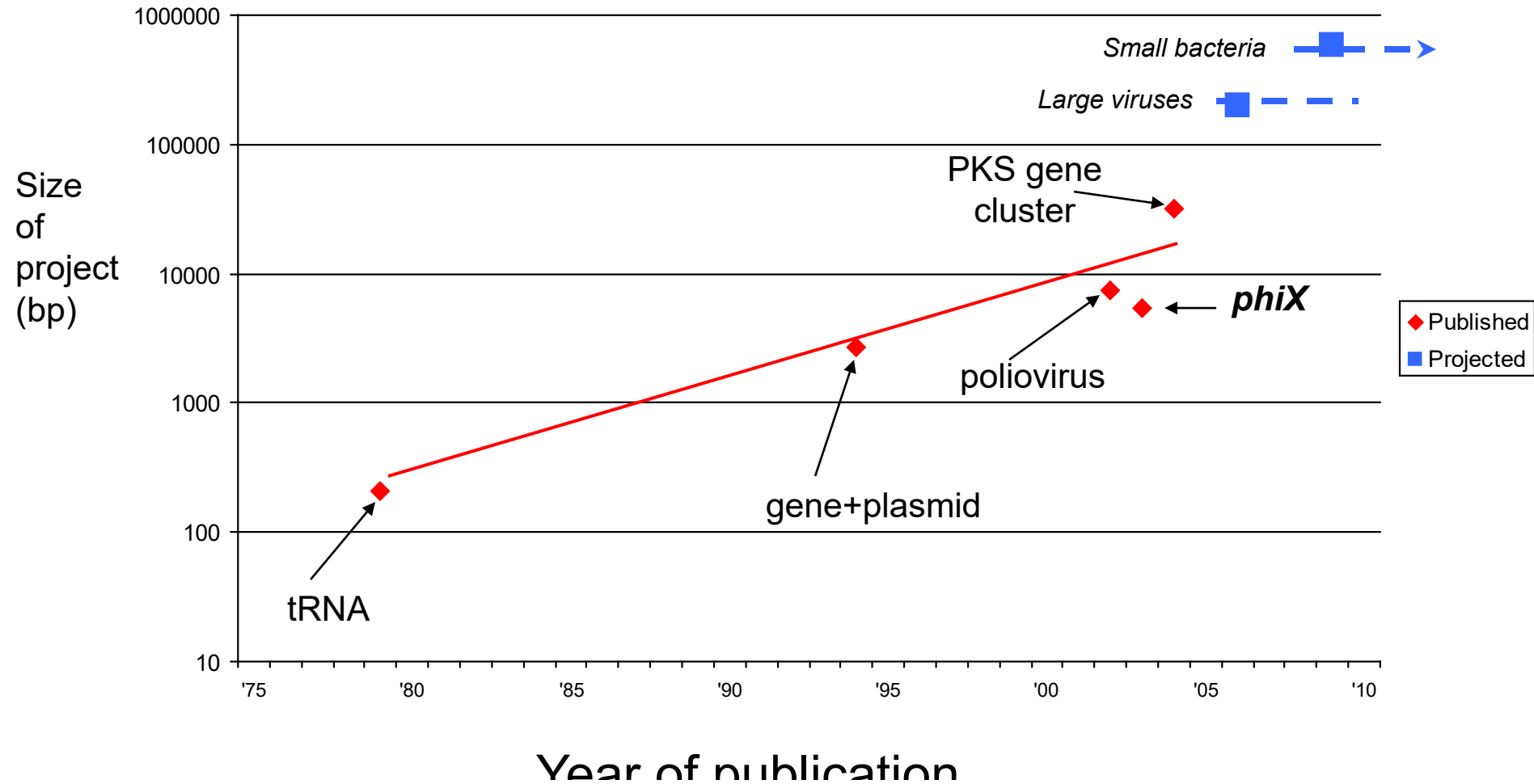
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Synthetic Genomics

Design and construction of
genomes from scratch

Chemical synthesis of DNA: from genes to genomes



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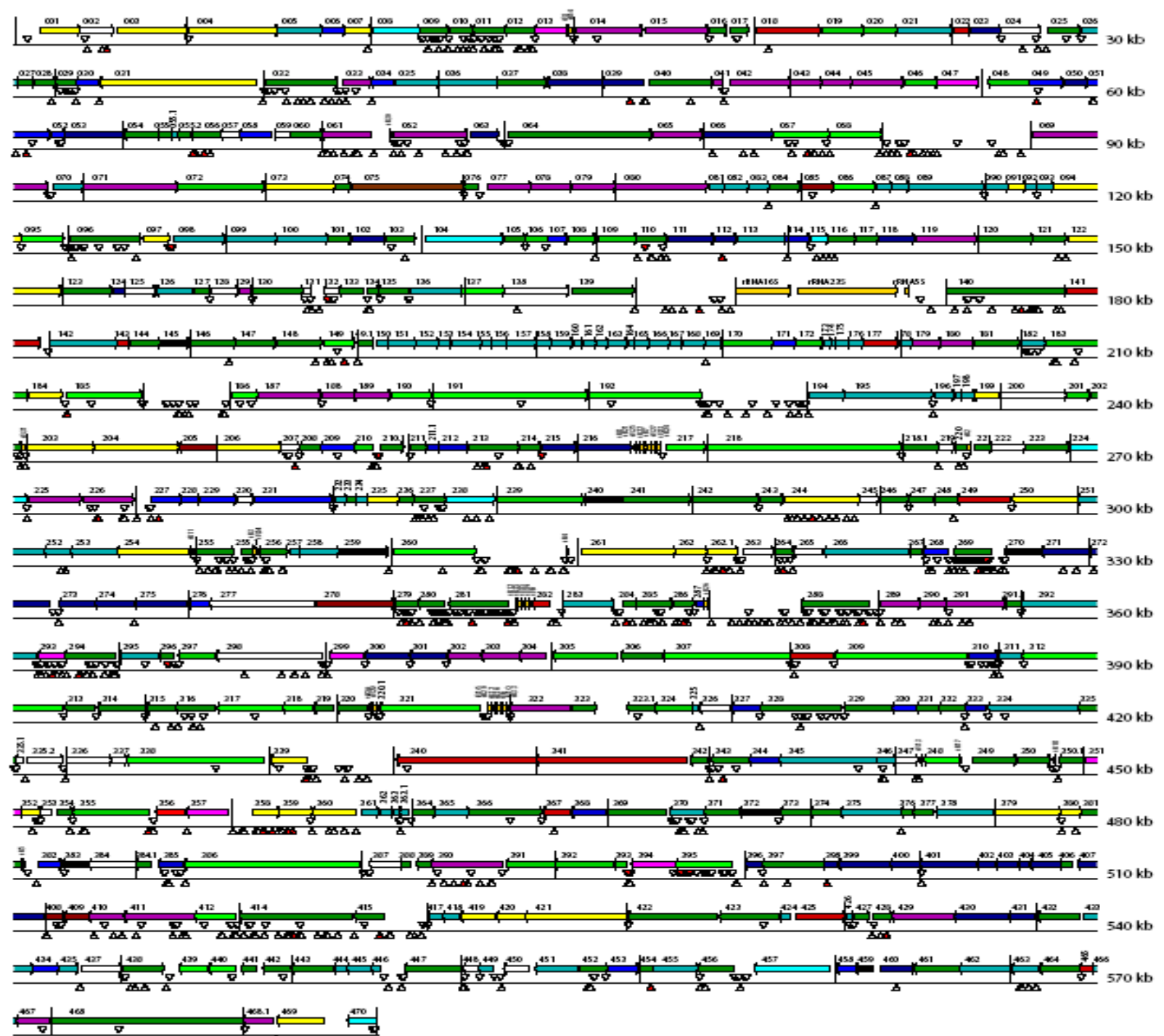
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M. genitalium: Living Organism With the Smallest Genome

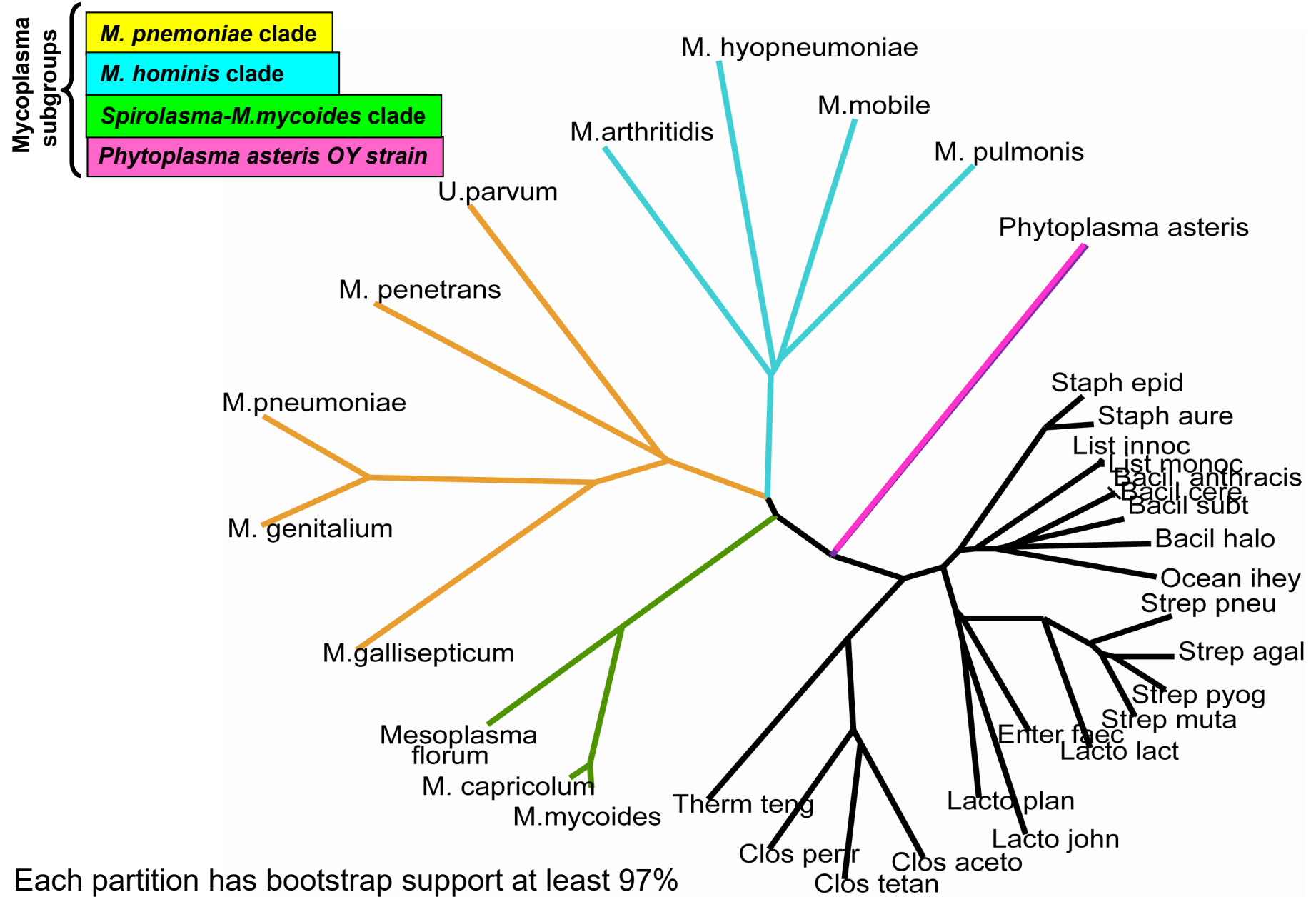


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Whole genome phylogeny of Firmicutes



The core mycoplasma genome is the set of genes common to all 13 complete sequences

Expanded core of 310 genes (90 because of non-orthologous gene displacements)

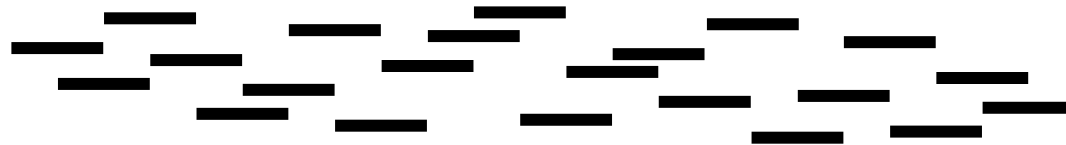
At least 36 genes in expanded core are non-essential based on gene disruption studies

173 genes common to all 13

220 core genes w/o obligate intracellular parasite

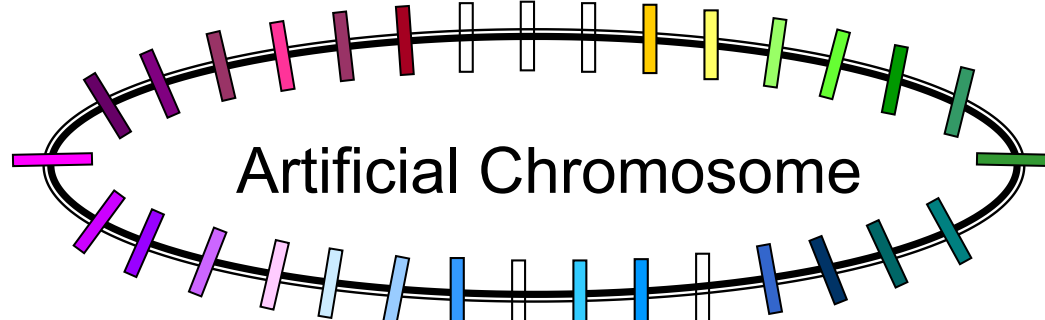
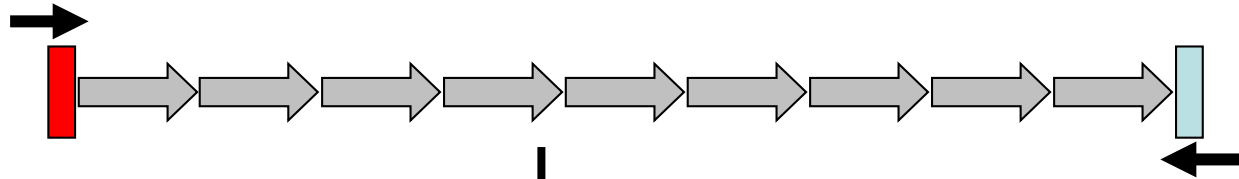
Construction of an Artificial Chromosome

Oligonucleotides



Taq Polymerase
Assembled Gene

PCR Products
~ 10 Kbp



Generating a synthetic genome by whole genome assembly: ϕ X174 bacteriophage from synthetic oligonucleotides

Hamilton O. Smith, Clyde A. Hutchison III[†], Cynthia Pfannkoch, and J. Craig Venter[‡]

Institute for Biological Energy Alternatives, 1901 Research Boulevard, Suite 600, Rockville, MD 20850

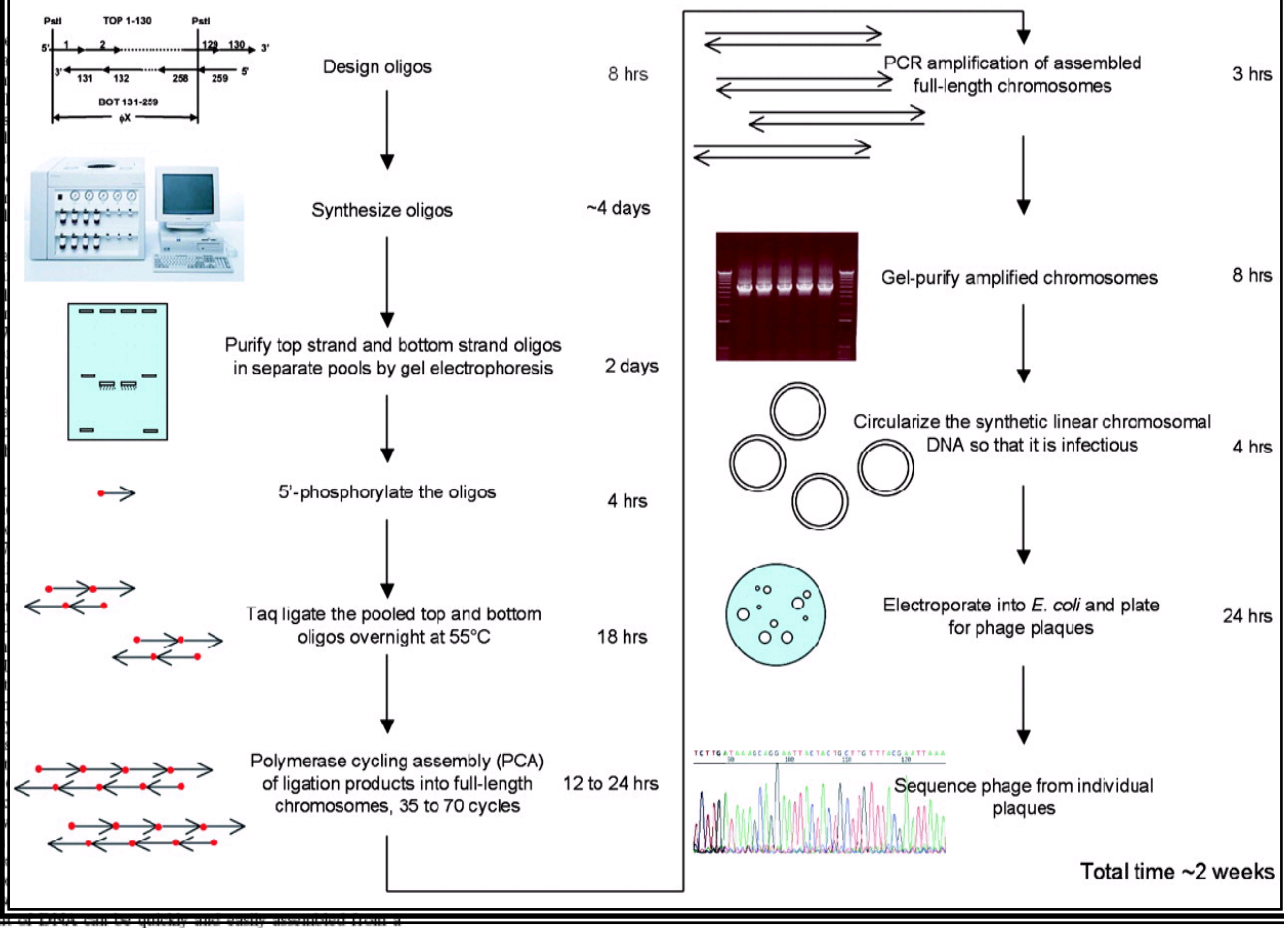
Contributed by J. Craig Venter, November 3, 2003

We have improved upon the methodology and dramatically shortened the time required for accurate assembly of 5- to 6-kb segments of DNA from synthetic oligonucleotides. As a test of this methodology, we have established conditions for the rapid (14-day) assembly of the complete infectious genome of bacteriophage ϕ X174 (5,386 bp) from a single pool of chemically synthesized oligonucleotides. The procedure involves three key steps: (i) gel purification of pooled oligonucleotides to reduce contamination with molecules of incorrect chain length, (ii) ligation of the oligonucleotides under stringent annealing conditions (55°C) to select against annealing of molecules with incorrect sequences, and (iii) assembly of ligation products into full-length genomes by polymerase cycling assembly, a nonexponential reaction in which each terminal oligonucleotide can be extended only once to produce a full-length molecule. We observed a discrete band of full-length assemblies upon gel analysis of the polymerase cycling assembly product, without any PCR amplification. PCR amplification was then used to obtain larger amounts of pure full-length genomes for circularization and infectivity measurements. The synthetic DNA had a lower infectivity than natural DNA, indicating approximately one lethal error per 500 bp. However, fully infectious ϕ X174 virions were recovered after electroporation into *Escherichia coli*. Sequence analysis of several infectious isolates verified the accuracy of these synthetic genomes. One such isolate had exactly the intended sequence. We propose to assemble larger genomes by joining separately assembled 5- to 6-kb segments; ~60 such segments would be required for a minimal cellular genome.

Chemical synthesis of life in the laboratory has been a standing challenge to synthetic organic chemistry since Wöhler's synthesis of urea in 1828 (1), and the doctrine of spontaneous generation was put to rest by an address by Louis Pasteur in 1864.[‡] With an understanding of the genetic role of DNA, much work has focused on the synthesis of oligonucleotides and genes. The synthesis of the 207-bp gene for tyrosine suppressor tRNA in 1979 by Khorana and 17 coworkers (2) was a monumental undertaking. Since then, the automated DNA synthesizer has been developed based on fundamental advances in synthetic methods from the laboratories of Letsinger (3, 4) and Caruthers (5, 6).

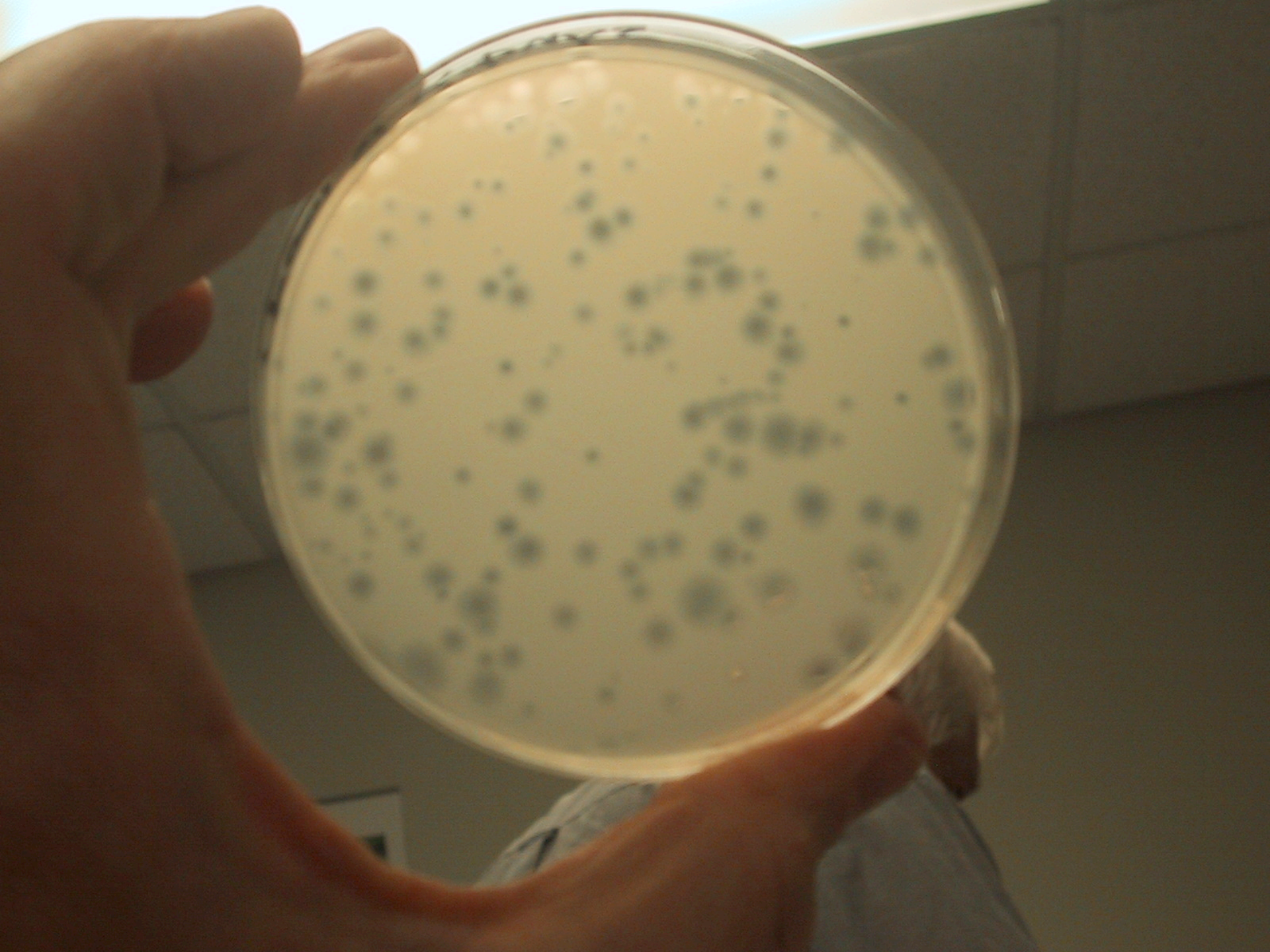
In 1999 we described a minimal prokaryotic genome based on results from random whole genome transposon mutagenesis that inactivated one gene per cell (7). By using this approach, ~300 essential genes for self-replicating cellular life were described, and we proposed to make a synthetic chromosome to test the viability of this hypothesis (7). Before attempting synthesis of a microbial chromosome, we commissioned an independent bioethical review of our proposed scientific plan (8). After >1 year of deliberation, the reviewers concluded that we were taking a reasonable scientific approach to an important biological question. The broader implications of the creation of life in the laboratory can now be considered a realistic possibility. However, there are several technical barriers to the synthesis of microbial chromosome-sized stretches of DNA that are hundreds of thousands to millions of nucleotides long, the most notable being the contamination of the oligonucleotides by

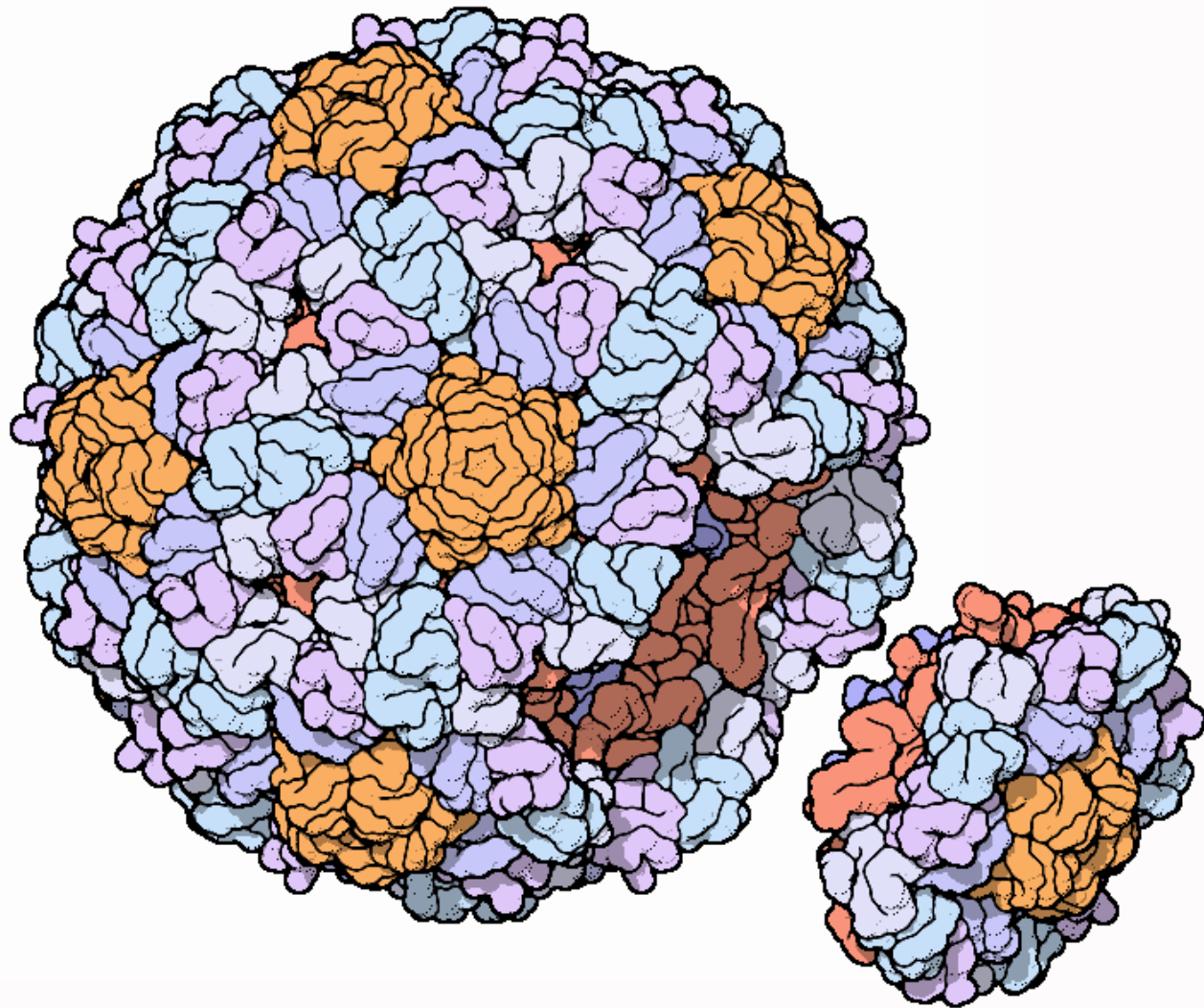
truncated molecules that are useful only as primers for PCR amplification. The general repair and assembly of segments could be used to assemble to find cleotides three assemblies would some. multiple of a established genome of chem known is not for sy sidera genome ϕ X174 phage begin single replic DNA ϕ X174 the first Gouli DNA nome in the DNA sequen with s region provide chro We sequ



Rapid gene synthesis from oligonucleotides

Hamilton Smith, Clyde Hutchison, Cindi Pfannkoch, Craig Venter





J. Craig Venter

I N S T I T U T E

This Software Builds Its Own Hardware

J. Craig Venter

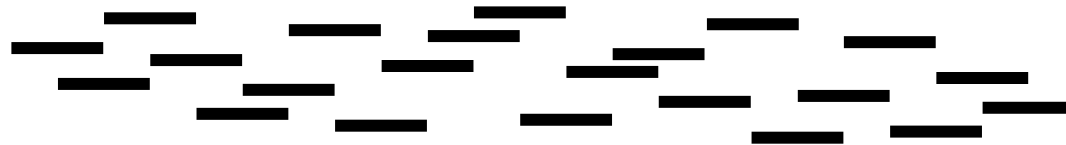
I N S T I T U T E

From Reading To Writing: What can be made and when?

- Any sequenced viral genome including select agents can be made *today*
- Designer viruses” are over a decade away
- Prokaryotes (bacteria): 2 years
- Single-cell eukaryotes: Within 10 years

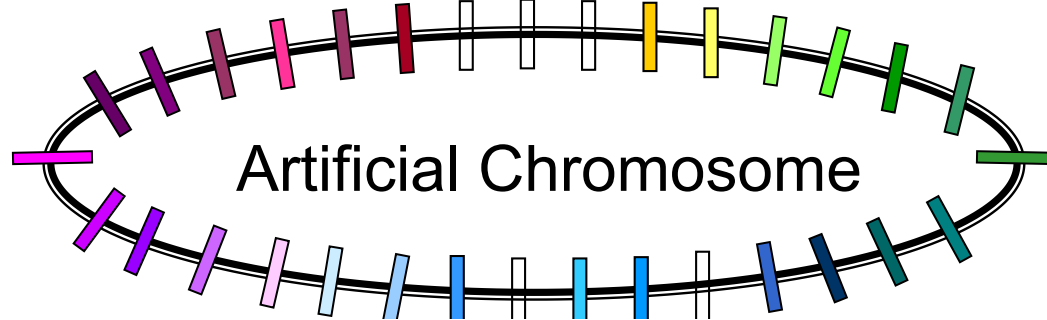
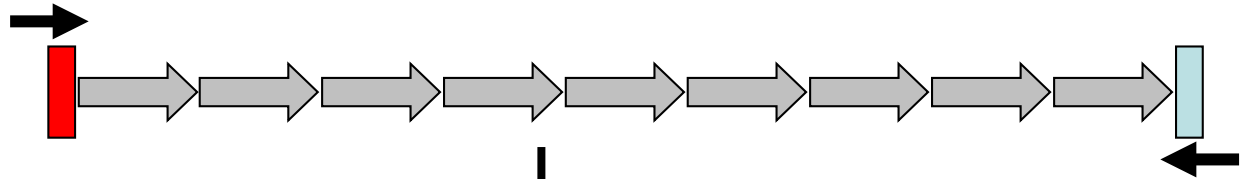
Construction of an Artificial Chromosome

Oligonucleotides



Taq Polymerase
Assembled Gene

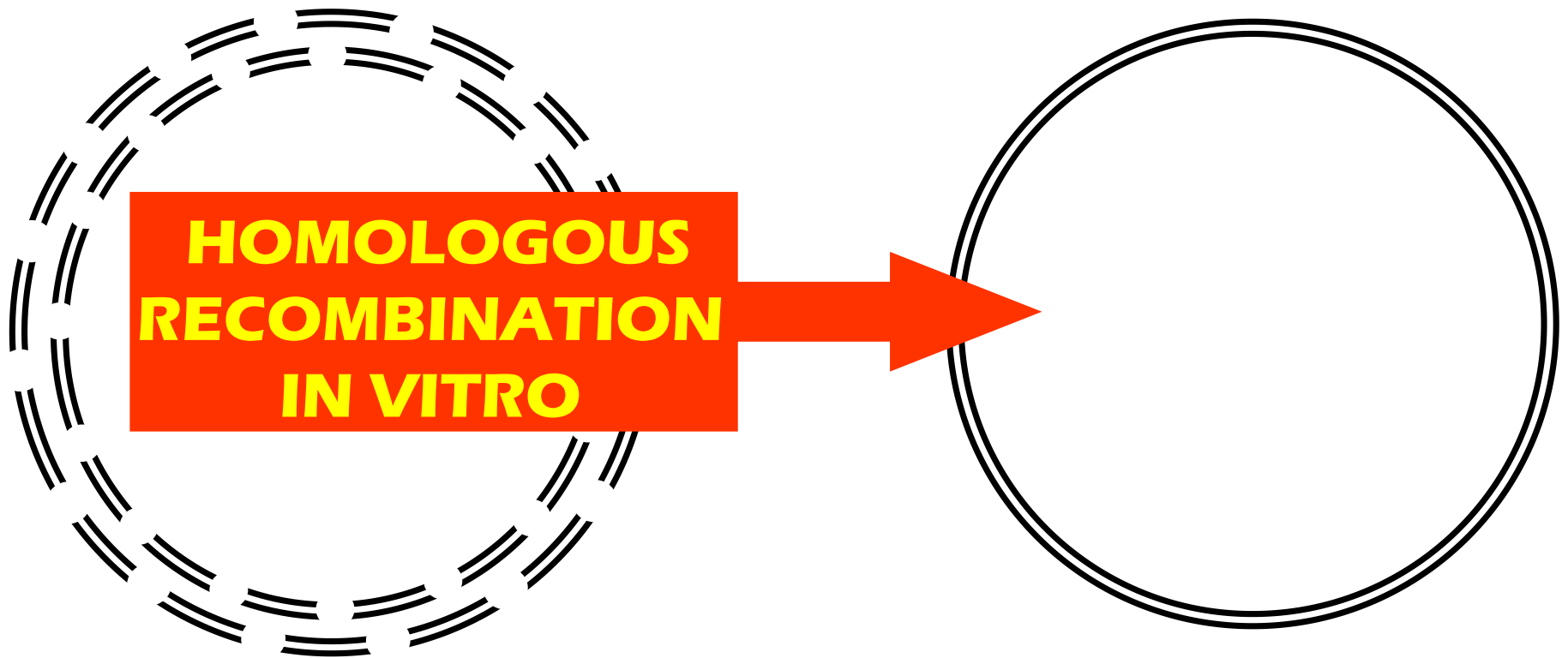
PCR Products
~ 10 Kbp



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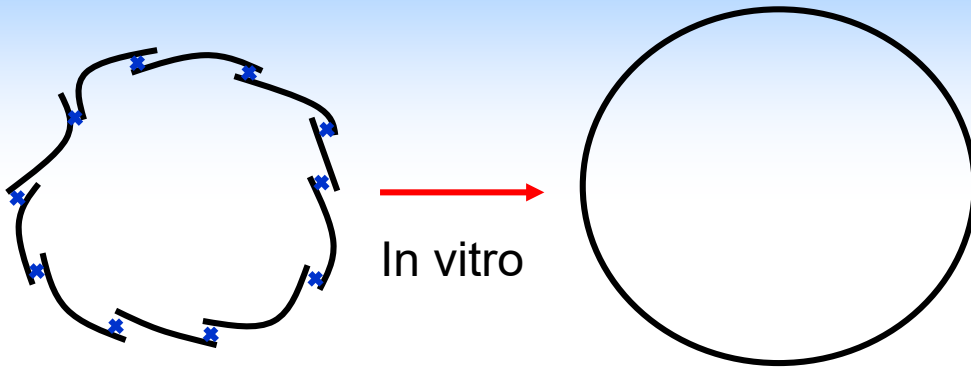
I N S T I T U T E

How do we connect many small synthetic genome fragments into a single circular chromosome?

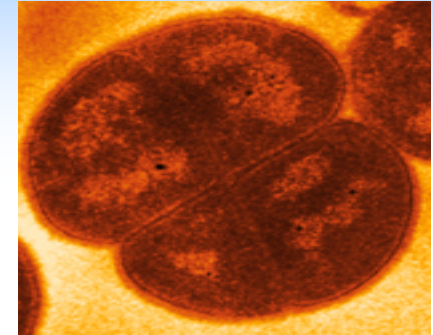


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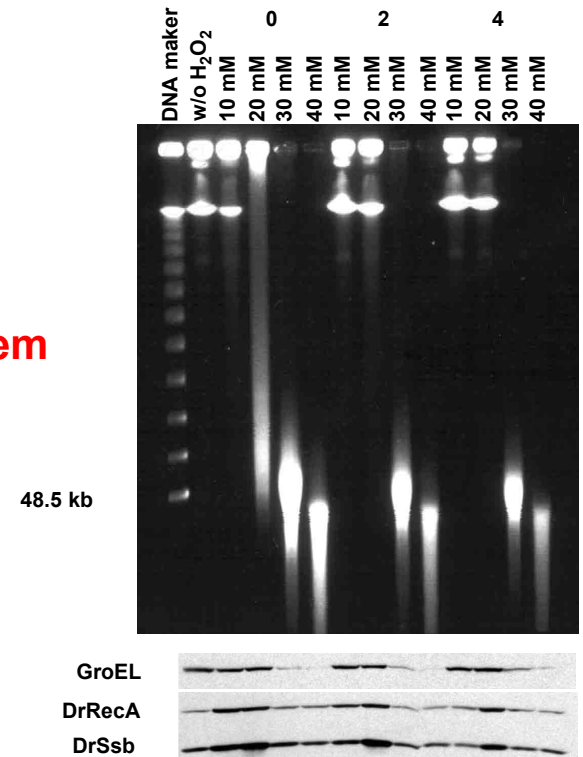
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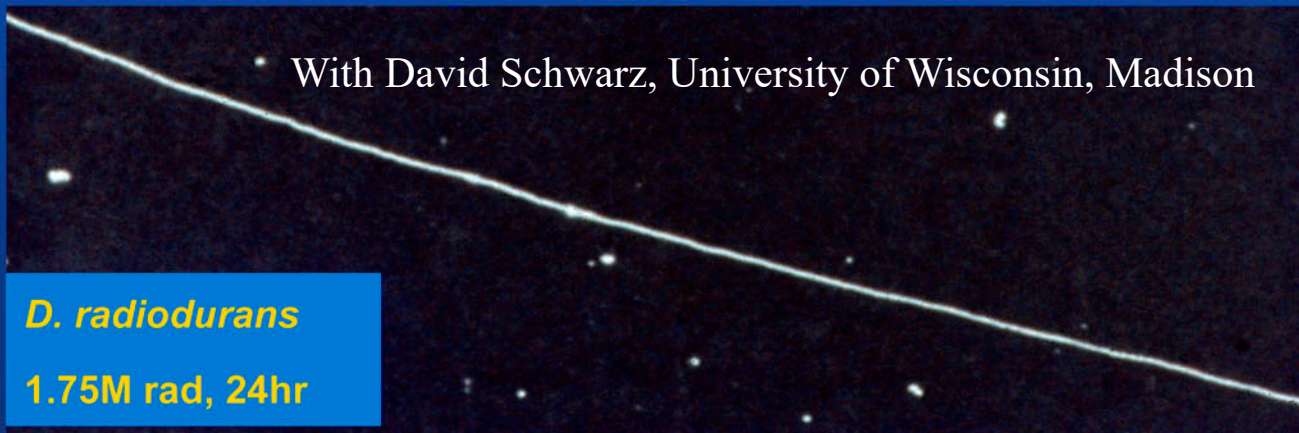
X homologous recombination



- Develop an in vitro *D. radiodurans* recombination system
- Express and characterize recombination proteins



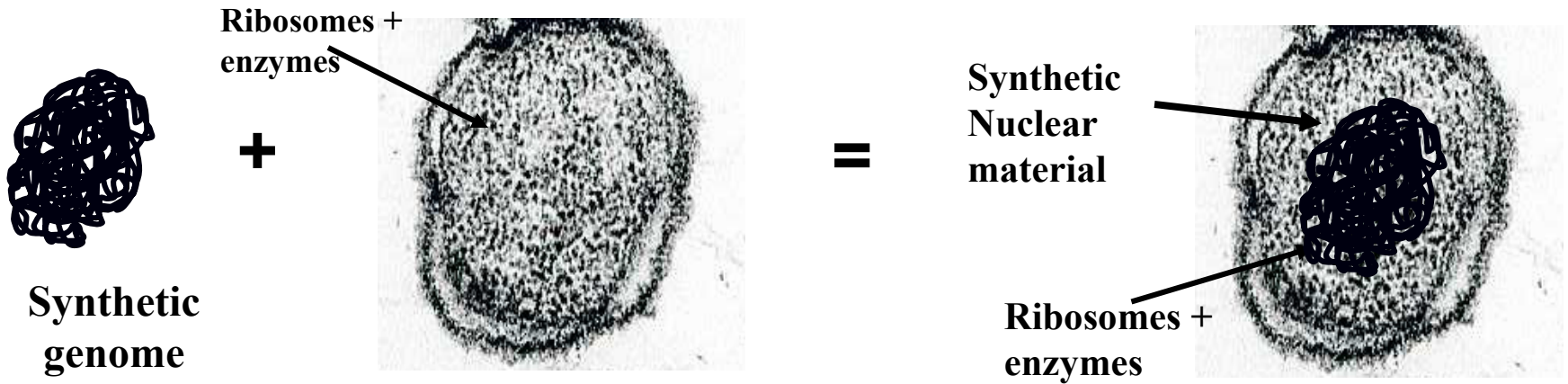
D. radiodurans: The Ultimate DNA Assembly Machine

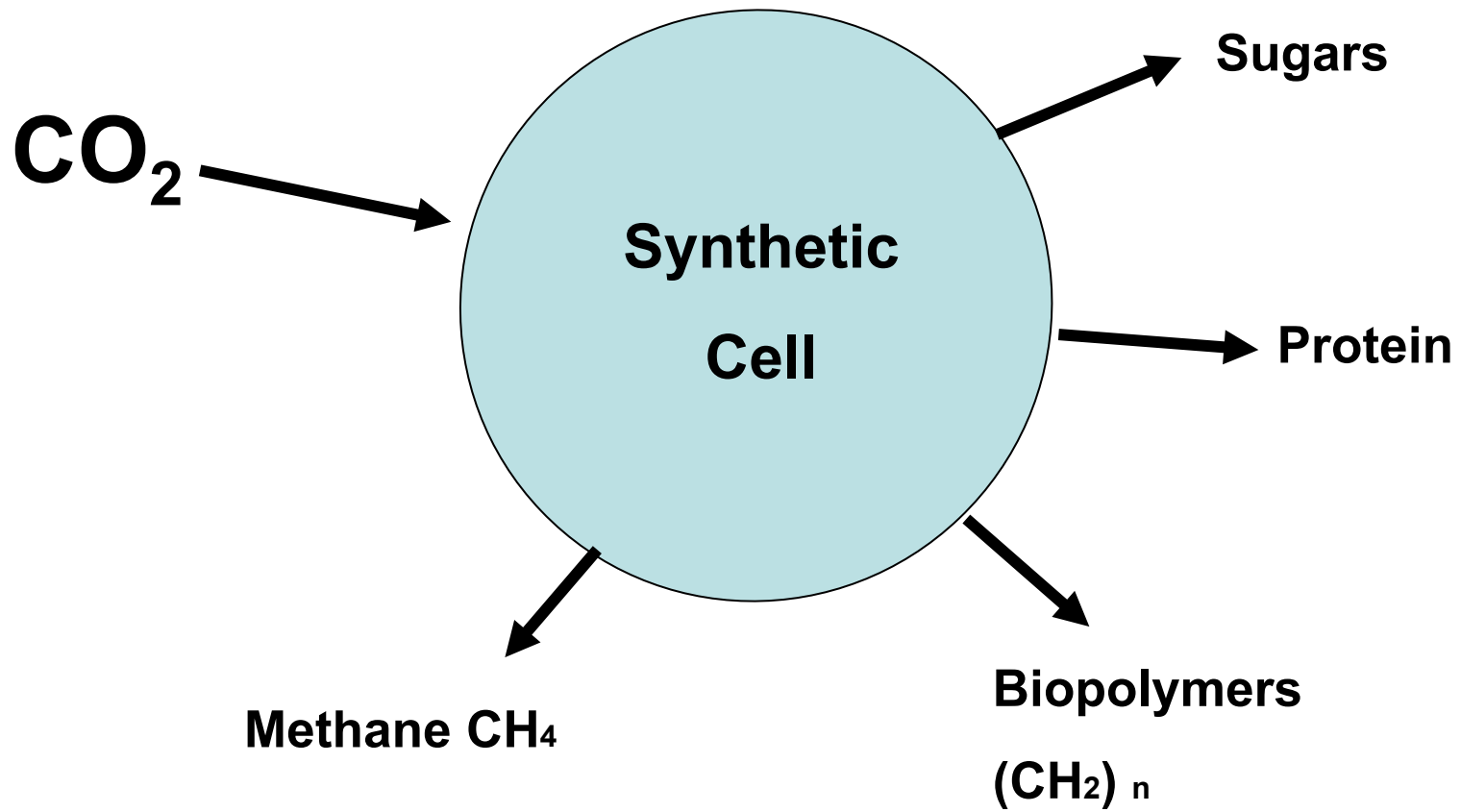


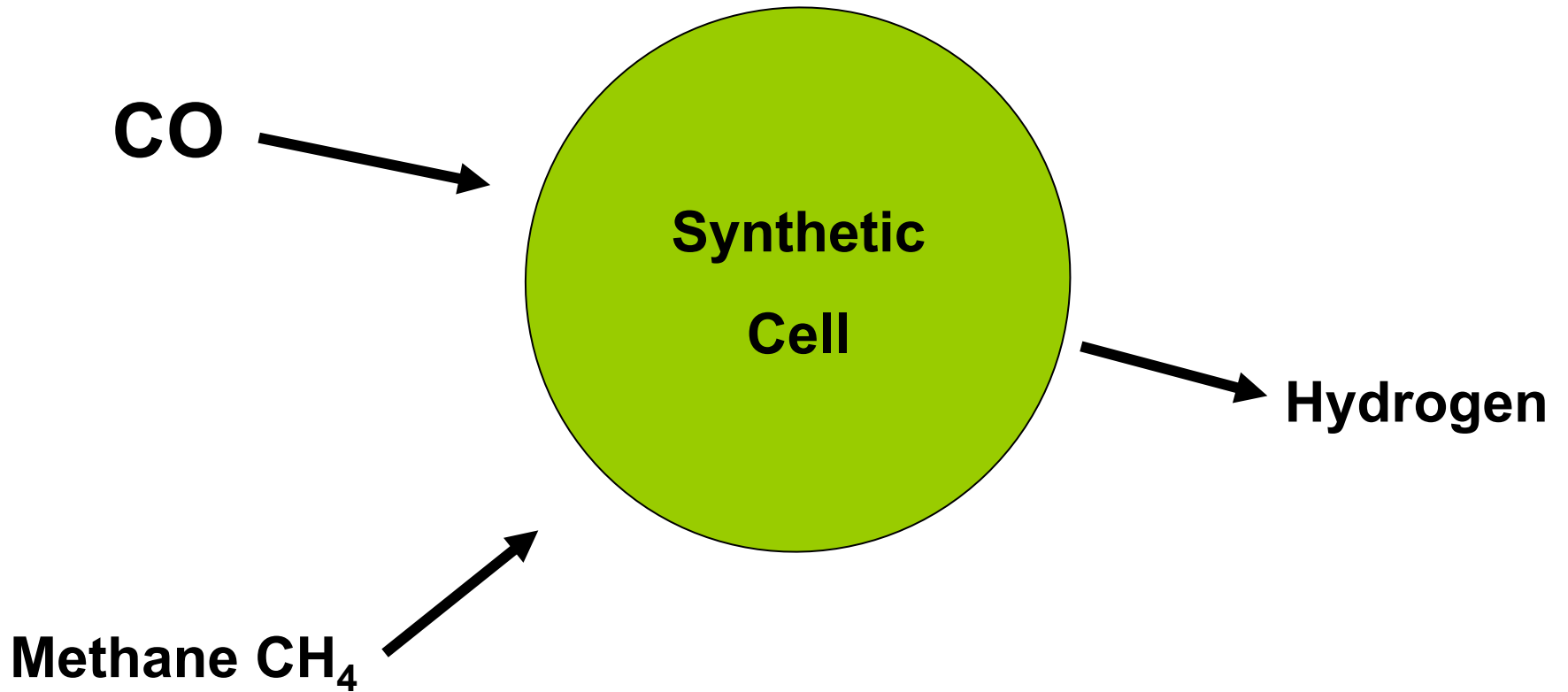
Combinatorial Genomics

- **Genes can be rapidly screened via cassette based construction of thousands to millions of genomes/day**
- **Selection through screening for**
 - **Chemical production**
 - **Viability**
 - **Hydrogen production etc.**

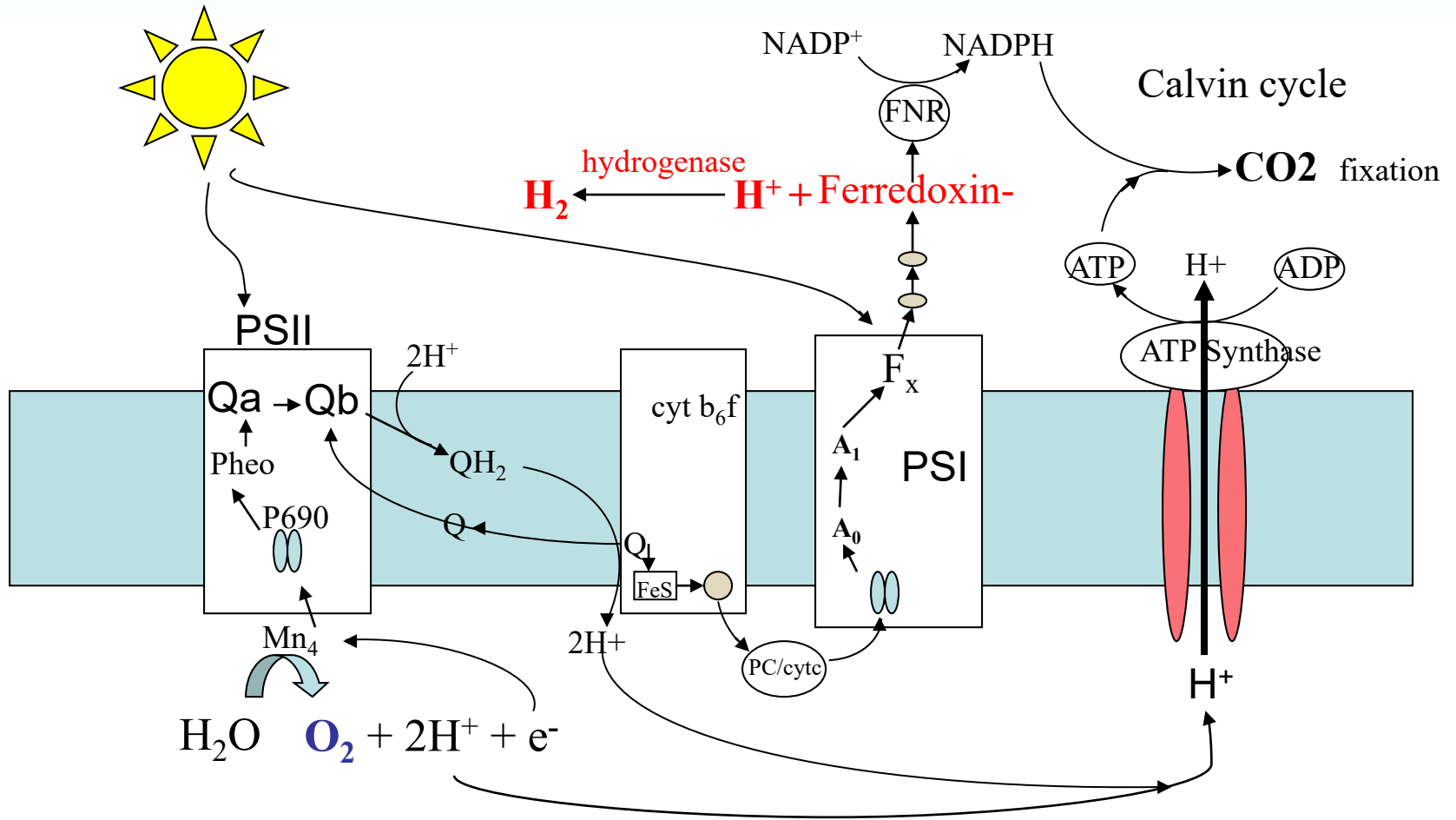
Genome transplantation







Photosynthetic production of hydrogen in cyanobacteria



Some Potential benefits

- **Basic biology**
 - Study evolution
 - Understand requirements for life
 - Confirm sequences
- **Human and animal health**
 - Vaccines (research and applications)
 - Gene therapy
 - Phage-based antibiotics
 - Drugs
- **Energy**
 - e.g., Renewable hydrogen (a JCVI project funded by DoE Office of Science)
- **New materials**
 - Bioplastics

Future of Engineered Species

- Designed and engineered species could replace petro-chemical industry
- Will be a source of future food
- A source of energy
- The basis of bioremediation

Regulation vs Good Scientific Standards

- **We Postponed Our research for Ethical/Policy Review in 1999**
 - Review indicated acceptable to proceed with minimal genome efforts*
- **Good Steward Standard**
 - Responsible lab precautions
 - Lab Bio Safety Level 3 for early stages
 - No human pathogens/No human genomes
 - No organism survival outside lab
 - Engineer out pathogenesis and self evolution
 - Open communication with non-science communities
- **Tremendous Opportunity for Good**
 - Carbon neutral energy sources
 - Environmental remediation
 - Carbon sequestration
 - Vaccine and other opportunities

* "Genetics: Ethical Considerations in Synthesizing a Minimal Genome" *Science*. 286. p. 2087
J. Craig Venter

Ethics and policy studies

- **Ethical and religious concerns surrounding work on minimal genomes (1999)**
 - ***Ethics of Genomics* group considered the implications of determining and/or synthesizing a minimal genome**
 - **Identified specific areas of concern, but determined that the research overall does not cross any bioethics boundaries**
 - **Cho et al., 1999. *Science* 286: 2087-2090.**
- **Societal implications (ongoing)**
 - ***Synthetic Genomics: Risks and Benefits for Science and Society***
 - **15-month study, funded by the Sloan Foundation**
 - **Focus on bioterrorism and environment, health, and safety**
 - **Partners**
 - **Policy Center, Venter Institute**
 - **Homeland Security Program, Center for Strategic & International Studies**
 - **Synthetic Biology Group, Massachusetts Institute of Technology**