





THE BCH III PROJECT

CEE REGIONAL BCH TRAINING WORKSHOP

Synthetic Biology

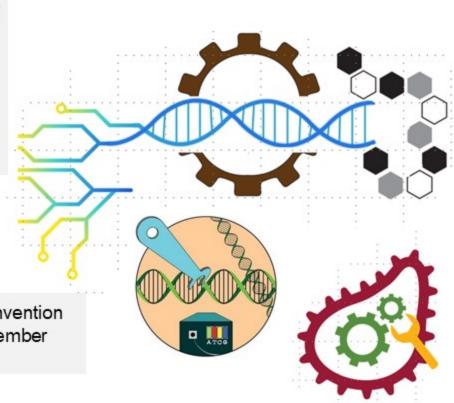
Prof Ossama AbdelKawy

2024

WHAT IS A SYNTHETIC BIOLOGY?

- "Synthetic Biology is a further development and new dimension of modern biotechnology that combines science, technology, and engineering to facilitate and accelerate the understanding, design, redesign, manufacture and/or modification of genetic materials, living organisms, and biological systems."

> Operational definition adopted by the UN Convention on Biological Diversity COP13, Cancun - December 2016.



WHAT IS A SYNTHETIC BIOLOGY?

- Humans always tried to make nature more 'engineerable













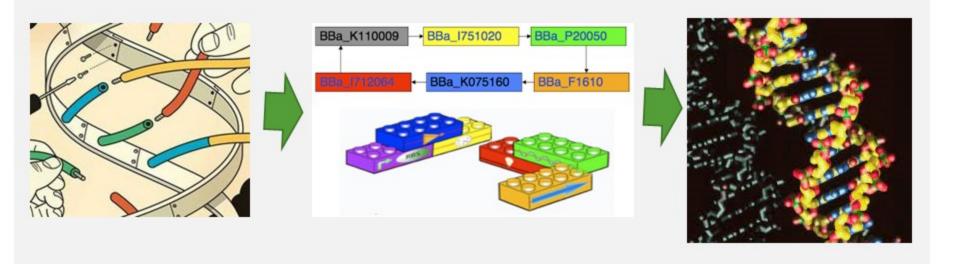






WHAT IS A SYNTHETIC BIOLOGY?

- Making 'engineerable' genetic systems based on standardized, predictable genetic parts (genetic circuits) to create new programmable life forms



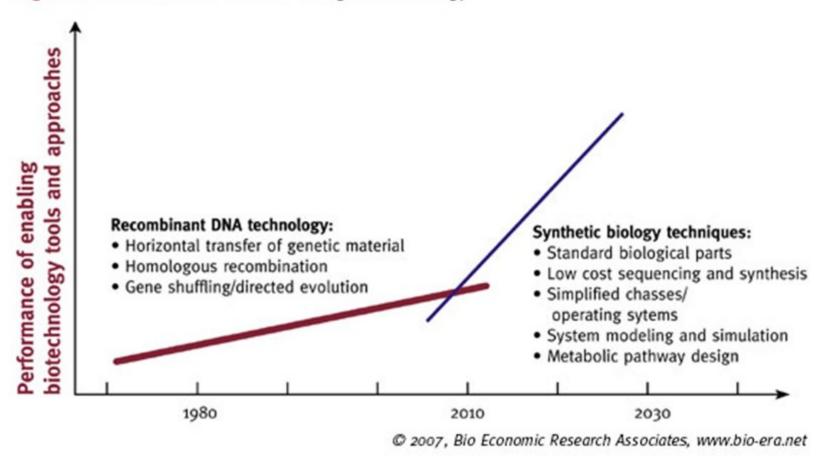
HOW IS IT DIFFERENT?

- Synthetic Biology is the next generation of genetic engineering.

	Recombinant DNA technology	Synthetic biology
Target	- Modifying existing biological systems	- Designing and fabricating new ones that are built with DNA that is partially or entirely artificial.
Level of complexity	- Focusing on expression of single genes or gene components	- Involves whole interacting genetic networks, genomes and entire organisms
What is it about?	- Introducing of naturally occurring, mutated or otherwise altered DNA into an organism with the source of DNA being an organism of a different or the same species. - Limited to the modification of natural organisms	- Introducing synthetically constructed parts - Extended to the construction of new life forms with no natural counterpart.

Both incorporate the techniques of molecular biology

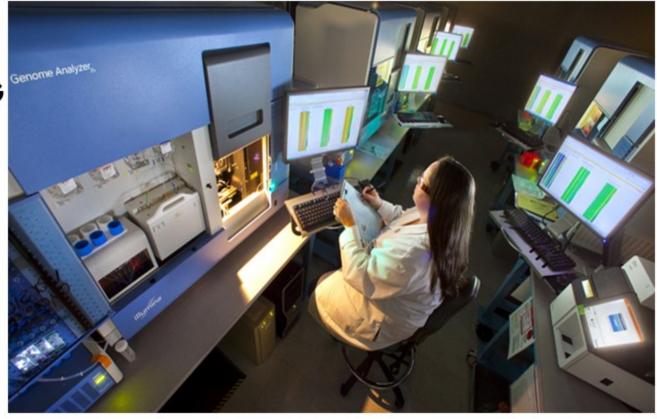
Figure 1-2: An Inflection Point for Biological Technology



This is now...

Genome READING





2015 Study: 2,500 high-throughput instruments, located in nearly 1,000 sequencing centers in 55 countries

PLoS Biol. 2015 Jul; 13(7): Stephens et al "Big Data: Astronomical or Genomical?"

Annual genomic data If 1 bp was a grain of sand... New industrial raw material



2015: 35 petabases of genome sequencing (35 thousand trillion BP) -32,000 microbial genomes, ~5,000 plant and animal genomes, and ~250,000 individual human genomes.



2025: 1 zetabase of genome sequencing (1 thousand million trillion BP).

Encompass All 1.2 million described species of plants and animals.

Estimated that there will be at least 2.5 million plant and animal genome sequences

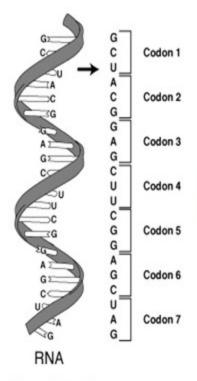
This is now... new industrial tools





Clustered Regularly Interspersed Short Palindomic Repeats (CRISPR), Directed Evolution, DNA-based genetic circuits, DNA Synthesis and Assembly, Epigenetic Modification, Expanded Genetic Alphabets, Genome Editing, Genome-level Engineering, Genome Shuffling, Gibson Assembly, Minimal Genomes, Multiplex Automated Genome Engineering, Oligonucleotide Directed Mutagenesis, Protocell Construction, Refactoring of Genomes, RNA-Directed DNA Methylation (RDDM). RNAi (RNA Interference) Standard Modular DNA 'parts' or 'Biobricks' Synthetic Metabolic Pathway Engineering, Synthetic Genomics, Transcription-Activator-like Effector Nucleases (TALENs), Xenobiology, Zinc Finger Nucleases(ZFN),

GENETIC CODE?



1st base

	U		С		A		G		
	UUU	Phenylalanine	UCU	Serine	UAU	Tyrosine	UGU	Cysteine	U
U	UUC	Phenylalanine	UCC	Serine	UAC	Tyrosine	UGC	Cysteine	C
U	UUA	Leucine	UCA	Serine	UAA	Stop	UGA	Stop	1
	UUG	Leucine	UCG	Serine	UAG	Stop	UGG	Tryptophan	0
•	CUU	Leucine	CCU	Proline	CAU	Histidine	CGU	Arginine	ı
	CUC	Leucine	ccc	Proline	CAC	Histidine	CGC	Arginine	(
C	CUA	Leucine	CCA	Proline	CAA	Glutamine	CGA	Arginine	1
	CUG	Leucine	CCG	Proline	CAG	Glutamine	CGG	Arginine	0
	AUU	Isoleucine	ACU	Threonine	AAU	Asparagine	AGU	Serine	ı
A	AUC	Isoleucine	ACC	Threonine	AAC	Asparagine	AGC	Serine	0
H	AUA	Isoleucine	ACA	Threonine	AAA	Lysine	AGA	Arginine	1
	AUG	Methionine (Start)	ACG	Threonine	AAG	Lysine	AGG	Arginine	0
	GUU	Valine	GCU	Alanine	GAU	Aspartic Acid	GGU	Glycine	ı
G	GUC	Valine	GCC	Alanine	GAC	Aspartic Acid	GGC	Glycine	(
G	GUA	Valine	GCA	Alanine	GAA	Glutamic Acid	GGA	Glycine	1
	GUG	Valine	GCG	Alanine	GAG	Glutamic Acid	GGG	Glycine	0

Ribonucleic acid

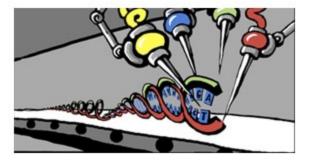
Nonpolar, aliphatic Polar, uncharged

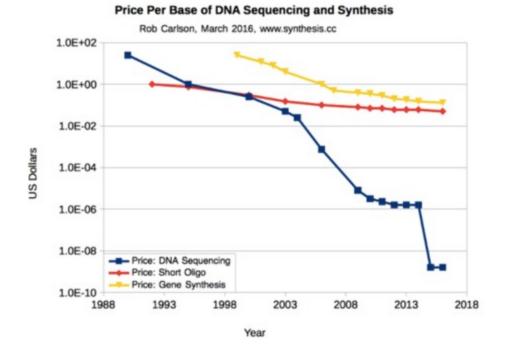
Aromatic

Positively charged

Negatively charged

Genome WRITING



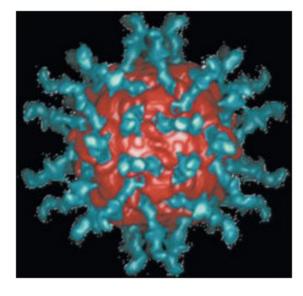


Commercial gene synthesis: 7-17 cents per base Currently, a billion base market – around a million genes.

Commercial Oligo Synthesis – 5 cents per base. Currently, a 4.8 billion base market

Roughly equivalent to one human genome per year.

Source Rob Carlson synthesis. cc – March 2016



Polio genome = Approx. \$500 to synthesize??

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7500bp

Genome WRITING

Human genome is currently \$21 billion

1/4 Gates (approx.)
 1/3 Zuckerberg
 1/5 Bezos
 1 week US military spending

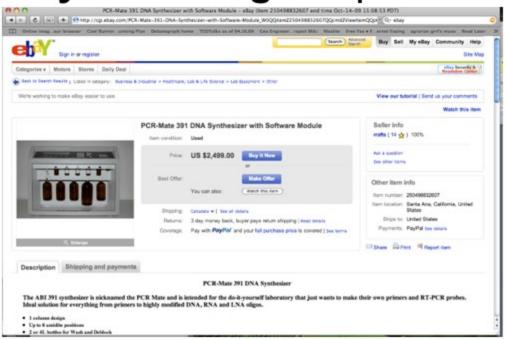


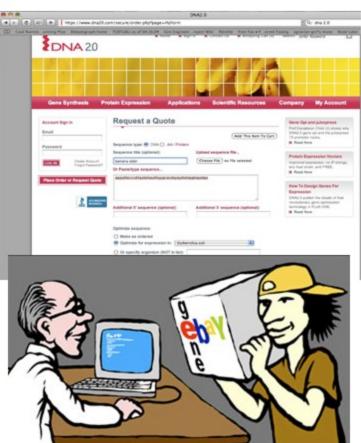
The Genome Project-write (GP-write) will be an open, international research project led by a multi-disciplinary group of scientific leaders who will oversee a reduction in the costs of engineering and testing large genomes in cell lines more than 1,000-fold within ten years.

CP-write will include whole genome engineering of human cell lines and other organisms of agricultural and public health significance. Thus, the Human Genome Project-write (HGP-write) will be a critical core activity within GP-write focused on synthesizing human genomes in whole or in part. It will also be explicitly limited to work in cells, and organoids derived from them only. Because of the special challenges surrounding human genomes, this activity will include an expanded examination of the

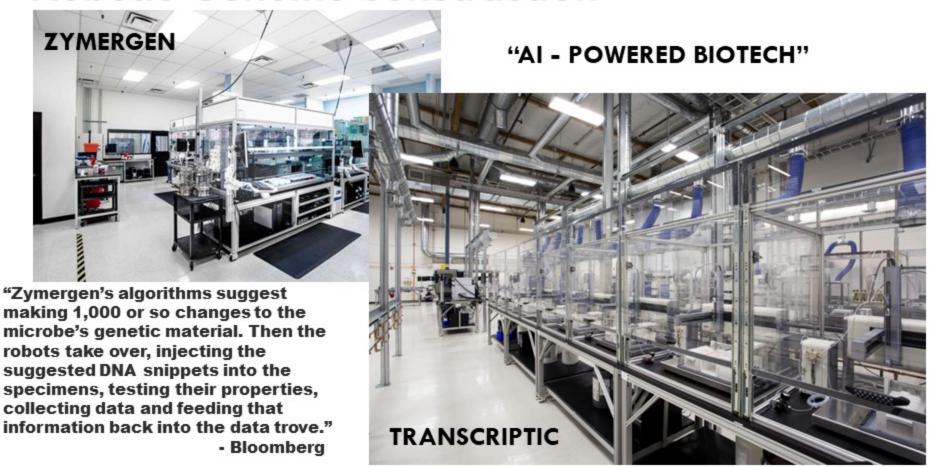
Download the GP-write White Paper

Learn How to Get Involved Synthesizing the parts of life





Robotic Genome construction



SYNTHETIC BIOLOGY INDUSTRY

- Rapid market growth (\$10.8 billon for 2016. \$38.7 billion in 2020)
- Govt funding rapidly growing (US: dominated by Defence/DARPA)
- Many deals with Fortune 500 companies

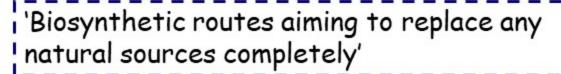
 food, flavor, chemicals, cosmetics, fuels, pharma, textiles.



"Programming life forms" > GTTCACTAGCCATTAGGTA



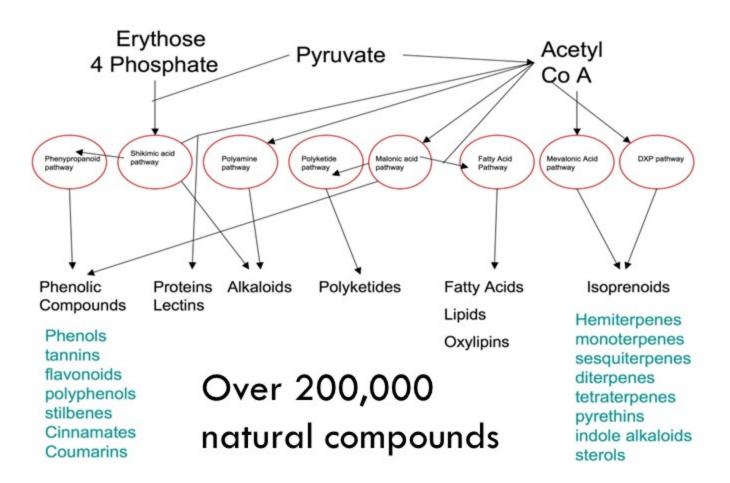












Evolva - a yeast "metro" for valuable products













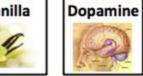


































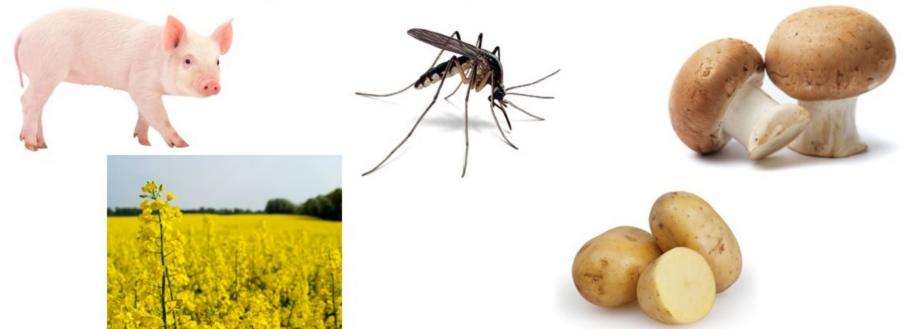




GMO 2.0 INDUSTRY

SECOND WAVE:

CROPS, INSECTS, ANIMALS



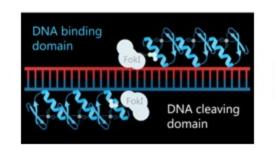
GENOME EDITING TECHNIQUES

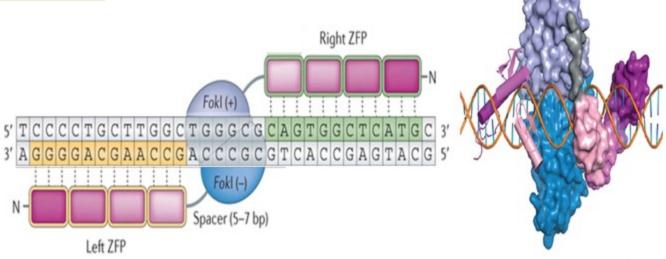
- Give scientists the ability to change an organism's DNA. These technologies allow genetic material to be added, removed, or altered at particular locations in the genome. Include Zinc Fingers, TALENS and CRISPR-CAS9,.





ZINC FINGERS NUCLEASES (ZFNs)

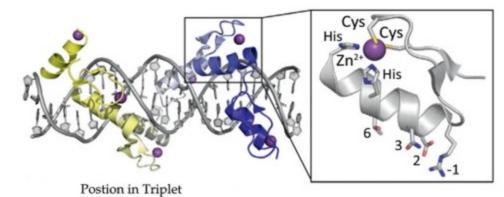




- Artificial restriction enzymes generated by fusing a zinc finger DNA-binding domain to a DNA-cleavage domain.
- The non-specific cleavage domain from the type IIs restriction endonuclease FokL is typically used as the cleavage domain in ZFNs. This cleavage domain must dimerize to cleave DNA; thus, a pair of ZFNs are required to target non-palindromic DNA sites. Standard ZFNs fuse the cleavage domain to the C-terminus of each zinc finger domain.

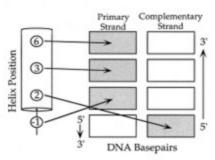
ZINC FINGERS NUCLEASES (ZFNs)

- The DNA-binding domains of individual ZFNs typically contain between three and six individual zinc finger repeats and can each recognize between 9 and 18 base pairs.
- The main drawback with this procedure is that the specificities of individual zinc fingers can overlap and depend on the context of the surrounding zinc fingers and DNA.



- 2	5'	Middle	3'
_ [*Arg 6 *Lys 6	*His 3	*Arg -1
G	*Asp 2† *Ser 2† *Phe 2†	*Lys 3	h h
A		*Asn 3	
	Gln 6	*Ser 3	*Gln -1
		*His 3	
		*Asp 3	
C	*Ser 2 [†]	Thr 3	*Asp -1
		Val 3	
т	Lys 6	Thr 3	*Leu -1
	Lyso	Ala 3	Thr -1
	*Asp 2 [†]	Ser 3 Val 3	Asn -1

Nucleotide

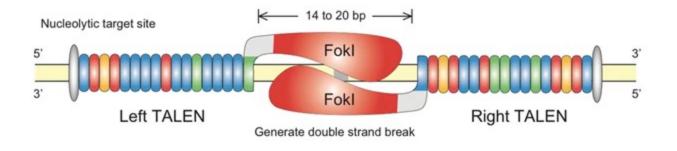








TRANSCRIPTION ACTIVATOR-LIKE EFFECTOR NUCLEASES (TALENS)

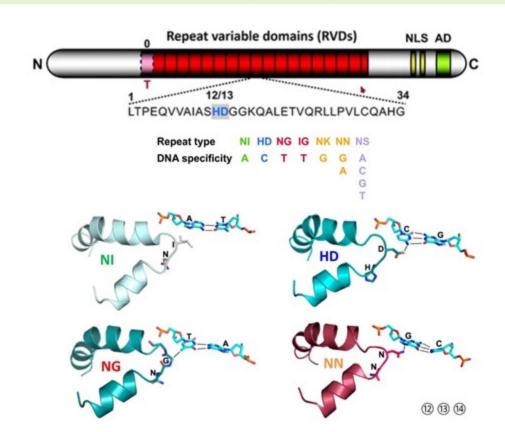




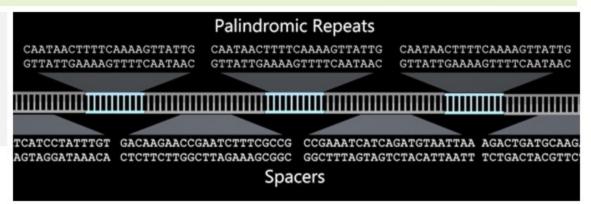
- Artificial restriction enzymes generated by fusing a TAL effector DNA-binding domain to a DNA cleavage domain.
- The non-specific cleavage domain from the type IIs restriction endonuclease FokI is typically used as the cleavage domain in TALENS. This cleavage domain must dimerize to cleave DNA; thus, TALENS s are required to target non-palindromic DNA sites.

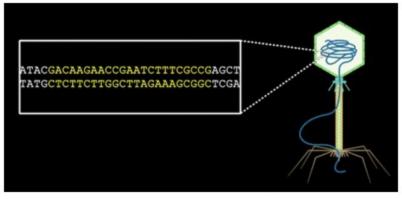
TRANSCRIPTION ACTIVATOR-LIKE EFFECTOR NUCLEASES (TALENS)

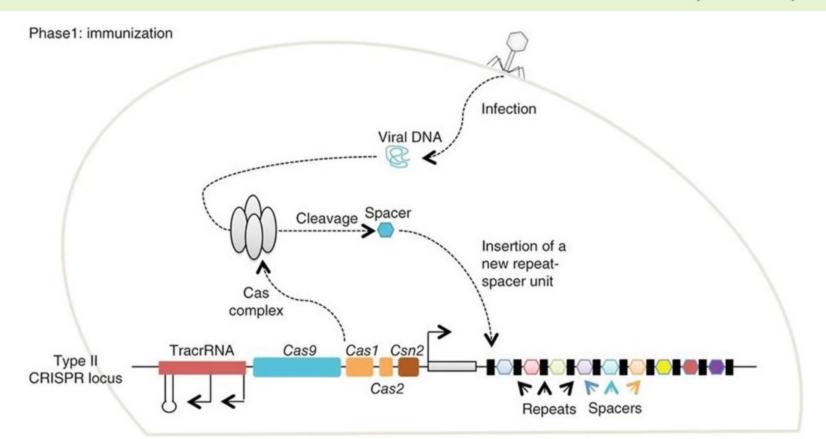
- TAL effectors are proteins secreted by Xanthomonas bacteria via their type III secretion system when infecting plants.
- They contain a repeated highly conserved 33-34 amino acid sequence with divergent 12th and 13th amino acids referred to as the Repeat Variable Diresidue (RVD) that strongly correlates with specific nucleotide recognition.

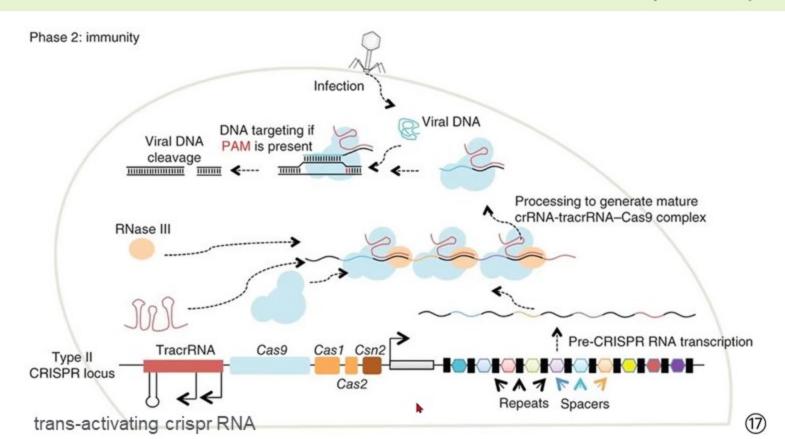


- CRISPR loci are found in roughly 40% of all bacterial and 90 % of archaeal species.
- It is an adaptive immunity system against bacteriophage.

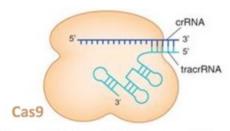




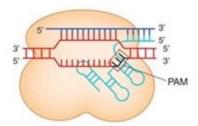




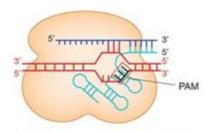
CLUSTERED REGULARLY INTERSPACED SHORT PALINDROMIC REPEAT (CRISPER)



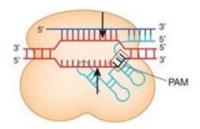
1) crRNA:tracrRNA base pairing and Cas9 binding



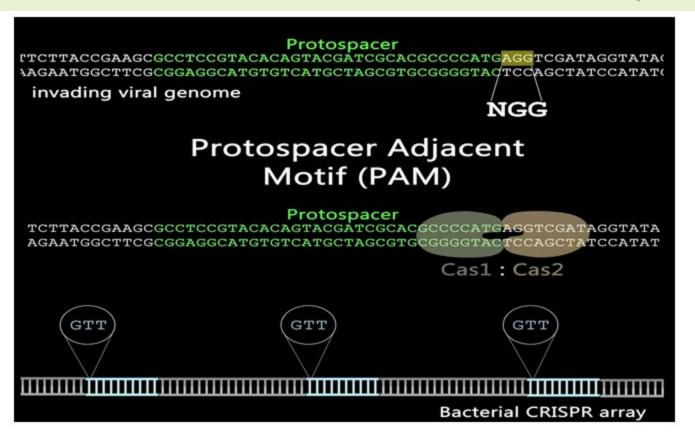
- crRNA:DNA base pairingstrand unwinding
 - R-loop formation



 Cas9 recognition of PAM in genomic DNA (protospacer adjacent motif)

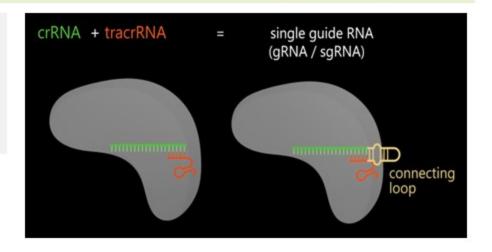


4) Sufficient base pairing triggers cleavage of both strands Creates a blunt DSB 3 bp from PAM



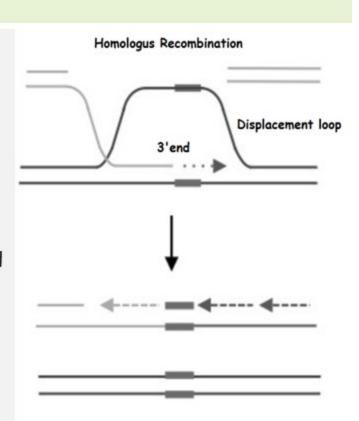
CLUSTERED REGULARLY INTERSPACED SHORT PALINDROMIC REPEAT (CRISPER)

- The bacterial immune system could be harnessed for gene editing. Create a simple connecting loop to combine the crRNA and tracrRNA into a single guide RNA. if you attach any sgRNAto CAS9 you can cut the corresponding DNA.



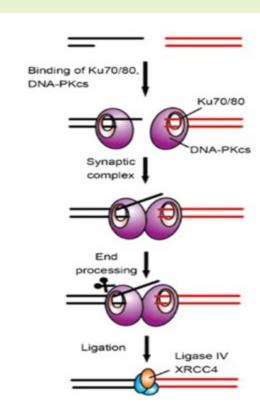
GENE EDITING — DSB REPAIR

- In homologous recombination, the DNA duplex that sustains the double-strand break (DSB) is resected at one or both ends by a 5' to 3' exonuclease. This generates a 3'-OH single-stranded extension that invades the intact homologous sister chromatid in a reaction that is catalyzed by the bacterial RecA protein (or its eukaryal homologue Rad51). The invading strand serves as a primer for a DNA polymerase (POL) that copies the chromatid information across the break. Resolution of the recombination intermediates rectifies the DSB by transferring a short segment of strand-templated DNA sequence to the original cyan chromatid. The residual single-strand nicks in the repaired duplex are eventually sealed by the replicative DNA ligase (LigA in bacteria).
- Host DSB repair by homologous recombination can facilitate insertions, deletions, inversions, etc. when homologous DNA is provided.

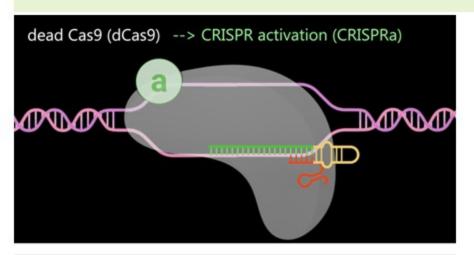


GENE EDITING - DSB REPAIR

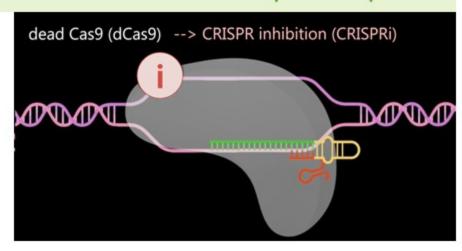
- Non-homologous end joining (NHEJ) brings the ends of the broken DNA molecule together by forming a synaptic complex consisting of two DNA ends, two Ku70/80, and two DNA-PKCS molecules. Non-compatible DNA ends are processed to form ligatable termini and then sealed by a specialized DNA ligase unique to NHEJ: ligase IV/XRCC4 complex in eukarya or LigD in bacteria.
- Host DSB repair by non-homologous end-joining results in small mutations, facilitating loss of gene function strategies.



CLUSTERED REGULARLY INTERSPACED SHORT PALINDROMIC REPEAT (CRISPER)



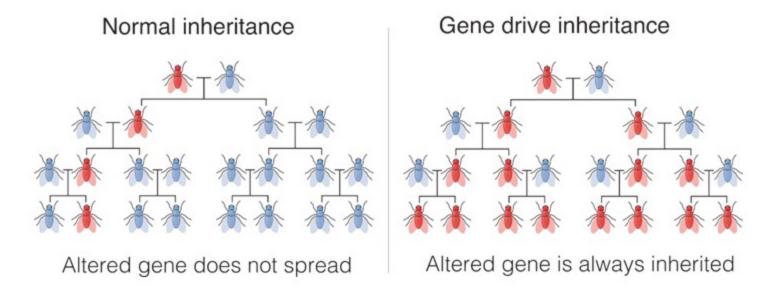
- you can use a dead version of CAS9 which can find a specific sequence of DNA but does not actually cut it. Scientists can then fuse an activator protein to dead CAS9 which forces the attached gene to become more active and transcribe more RNA



- Similarly, they could attach an inhibitor protein that turns off the target gene.

GENE DRIVE

- is a technology of genetic engineering that propagates a particular suite of genes throughout a population by altering the probability that a specific allele will be transmitted to offspring (instead of the Mendelian 50% probability).



GENE DRIVE

- Gene drives have been proposed to provide an effective means of genetically modifying specific populations and entire species. Proposed applications include exterminating insects that carry pathogens, controlling invasive species, or eliminating herbicide or pesticide resistance.
- As with any potentially powerful technique, gene drives can be misused in various ways or induce unintended consequences.
 - Gene drives eradicating populations of invasive species in their non-native habitats may have consequences for the species as a whole, even in its native habitat. Any accidental return of individuals of the species to its original habitats through natural migration, environmental disruption (storms, floods, etc.), accidental human transportation, or purposeful relocation could unintentionally drive the species to extinction if the relocated individuals carried harmful gene drives.

A STRUCTURE OF SELF-PROPAGATING GENE DRIVES

A repair template containing



a homing endonuclease or an RNA-guided endonuclease (e.g., Cas9 or Cas12a) and its guide RNA that cuts the chromosome at a specific site that does not encode the drive in recipient cells

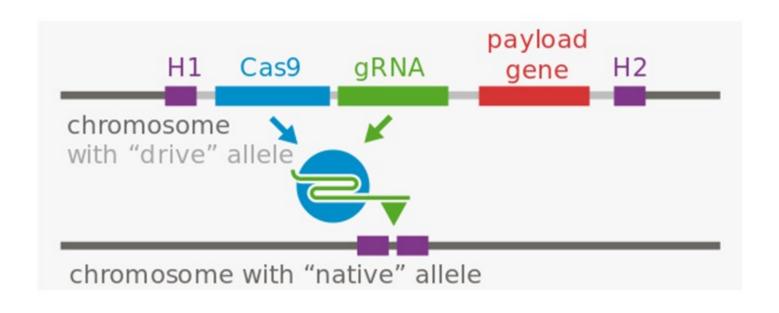
A STRUCTURE OF SELF-PROPAGATING GENE DRIVES

A repair template containing

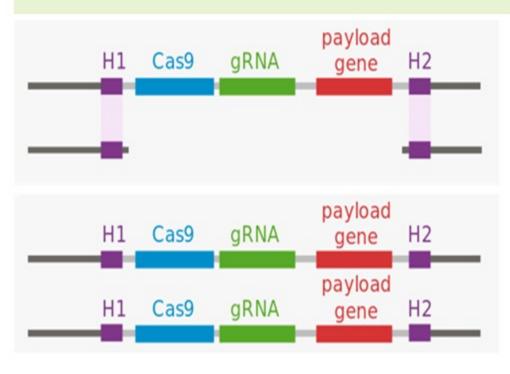


sides homologous to the sequences that are adjacent to the cutting site in the host genome

STEP 1: SITE-SPECIFIC DNA CLEAVAGE



STEP2: HOMOLOGY DIRECTED REPAIR



- As a result, the gene drive insertion in the genome will re-occur in each organism that inherits one copy of the modification and one copy of the wild-type gene.
- If the gene drive is already present in the egg cell (e.g. when received from one parent), all the gametes of the individual will carry the gene drive (instead of 50% in the case of a normal gene)

GENE DRIVES IN VIRUSES

- A gene drive strategy that relies on the co-infection of a given cell by a
 naturally occurring and engineered virus. Upon co-infection, the unmodified
 genome is cut and repaired by homologous recombination, producing new
 gene-driven viruses that can progressively replace the naturally occurring
 population.
- Recombination between viral genomes is a well-known and widespread source
 of diversity for many viruses. In particular, herpesviruses are nuclearreplicating DNA viruses with large double-stranded DNA genomes and
 frequently undergo homologous recombination during their replication cycle.



"New Plant Breeding techniques"

Genome edited crops:

- CRISPR-CAS9
- Zinc Finger Nucleases
- TALENS
- Oligo-Directed Mutagenesis

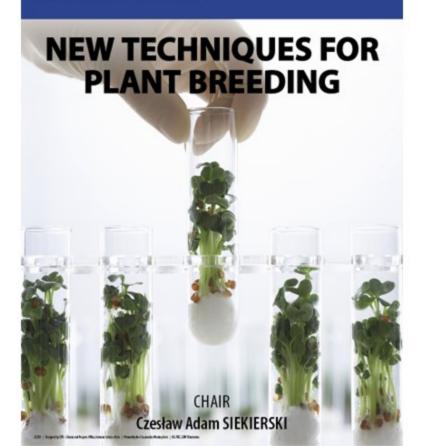
Epigenetic Engineering

- RNAi (RNA Interference)
- RDDM (RNA Directed DNA Methylation)

PUBLIC HEARING COMMITTEE ON AGRICULTURE AND RURAL DEVELOPMENT



Tuesday 01.12.2015 - **15:00-17:00**JÓZSEF ANTALL BUILDING - ROOM **602**





SHORT SHARP SCENCE 23 Seasonber 2004

Monsanto cuts deal to use CRISPR to engineer food





POPULAR SUBSCIENCE

pricelline...











SCIENCE

CRISPR-MODIFIED CORN MAY SOON BE READY FOR MARKET

IT WOULD BE THE FIRST CROP TO GO ON SALE THAT HAS BEEN GENETICALLY ALTERED WITH THE ENZYME

By Alexandra Ossola September 6, 2016



Cas Public/Private Partnership

Dulbert Risease and the International Malate and Wheat improvement Center (CIMMPT) have entered into a Master Alliance Agreement to jointly develop improved crops using CRESPR-Cas advanced plant breeding technology for characteristics that address the needs of smallholder farmers around the world. The collaboration amountement coincides with CAMMPT's Still annexasy celebrations being held this week in CIMMPT's Still annexasy celebrations being held this week in CIMMPT.

"Working together with CMMhTI will enable smallholder farmers to benefit from technology like CRISPR-Cas, helping them solve their challenges," said DuPort Pioneer President Paul Schlickler.

Phoneer and CIMMYT collaborations span decades and have contributed significantly to the food security and livelihoods of farmers and consumers in developing countries.

"in a world of rapid technology evolution, it's essential that new approaches such as CRESPR Cas are applied widely to benefit both poorer and wealthier farmers," said CMMNT Director General Martin Knopft. "This collaboration with DuPont Romeir will allow us to provide climate and disease



Paul Schickler DuPont Pioneer President, and CIMMYT Director General, Martin Krooff, sign CRISPR-Cas collaboration agreement at CIMMYT 50th anniversary celebration in Mexico.

GMO +

Biotech Industry argues:

- Not GMO's according to regulations (legal argument around wording) the techniques do not give rise to 'a GMO'
- More 'precise' / less intervention ('editing')
- Do not use 'foreign DNA' therefore consumers will not be concerned.
- In some cases, do not even involve modifying DNA.

NGO's/critics argue:

- This is genetic engineering 2.0 therefore should be regarded as GMOs
- Genome editing has similar 'off-target' effects as 1st gen GMOs risks.
- Techniques are new and more powerful; therefore, GMO risk concerns are magnified.
- Creates entirely novel sequences.
- Wrong to claim that new edited sequences are 'predictable'/well understood. Small genome changes > big changes in organisms.



MISSION



ABOUT

THE CROPS

CANOLA

Cibus' new *SU Canola™* is a non-transgenic (non-GMO) sulfonylurea (SU) herbic canola that is

now available in the United States;

TECHNOLOGY

- 2) on track to be available in Canada in 2017; and,
- 3) expected to be launched in other major global markets after 2018.

Bloomberg Technology

IN THE NEWS

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Americans Are Buying Gene-Edited Food That's Not Labeled GMO

by Craig Giammona and Jack Kaskey

July 14, 2016 - 5:00 AM EDT

- USDA passes on oversight of cooking oil new to store shelves
- Monsanto, DuPont, Dow developing crops with the new technology



nature biotechnology

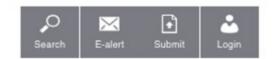


Table 1: CRISPR-edited plants in the pipeline that USDA will not oversee

From: With a free pass, CRISPR-edited plants reach market in record time

Inquiring institution (location)	Plant trait engineered with CRISPR-Cas9
USDA ARS, Plant Science Research Unit (St. Paul, Minnesota)	Soybean (Glycine max) with drought and salt tolerance; achieved by disrupting the Drb2a and Drb2b genes (double-stranded RNA-binding protein2 genes)
Yield10 Bioscience (Woburn, Massachusetts)	Camelina with increased oil content; target genes not disclosed
Donald Danforth Plant Science Center (St. Louis)	Setaria viridis, or green bristlegrass, with delayed flowering time; achieved by deactivating the S. viridis homolog of the Zea mays ID1 gene
DuPont Pioneer (Johnston, Iowa)	Waxy corn with starch composed exclusively of amylopectin; achieved by inactivating the endogenous waxy gene Wx1 that encodes a granule-bound start synthase catalyzing production of amylose
The Pennsylvania State University (University Park, Pennsylvania)	White button mushroom (Agaricus bisporus) with anti-browning properties; achieved by knocking out a gene coding for polyphenol oxidase (PPO)
	USDA ARS, Plant Science Research Unit (St. Paul, Minnesota) Yield10 Bioscience (Woburn, Massachusetts) Donald Danforth Plant Science Center (St. Louis) DuPont Pioneer (Johnston, Iowa) The Pennsylvania State University



"Gene editing could, for example, be used to knock out the receptor that the fungus uses to invade cells



RNAi (RNA Interference)

Spraying synthetic RNA on crops to interfere with DNA functioning.

Big Ag very invested: Monsanto, Syngenta



Biomedicine

The Next Great **GMO Debate**

Deep inside its labs, Monsanto is learning how to modify crops by spraying them with RNA rather than tinkering with their genes.

by Antonio Regalado August 11, 2015

he Colorado potato beetle is a voracious eater. The insect can chew through 10 square centimeters of leaf a day, and left unchecked it will strip a plant bare. But the beetles I was

looking at were doomed. The plant they were feeding on-bright green and carefully netted in Monsanto's labs outside St. Louis-had been doused with a spray of RNA.

The experiment took advantage of a mechanism called RNA interference. It's a way to temporarily turn off the activity of any gene. In this case, the gene being shut down was one vital to the insect's survival. "I am pretty sure 99 percent of them will be dead soon," said Jodi Beattie, a Monsanto scientist who showed me her experiment.

The discovery of RNA interference earned two academics a Nobel Prize

"non-GMO"

GENETIC ENGINEERING — SYNTHETIC BIOLOGY

MAIN BIOSAFETY ISSUES

- The behavior of synthetic biological systems is inherently uncertain and unpredictable, especially when it comes to potential ecological risks
- No risk assessment protocols have been developed to assess all potential risks associated with synthetic biology
- Assured containment of organisms developed with synthetic biology is not always practical or possible. (Xenobiology does not offer safe or reliable tools to ensure confinement or biological containment)
- Synthetic biology Researchers are not necessarily trained in biological sciences or biosafety.
- Currently, there is no comprehensive regulatory apparatus for the oversight and governance of synthetic biology
- Synthetic biology could profoundly alter current practices related to biodiversity conservation and sustainable use and rules governing access and benefit sharing. It will also affect Food and Livelihood Security, especially in the developing World

GENETIC ENGINEERING — SYNTHETIC BIOLOGY

MAIN BIOSAFETY ISSUES

- The Cartagena Protocol does not sufficiently cover synthetic biology and its potential impacts on biodiversity.
 - ·i. virtual (digital) transfer of LMOs
 - ·ii. transfer of constituent parts of an LMO
 - · iii. import of synthetic organisms for contained use.
- The absence of adequate tools to monitor and detect Synthetic biology products

Thank you!

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