B·DEBATE International Center for Scientific Debate BARCELONA

upf. Universitat Pompeu Fabra Barcelona

FARREN ISAACS

CV

PARTICIPANT AT:

SYNTHETIC BIOLOGY.
FROM STANDARD BIOLOGICAL PARTS TO ARTIFICIAL LIFE

September, 17th-18th, 2015, Barcelona

Farren Isaacs, assistant professor of Molecular, Cellular and Developmental Biology and Systems Biology, Yale University, New Haven, USA

Farren Isaacs is assistant professor of Molecular, Cellular and Developmental Biology and Systems Biology at Yale University. He received a B.S.E in Bioengineering from the University of Pennsylvania and Ph.D. in Biomedical Engineering-Bioinformatics at Boston University, where he pioneered the development of synthetic RNA molecules capable of probing and programming cellular function. As a research fellow in genetics at Harvard, he invented enabling technologies for genome engineering. His research is focused on finding ways to construct new genetic codes and reprogrammable cells that serve as factories for chemical, drug and biofuel production. He has been named a "rising young star of science" by Genome Technology Magazine, a Beckman Young Investigator by the Arnold and Mabel Beckman Foundation and recipient of a Young Professor award from DuPont.

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ABSTRACT

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Design, Construction & Function of Genomically Recoded Organisms

The conservation of the genetic code, with minor exceptions, enables exchange of gene function among species, viruses and across ecosystems. Fundamental changes to the genetic code could significantly enhance our understanding of the origins of the canonical code and reveal new subtleties of how genetic information is encoded and exchanged. Modifying the canonical genetic code could also lead to orthogonal biological systems with new properties. I will first present the development of genome engineering technologies – MAGE (multiplex automated genome engineering) and CAGE (conjugative assembly genome engineering) – that permit versatile genome modifications. Next, I will discuss the design and construction of a genomically recoded organism (GRO) using MAGE and CAGE. In the GRO, all known UAG stop codons in Escherichia coli MG1655 were replaced with synonymous UAA codons, which permitted the deletion of release factor 1 and reassignment of UAG translation function. This GRO exhibited improved properties for incorporation of nonstandard amino acids that expand the chemical diversity of proteins in vivo. The GRO also exhibited increased resistance to T7 bacteriophage, demonstrating that new genetic codes could enable increased viral resistance. Finally, I will describe the engineering of the GRO to depend on synthetic amino acids aimed at construction of safe GMOs unable to grow in the wild. This work increases the toolbox for genomic and cellular engineering with the goal of expanding the functional repertoire of organisms.

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