

Synthetic Biology



The promise of engineered biology for a multitude of applications.

Enabled capabilities

- Bio-production including bio-fuels
- Bio-sensors
- Tissue regeneration
- New and faster ways to produce vaccines
- Algae-based food production
- Clean water as a bio-based capability

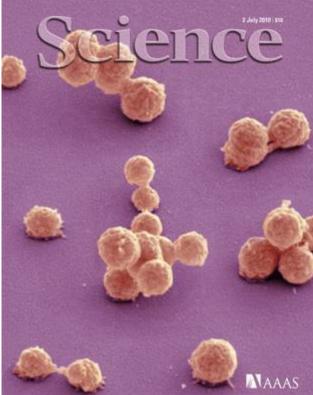
Key research challenges:

- Modeling and simulation to address complexity of pathways
- Automation of trials
- Selection of appropriate host cell compatible with synthetic genome
- Regulation and societal acceptance



Creation of a Bacterial Cell Controlled by a Chemically Synthesized Genome David G. Glibon¹ John I. Glass¹ Grole Lartique³ Vladimir M. Noskov¹ Ray-Yuan Chuang¹

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crude *M. mycoides* or *M. capricolum* extracts, or by simply disrupting the recipient cell's restriction system (8).

We now have combined all of our previously established procedures and report the synthesis, assembly, cloning, and successful amagination of the 1.08-Mhp *M. mycoider JCVI*-syn1.0 geneme, to create a new cell controlled by this synthesic genome.

ir genome design. Design of the VI-syn1.0 genome was based on the te finished genome sequences of two ains of M. myapides subspecies cars II). One was the geno e donor us al KienBank accession (2001621) r was a strain created by trans that had been ckned and west VCnMmwc1 1-Atunelling on CP001668] (8). This project Ithough we believe that both finder genome sequences are reli which they differ W the synthetic genome before both 1621 sequence (11). When it was ose the sequence of the senom nsplanted from yeast (CP001668 reference (excent that we kent the hes gene). All differences that apically significant between CP001668 synthesized cassettes were cor nactly (11). Sequence difference amphetic cassettes and CP001668 at 19 sites appeared harmless and so ed. These provide 19 polymorph hetween our synthetic genom) and the natural (non-synthetic) se fmyc1.1) that we have ckned i as a standard for senome trans veast (8). To further differentiat nthetic genome and the natural one bur watermark sequences (fig. S1) to or more cassettes in regions expe onstrated [watermarks 1 (1246 bp [1 bp)] or predicted [watermarks d 4 (1222 hp)] to not interfere with These watermark sequences encode fiers while limiting their translation Table S1 lists the differe thetic genome and this natural sta-S2 shows a map of the M_mycoide watermarks deletions inco es of the M. mucoides JCVI syn1.0 fig. S2, and the sequence of th mlasma ckne sMmYCn235tied to GenBank (accessi

ic genome assembly strategy. The assettes were generally 1080 hp with laps to adjacent cassettes (*II*). They oducad by assembly of chemically