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High Throughput, Sequence Independent and Ordered Nucleic Acid Assembly

Tech ID: 25452 / UC Case 2015-195-0

BACKGROUND

Currently DNA fragments are assembled from smaller oligonucleotides that contain overlapping DNA sequences. After overlapping sequences are annealed, each oligo will act as primer for polymerization, eventually fusing the two fragments together. This method relies on unique overlapping sequences that are favorable to anneal at a specific temperature. This strategy becomes problematic when you try to assemble more than two fragments, when the uniqueness of annealing sequences, the correct order of fragments annealing and optimal temperature for all the annealing reactions are major concerns. On the other hand, annealing only two fragments at a time is time consuming and low in scalability. There is a great need for a cost-effective and accurate approach.

TECHNOLOGY DESCRIPTION

Researchers at UC San Diego have discovered a novel approach to synthesize large DNA fragments without any of the aforementioned limitations. First, it is sequence independent and does not depend on the overlapping sequences on oligonucleotides being assembled. Thus, it can assemble repetitive sequences, or sequences with either high or low G/C or A/T content. DNAs are assembled in solution; which allows for the parallel synthesis of many smaller pieces.

APPLICATIONS

The ability to assemble DNA fragments in a sequence independent manner has special implications on synthetic biology. This technology will enable a "gene synthesis machine" that allows a user to enter a desired DNA sequence and have it printed. In addition, there is a cost-saving potential in the fact that this strategy allows for the parallel synthesis of a mixture of many smaller pieces of DNA.

PATENT STATUS

Country	Туре	Number	Dated	Case
United States Of America	Issued Patent	10,407,460	09/10/2019	2015-195
Patent Cooperation Treaty	Published Application	2016179602	11/10/2016	2015-195

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OTHER INFORMATION

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2015-195-0

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