



AN EVOLUTIONARY APPROACH FOR COMBINATORIAL CHEMISTRY BY GENETICS

Pablo Cruz-Morales^{* 1,2,3,4}, Yuka Murofushi ^{1,5}, Cuauhtemoc Licona-Cassani⁴, Jay D Keasling^{1,2,3}

1: Joint Bioenergy Institute, 5885 Hollis Street, Emeryville, CA 94608, USA

eón, Guanajuato

019

23 al 28 de iunio

2: Biological Systems & Engineering Division, Lawrence Berkeley National Laboratory,

3: Department of Chemical and Biomolecular Engineering, University of California, Berkeley,

4: Centro de Biotecnología FEMSA, Tecnológico de Monterrey, NL, México

5: Tokyo Institute of Technology, Japan

Discovering a bioactive natural product with pharmacological potential is expensive and time consuming. Current strategies implement a "culture-extract-screen" approach which involves large-scale and costly experiments. We have developed a method that may accelerate early stages of drug discovery pipelines by diversifying known bioactive natural products. We used Beta-lactams and aminoglycosides as proof-of-concept models as they represent classic scaffolds that have been widely characterized.

Our work incorporates synthetic biology methods, with phylogenomic analysis and *in vivo* screening into a combinatorial chemistry by genetics approach to explore chemical diversity around bioactive chemical scaffolds in short time at low cost. We believe this approach could positively impact the biodiscovery pipeline for most pharmacologically relevant natural product classes, effectively discovering novel drugs, cheaper and faster.





