A S Kolaskar et al., J Genet Mol Biol 2018, Volume 2

CATEGORIZATION OF METABOLIC PATHWAYS IN BACTERIA

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Fully sequenced bacterial genomes having more than ≥250 well annotated metabolic pathways were analysed to find out identical pathways in all these bacteria in more than 100 well annotated bacteria ≥250 well annotated pathways and fully sequenced genomes, 42 identical pathways were found in each of these bacteria. These pathways were called as stage I pathways or Fundamental pathways. The categorization of pathways was carried out by comparing compounds for each of the stage I pathways with compounds from remaining pathways. Pathways having common compounds with stage I pathways are categorized as stage II pathways. Following the logic of identifying common compounds between newly categorized pathways and the remaining pathways, this tool categorizes the metabolome iteratively. Categorization process is stopped when no common compounds exist between newly categorized pathways and remaining pathways. This was termed as metabolic categorization. In each metabolome, non-interacting pathways can be used to engineer bacteria without affecting other networks/ interacting pathways. The case study of *Escherichia coli* O157, having 433 annotated pathways, shows that 376 pathways interact directly or indirectly with 42 stage I pathways while 17 pathways are non-interacting. These 376 pathways are distributed in the stage II (285), stage III (76), stage IV (13) and stage V (two) category. This approach allows a better understanding of the complexity of metabolic networks. This approach suggests that stage I pathways could be the most ancient pathways and compounds that interact with maximum pathways maybe compounds with high biosynthetic potential, which can be easily identified. Further, it has been shown that interactions of pathways at various stages could be one to one, one to many, many to one, many to many mappings through interacting compounds. The granularity of the method being high, the impact of pathway perturbation on the metabolome and particularly sub-networks can be studied precisely. This can help in engineering a bacterium with desired characteristics.

BIOGRAPHY

A S Kolaskar has played a key role in shaping India's educational direction. Currently, he splits his time between being the Honorary Vice Chancellor at the University of Pune in India, the Director of the Bioinformatics Program for the American Type Culture Collection and an affiliate professor in the School of Computational Sciences at George Mason University. For the past 13 years, he has served as a professor and as Director of the Bioinformatics Center at the University of Pune. His main areas of research include theoretical molecular biophysics work and bioinformatics. He also has spent time in various management positions, from advising PhD students as a chairman of the post-graduate department at the University of Pune and as the chief investigator of large research and infra-structural grants and contracts from the Indian government. He has also been actively involved with international scientific organizations from the Technology Transfer Society to the American Association for the Advancement of Science and the Maharashtra Association for the Cultivation of Science. He has implemented major reforms in the university governance during his tenure as Vice Chancellor of the University of Pune, one of the largest universities in India.

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