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Categorization of metabolic pathways in bacteria

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Abstract

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.

Analyses of biological databases such as those of genome, proteome, metabolome etc., have given insights in organization of biological systems. However, current efforts do not utilize the complete potential of available metabolome data. In this study, metabolome of bacterial systems with reliable annotations are analyzed and a simple method is developed to categorize pathways hierarchically, using rational approach. Ninety-four bacterial systems having for each ≥ 250 annotated metabolic pathways were used to identify a set of common pathways. 42 pathways were present in all bacteria which are termed as Core/Stage I pathways. This set of pathways was used along with interacting compounds to categorize pathways in the metabolome hierarchically. In each metabolome non-interacting pathways were identified including at each stage.

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