

Cultivating the uncultivable environmental microbe using insights from whole genome sequence that define a growth medium

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Abstract

While many microbes could be cultivated in the laboratory, many more resist attempts at bringing them under cultivation through a variety of environmental and nutritional conditions. This represents the current state of microbiology where we still lack knowledge and tools concerning the appropriate conditions and medium for cultivating hitherto unculturable microbes. Many approaches have been proposed for improving the subset of environmental microbes that could be cultivated, but these remain specific methods not generally applicable under all circumstances. One potential general solution to the problem is to use insights from whole genome sequence of environmental microbes for understanding the environmental and nutritional conditions conducive for its cultivation. For example, reconstruction of the metabolic network of a microbe from annotated whole genome data would reveal whether the microbe pursue an aerobic or anaerobic lifestyle. Specifically, presence of enzymes mediating processes involving anaerobic electron acceptors strongly suggest an anaerobic lifestyle. After fixing the oxygen tension of the cultivation medium, the next question to ask involves the types of nutrients that could be uptake by cells. Profiling the types of transporters available to the microbe would largely answer its capability of transporting different nutrients into the cell. When such nutrients are coupled to metabolic pathway that aid their catabolism, they can be provided in the medium to provide the carbon backbone for forming different intermediates needed by the cell. But, most microbes are deficient in some enzymes that build specific intermediates required for biomass formation. Lack of such intermediates would thus prevent cell growth, and these metabolites would need to be provided in the nutrient medium. Moving beyond nutrients, the genome sequence could also offer clues to the pH requirement of the microbe. This can be gleaned from the presence of homologous enzymes known to facilitate survival at low or high pH. However, such knowledge remains guesswork where experiments are needed to fine tune the pH for optimal cell growth. Finally, requirement for essential micronutrients such as trace metals could be deciphered from the presence of metal-cofactor enzymes in the annotated genome. Requirement for vitamins in the growth medium could similarly be deduced from the presence/absence of vitamin synthesis pathways in the microbe. This helps to concoct the trace metal and nutrient solution needed by the cells. Collectively, while the approach outlined above is theoretically feasible, experimental work remain essential in delineating the nutritional and environmental conditions needed by particular microbe for growth. But, information from whole genome sequence do offer help in selecting the range of conditions for experimentation; thereby, reducing the time, expense and effort needed to bring a microbe into cultivation in the laboratory.

Keywords: environmental microbe, aerobic, anaerobic, nutrients, transporters, whole genome sequence, genome-scale metabolic network, cell growth, electron acceptors, vitamin synthesis pathways,

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Conflicts of interest

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