MiDAS: A Novel Approach Reveals Microbiome Selection for Wastewater Treatment System

Pratibha Yadav¹ and Kamlesh Kumar Yadav²*

¹SBN Govt.PG College, Barwani, Madhya Pradesh, India
²Brandenburg Innovation India Pvt. Ltd., Bangalore, Karnataka, India

Corresponding Author: Kamlesh Kumar Yadav, Brandenburg Innovation India Pvt. Ltd., Bangalore, Karnataka, India.

Waterborne infectious diseases are caused by viruses and bacteria that are ingested into the body through contaminated water or contact with faeces. Industrial waste, chemical effluents, untreated sewage, human waste, animal waste, garbage, and other pollutants are the most common sources of contamination of water. If the effluent is not properly treated, it may cause serious harm to humans and the environment.

Microorganisms are a crucial component of wastewater treatment systems, as they remove pollutants and disease-causing pathogens, recycle nutrients and energy, and produce clean water. There is a diversity of microorganisms employed in sewage treatment, however, the exact number is unknown, which play a vital role in wastewater treatment. Each of these bacteria contributes to the treatment process in a different way, ensuring that there is little to no influence on the environment. Diverse microorganisms are in the systems; however, only a few of them have information about their identification and functions that are involved in the treatment system. Microbial community surveillance might be used as a standard approach of controlling and optimising wastewater treatment processes. It is only possible to determine whether the correct processes are in right place when the identity and function of the majority of microorganisms are known, which is difficult to do today [1]. To make appropriate decisions about the management of the treatment systems, detail information about the microorganism is essential. This will be extremely crucial in the coming years, given the global trend toward advanced water resource recovery systems for sustainable development.

The majority of the species discovered are new and unknown, and many of them belong to unnamed genera. It is true that determining the functions of bacteria is difficult, however there are several approaches for doing so. This landscape has been significantly changed by novel DNA-based technologies without growing pure culture. Bacteria can now be identified to species level for the first time [2]. The gold standard for microbe identification is an advanced technique for bacterial identification, is to identifying specific marker genes in their chromosome - a fingerprint gene. The DNA sequence of this marker gene is compared to a reference database for the identification of bacteria based on the present or absent the sequence in the database [3]. Furthermore, global mapping of all microorganisms in these systems is undertaken.

Once the fingerprint gene has been identified, the markers can be designed to visualise its fingerprint gene using fluorescence microscopy, a process known as fluorescence *in situ* hybridisation (FISH). The FISH can combine with other staining or spectroscopic techniques, such as Raman microspectroscopy to obtain about physiological traits.

Enabling online identification of the microbes is one of the ultimate goals for wastewater treatment plant operators and uses that information for monitoring and controlling the microbial ecosystems. With the modern sequencing technologies, it is possible to keep pocket-sized sequencing devices to treatment plants and have results within the hours, making this a quick and inexpensive process.

A new ecosystem-specific database based on the SILVA database was founded in 2015 that contains sequences from nearly all microbes present in wastewater treatment plants, known as MiDAS (Microbial Database for Activated Sludge). The Microbial Database for Activated Sludge (MiDAS) field guide is a free online resource that connects the identities of abundant and process-critical microorganisms in activated sludge wastewater treatment systems with data on their functional value. It provides manually catalogued taxonomic assignment (MiDAS taxonomy 1.0) and associated physiological information profiles (midasfieldguide.org) for all abundant and process-critical genera in activated sludge (AS) [3]. Quick and accurate identification is now possible with the new MiDAS reference database. Recent advancement in sequencing technology and bioinformatics tools has made it possible to generate millions of high-quality full-length 16S rRNA gene reference sequences from any environmental ecosystem [4-6]. MiDAS 3.6 is the latest version, an improved taxonomy with comprehensive 16S RNA gene reference database based on high-quality sequences derived from activated sludge and anaerobic digester systems.

The proposed MiDAS genus names can provide a uniform language for all field researchers, making data exchange easier and benefitting studies into the ecology of these industrially important ecosystems. MiDAS is a live project that will be updated on a regular basis to reflect new developments in the industry. It may be possible to identify problematic filamentous bacteria and receive advice on how to control them; it may also be possible to determine whether the appropriate amount and composition of nitrifiers are present; or to test the quality of effluent, in relation to the presence of pathogens.

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