

Fitriana Puspitasari Pingkan, 2012. **Abundance of Indigenous Organic Compounds Decomposers Bacteria in the Wastewater Treatment Reactor.** This study was written under guided by Dr. Ni'matuzahroh and Tri Nurhariyati, S. Si., M. Kes. Biology Undergraduate Study Program, Biology Department of Science and Technology Faculty, Airlangga University.

Abstract

The purpose of this research was to know the abundance, macroscopic and microscopic characteristics, and genus name of dominant indigenous organic compounds, especially starch, protein, and lipid decomposers bacteria that were in the every part of the wastewater treatment reactor. This research was an explorative research. The method of the research was taking wastewater samples from every part of the reactor. Samples were put in a 10 ml sterile sample bottles. Samples then diluted in series. The level of dilutions were varied depend on the level of samples turbidity. Samples that had been diluted were cultured in petri dish with Nutrient Agar media (NA) and amylytic, proteolytic, and lipolytic test medium with pour plate method. Samples then incubated for 24 hours at room temperature. After incubated, cultures were observed and counted for the Total Plate Count value. Different colonies of heterotrophic bacteria from the inlet and outlet part of the reactor were separated until pure isolates were obtained and then macroscopic and microscopic identification were performed. Genus identification was done for bacteria colony that most often appeared on the NA media by doing physiology tests. The abundance of indigenous organic compounds, especially starch, protein, and lipid decomposers bacteria that stated in Total Plate Count value was different for every part of the reactor. The highest Total Plate Count result was at the second part of the reactor that indicates that organic compounds hydrolyzing process mostly happened in this part of reactor. Isolation and identification process showed that a lot of Gram-negative coccoid shaped bacteria, Gram-positive rod shaped bacteria, and Gram-positive coccus shaped bacteria occurred. The genus names of the dominant bacteria from the reactor were identified as *Bacillus* and *Micrococcus*. These two isolates can hydrolyze protein, but only *Bacillus sp.F.* can hydrolyze starch.

Keywords : *Total Plate Count* (TPC), isolation, identification, organic compounds decomposers bacteria, wastewater treatment reactor.