Microplastic (MP) pollution has become a global environmental issue, negatively impacting aquatic ecosystems and public health. The doctoral thesis aimed to determine the potential for MP removal in wastewater treatment systems and its effect on biological processes. The research was divided into three stages. The potential for MP removal in primary settling tanks was investigated in the first stage. The studies showed that using coagulants and flocculants can significantly increase the effectiveness of MP removal. The application of FPM at a dose of 25 μ g/L enabled the removal of 96% of MPs with a diameter of 80–212 μ m. MPs sized 710–850 µm were utterly removed from the wastewater after using PIX (38%) at a dose of 95 μ l/L, PEL at a dose of 6.25 μ g/L, and PAX (36%) at a dose of 90 and 189 μ l/L. In the second stage of the research, the influence of MPs on pollutant removal efficiency and microbiome in GSBR was determined. The type of MP in wastewater influenced the accumulation of MPs in biomass (TM>PET>PE) and the transformation of organic compounds, nitrogen, and phosphorus. The presence of TM affected the efficiency and kinetics of N-NH4 removal and the rates of N-NO₂ and N-NO₃ removal/production. The presence of PET in wastewater reduced the efficiency of COD and N-NH4 removal while increasing the efficiency of P-PO₄ removal. The dosing of PE affected the kinetics of COD, N-NH₄, N-NO₂, N-NO₃, and P-PO₄ transformations and reduced the concentration of N-NO₂ in treated wastewater. It was found that AGS degraded over 60% of compounds leached from TM. The TM dose in wastewater was correlated with an increase in the proportion of microorganism biomass belonging to genera Xanthomonas, Ferruginibacter, Luteimonas, Hydrogenophaga, Devosia, Geobacter, Thiobacillus, Rubrivivax, Gemmatimonas and Acidovorax capable of degrading micropollutants. Additionally, genome annotation using the KEGG database indicated an increase in the metabolic potential of the community associated with genetic material repair or synthesis and biodegradation with increasing TM dose in wastewater. Dosing PET with wastewater increased the abundance of microorganisms from Bacteroides, Singulisphaera, Gemmata, Ectothiorhodospira, Devosia, Dechloromonas, Woodsholea and Microcystis genera in aerobic granules. In GSBR dosed with PE, the abundance of microorganisms from Mycobacterium, Oscillochloris, Fusobacterium, Lactobacillus, Stenotrophomonas, Bacteroides and Microcystis genera increased. PET and PE in the tested doses did not affect the activity of microorganisms based on the abundance of 16S rDNA, amoA, nirK, and nirS genes in the biomass. However, the presence of PET increased the abundance of nosZ and ppk1 genes in the biomass in the GSBR cycle. In the third stage, the influence of nitrogen concentration in the environment on the surface characteristics of MPs and the microbial community in the biofilm colonizing MPs was determined. Morphological analysis showed increased roughness and the formation of cracks on the surface of MPs throughout the experiment; the decrease in MP mass during the experiment was approximately 7%. The N-NH₄ concentration in the environment was positively correlated with TN sorption on the MP surface. The presence of microorganisms with colonization and degradation potential for plastics (genera Acidovorax, Aneurinibacillus, Aquabacterium, Bacillus, Brevibacillus, Enterobacter, Gordonia, Hydrogenophaga, Ideonella, Pseudomonas, Rhodococcus, Rhodopseudomonas, Sphingomonas, Sphingopyxis, Streptomyces, and Thermoactinomyce) was demonstrated in the biofilm. Although many bacterial genera capable of degrading MPs were observed; their relative proportion in the biomass was low. Potentially pathogenic microorganisms such as Enterobacter, Pseudomonas, Mycobacterium, Sphingopyxis, Aquabacterium, and Brevundimonas were found on the MP surface. These studies expand knowledge regarding the impact of MPs on the microbiome and wastewater treatment efficiency. They may serve as a basis for developing effective strategies for MP elimination from the aquatic environment.