



Dinamika Keragaman Bakteri Air dan Sedimen pada Mina Padi di Seyegan, Sleman

Afri Herlabang
17/419960/PMU/09171

INTISARI

Mina padi merupakan salah satu sistem budidaya yang memadukan antara budidaya ikan dan tanaman padi pada satu area. Dalam ekosistem budidaya, bakteri memiliki peran penting dalam siklus biogeokimia. Studi tentang kelimpahan dan keanekaragaman bakteri diperlukan untuk meningkatkan pemahaman tentang ekologi mikroba guna mengoptimalkan produksi akuakultur dan kualitas air. Penelitian ini bertujuan untuk mengetahui keragaman dan dinamika komposisi komunitas bakteri selama pemeliharaan mina padi. Gen 16S rRNA dianalisis dengan teknik *Next Generation Sequencing* (NGS) untuk mengidentifikasi komunitas bakteri di air dan sedimen dari bagian kolam, sawah, dan caren pada mina padi. Hasil penelitian ini menunjukkan bahwa rata-rata sebanyak 4337 dan 1184 *Operational Taxonomic Unit* (OTU) teridentifikasi masing-masing di sampel sedimen dan air. Secara keseluruhan, filum Proteobacteria, Acidobacteria, dan Chloroflexi melimpah di sampel sedimen, sedangkan filum Proteobacteria, Bacteroidetes, dan Actinobacteria terdeteksi dominan di sampel air mina padi. Dinamika komposisi komunitas bakteri teramati selama pemeliharaan mina padi yang dimulai dari tingkat filum untuk sampel air dan tingkat genus untuk sampel sedimen. Komunitas bakteri pada tingkat genus menunjukkan dominasi bakteri yang diduga terlibat dalam siklus biogeokimia, seperti *Desulfobacca* dalam reduksi sulfat, *Methylophilus* dalam oksidasi amoniak, serta *Methylothena* dalam siklus karbon dan denitrifikasi.

Kata kunci: bakteri, dinamika, keragaman, mina padi, NGS



The Dynamic of Bacterial Diversity in Water and Sediment of Mina Padi at Seyegan, Sleman

Afri Herlambang

17/419960/PMU/09171

ABSTRACT

Mina padi (integrated rice-fish farming) is a culture system that integrates fish and rice cultivation in one area. In aquaculture ecosystems, bacteria play an important role in biogeochemical cycle. The study of bacterial abundance and diversity is needed to improve an understanding of microbial ecology to optimize aquaculture production and water quality. This study aimed to determine the diversity and dynamics of the composition of the bacterial community during the cultivation of mina padi. The 16S rRNA gene was analyzed using the Next Generation Sequencing (NGS) to identify bacterial communities in the water and sediment from the ponds, rice fields, and trenches in mina padi. The results indicated that an average of 4337 and 1184 Operational Taxonomic Units (OTU) were identified in sediments and water samples, respectively. Overall, the phyla Proteobacteria, Acidobacteria, and Chloroflexi were abundant in sediment samples, while the phyla Proteobacteria, Bacteroidetes, and Actinobacteria were detected predominantly in water samples. The dynamics of the composition of bacterial community in water and sediment were clearly observed at the phylum and genus levels, respectively. Bacterial community at the genus level showed a predominance of bacteria predicted to be involved in the biogeochemical cycle, such as *Desulfobacca* in sulfate reduction, *Methylophilus* in ammonia oxidation, and *Methylothera* in the carbon cycle and denitrification.

Keywords: bacteria, diversity, dynamics, *mina padi*, NGS