



Diversity of Greenhouse Gas Producing and Mitigating Microbes in the Soil - A Review Article

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Abstract

Climate change is a serious issue for our planet. Climate change is the consequence of greenhouse gas emissions deliberately without nature's permission. The challenge is until now continued broadly. Exploring and exploiting soil microbes are one of the solutions to overcome permanently. Soil microbes are not only producers but users of greenhouse gases for their metabolic pathway. Diverse greenhouse gas-producing and mitigating microbes are involved. Microbes are providing secured positive and negative responses to global warming. But a microbial community has not been studied in detail yet. Overall, it needs an urgent metagenomics study.

Introduction

Our world is faced with many problems and daggered situations like Political instability, Economic crisis, Civil war, Immigration, Illegal trades, and Emerging virus pandemic. Notice for the last and most chronic one is Climate change. The hot topic and breaking news are the increment of global warming alarmingly. Politicians, Environmentalist, Scientist, Researchers, and Journalists are actively engaged to overcome shortly, but the challenge is until now continued.

Climate change is a serious issue for our planet. To overcome the problem numerous possible solutions and influence ideas are suggested from different stakeholders, but the crisis until now continued extremely. Hence, Climate change is a matter of survival for all life forms. Climate change is the consequence of greenhouse gas emission deliberately without nature's permission. Our world is speaking in "One word, One mouth" about the effect of global warming on living things daily. Countless scientific papers were published and situated on the academic's shelf, but they are insignificant to save nature.

Increasing soil microbes is also a competitive strategy for sequestering Carbon Dioxide (CO₂) to mitigate anthropogenic greenhouse gasses emissions. Microorganisms have beneficial to speed up and slow down climate change over time. Microorganisms affect climate change. At the same time, Climate change also affects the diversity of microorganisms [1]. The most novel microorganisms were originated from the soil. Concurrently, soil is performing as source and sink for greenhouse gases such as Carbon Dioxide (CO₂), Methane (CH₄), and Nitrous Oxide (N₂O).

As Endeshaw et al. reviewed a vast number of researches were overdone previously on the area of the biogeochemical process to clearly show greenhouse gas production and consumption pattern [2]. The role of microbes in climate change cannot be ignored. Soil microbes play an important role as both users and producers of greenhouse gases. Both natural and human-induced fluxes of carbon dioxide, methane, and nitrous oxide are dominated by microbiology. There are a few research efforts on the exploring of soil microbial community that responsible for either producing or mitigating greenhouse gases until now. The author is tried to address the diversity of soil microorganisms at the taxonomic unit level shortly.

Conclusion and Recommendation

Overall, the ultimate cause of climate change is sourced from anthropogenic greenhouse gas emission without restriction. Microbes are providing secured positive and negative responses to global warming. The diversity of greenhouse-gas producing and mitigating microbial communities has not been studied in detail yet. It needs an urgent Metagenomics study to fully understand soil-microbes interaction.

OPEN ACCESS

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Received Date: 25 Nov 2021

Accepted Date: 07 Dec 2021

Published Date: 13 Dec 2021

Citation:

Abatenh E. Diversity of Greenhouse Gas Producing and Mitigating Microbes in the Soil - A Review Article. *Ann Microbiol Immunol.* 2021; 4(1): 1026.

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Table 1: The diversity of greenhouse gas producing microbes in soil.

No	Greenhouse Gas Producing Microbes	Reference	
1	<i>Nitrosomonas</i> spp.	Heil et al. 2016 [3].	
2	<i>Nitrosolobus</i> spp.		
3	<i>Nitrospira</i> spp.		
4	<i>Acidobacteria</i> spp.	Hester et al. 2018 [4]	
5	<i>Sphingobacteriales</i> spp.		
6	<i>Opitutales</i> spp.		
7	<i>Rhizomicrobium</i> spp.	Samad et al. 2016 [5]	
8	<i>Sphingomonas</i> spp.		
9	<i>Haliangium</i> spp.		
10	<i>Variovorax</i> spp.		
11	<i>Bryobacter</i> spp.		
12	<i>Candidatus</i> spp.		
13	<i>Blastocatella</i> spp.		
14	<i>Acidothermus</i> spp.		
15	<i>Nocardioides</i> spp.		
16	<i>Streptomyces</i> spp.		
17	<i>Gaiella</i> spp.		
18	<i>Ktedonobacter</i> spp.		
19	<i>Bacillus</i> spp.		
20	<i>Gemmatimonas</i> spp.		
21	<i>Nitrospira</i> spp.		
22	<i>Anaeromyxobacter</i> spp.		Orellana et al. 2014 [6]
23	<i>Pseudomonas</i> spp.		
24	<i>Ignavibacterium</i> spp.		
25	<i>Gemmatimonas</i> spp.		
26	<i>Opitutus</i> spp.		
27	<i>Hydrogenobacter</i> spp.		
28	<i>Raistona</i> spp.		
29	<i>Thiobacillus</i> spp.		
30	<i>Rhodopseudomonas</i> spp.		
31	<i>Bradyrhizobium</i> spp.		
32	<i>Aromatelum</i> spp.		
33	<i>Thauera</i> spp.		

Table 2: The diversity of greenhouse gas mitigating microbes in soil.

No	Greenhouse Gas Mitigating Microbes	Reference
1	<i>Dyadobacter fermentans</i>	Domeignoz-Horta et al. 2016 [7]
2	<i>Azotobacter</i> spp.	Armada et al. 2015 [8]
3	<i>Rhizobium</i> spp.	Casanovas et al. 2002 [9]
4	<i>Bradyrhizobium japonicum</i>	
5	<i>Sinorhizobium fredii</i>	
6	<i>Bacillus</i> spp.	
7	<i>Azospirillum</i> spp.	Couradeau et al. 2012 [10]
8	<i>Microcoleus vaginatus</i>	
9	<i>Pseudomonas putida</i>	DeKempeneer et al. 2004
10	<i>Burkholderia cepacia</i>	Barac et al. 2004
11	<i>Methylobacterium</i> spp.	Van Aken et al. 2004

12	<i>Proteobacteria</i> spp.	Hallin et al. 2018 [11]
13	<i>Nitrospira</i> spp.	
14	<i>Actinobacteria</i> spp.	
15	<i>Bacteroidetes</i> spp.	
16	<i>Firmicutes</i> spp.	
17	<i>Chloroflexi</i> spp.	
18	<i>Nitrospirae</i> spp.	Hallin et al. 2018 [11]
19	<i>Verrucomicrobia</i> spp.	
20	<i>Euryarcheota</i> spp.	
21	<i>Thaumarcheota</i> spp.	
22	<i>Crenarcheota</i> spp.	Maeda et al. 2015 [12]
23	<i>Hypocreales</i> spp.	
24	<i>Eurotiales</i> spp.	
25	<i>Sordariales</i> spp.	
26	<i>Chetosphaeriales</i> spp.	
27	<i>Mucorales</i> spp.	
28	<i>Pleosporales</i> spp.	
29	<i>Glomerellales</i> spp.	Huang et al. 2020 [13]
30	<i>Ophiostomatales</i> spp.	
31	<i>Rubrivivax</i> spp.	
32	<i>Bradyrhizobium</i> spp.	
33	<i>Ideonella</i> spp.	Akiyama et al. 2016 [14]
34	<i>Azoarcus</i> spp.	
35	<i>Polymophum</i> spp.	Endeshaw et al. 2018 [2]
36	<i>Bradyrhizobium diazoefficiens</i>	
37	<i>Thiobacillus ferrooxidans</i>	
38	<i>Bacteroides succinogenes</i> ,.	
39	<i>Clostridium butyricum</i>	
40	<i>Syntrophomonas</i> spp.	
41	<i>Rhizobium trifolium</i>	
42	<i>Pseudomonas</i> spp.	
43	<i>Beijerinckia</i>	
44	<i>Anabaena</i> spp.	
45	<i>Nostoc</i> spp.	

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