

---

## 10. Effect of Chemical Fertilizer and Biofertilizer on Rhizosphere Soil Microbiome Composition and Functions

**Dr. Maitreyee Mondal**

Assistant Professor,  
Department of Microbiology,  
Dinabandhu Andrews College, Baishnabghata,  
Garia, Kolkata, West Bengal, India.

### **Abstract:**

*Fertilization influences the soil microbiome. Fertilizer application significantly changed the soil C/N ratio. Chemical fertilizer (NPK) treatment decreased soil pH. NPK application does not change the soil microbiome composition or dominant phylum but changed the relative abundances of microbiome components. Moreover, fertilizer significantly influenced metabolic processes, cellular processes and single-organism processes. Compared with a no-fertilizer treatment, the NPK treatment resulted in more differentially expressed gene pathways, and these pathways significantly correlated with soil nitrate nitrogen, available phosphorus and the moisture content of soil. KEGG analysis found that fertilizer application mainly affected the ribosome, photosynthesis and oxidative phosphorylation pathways. It has found that, organic fertilizer increased Nitrogen fixation and nitrification, and inorganic Nitrogen fertilizer accelerated denitrification. We found that the function of the soil microbiome under different fertilizer applications could be important for the rational application of fertilizer and for environmental and sustainable development.*

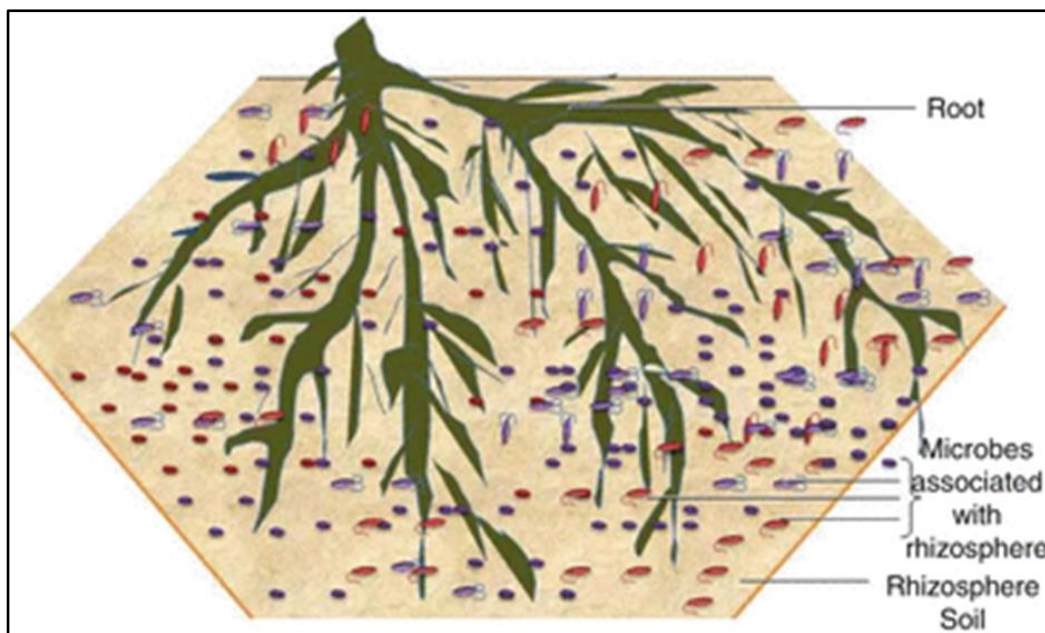
**Keywords:** rhizosphere; soil microbiome; microbiome function; fertilizer, meta-genomics.

### **10.1 Introduction:**

Fertilization is an important method of improving soil fertility and quality and increasing crop yield [1], although it also influences the level of soil pollution [2], leaching of nitrate in ground water and surface waters, enhanced emissions of nitrous oxide [3], soil hardness and organic matter mineralization. In recent years, to mitigate the environmental impacts of excessive rates of chemical fertilization in agro ecosystems, the combined use of inorganic fertilizers with organic manures has attracted increasing interest. Organic fertilizer application not only improves soil organic matter content, preserves moisture and fertility and reduces losses of soil nutrients such as N, P and K, but also helps maintain soil pH stability [5]. In addition, an increasing number of research studies have demonstrated that highly anthropogenic fertilizers with straw significantly enhance bacterial activity [6] and greenhouse gas emissions [7]. The soil rhizosphere microbiome has a critical role in plant growth, nutrition, health and breeding [8, 9]. Kalivas et al. [2] concluded that the proportion of soil rhizosphere microorganisms (Proteobacteria and Acid bacteria) was higher in a no-fertilizer treatment. Fertilizers can exert profound effects on the biodiversity and structure

and functions of soil microbial communities [10]. Soil microbial and fungal diversity was found to decrease significantly with fertilization [11]. Previous studies have found that dominant microbes are adapted to particular soil conditions and play significant roles in the preservation and regulation of key processes [12, 13]. Ahmed et al. [14] reported that Proteobacteria, Actinobacteria, Gemmatimonadetes, Bacteroides, Formicetes and Acid bacteria can tolerate salty soil. The dominant microbes differ in different types of soil and are altered by fertilizers [15]. The nitrogen (N) cycle is a collection of important biogeochemical pathways mediated by microbial communities [16].

Microbial transformations of nitrogen are often depicted as cycles consisting of nitrogen fixation, nitrification, denitrification, anammox, assimilation and ammonification [17]. Studies have shown that ammonia-oxidizing bacteria, nitrogen fixing bacteria, nitrifying bacteria, denitrifying bacteria and cellulose-decomposing bacteria have an important impact on the nitrogen cycle, and most ammonia-oxidizing bacteria belong to Proteobacteria. At the taxonomic level, these are the largest and most diverse microbial species involved in soil organic nitrogen metabolism and nitrate reduction. Deng et al. [19] suggested that metagenomics can be used to reflect the structure and potential function of microbial communities. However, the role of microbes in ecosystem functions and agricultural productivity in response to the different fertilizers is complicated and elusive.



**Figure 10.1: Plant Rhizosphere Microbiome [18]**

## **10.2 Soil Microbiome Community and Function:**

The soil composition (bacteria, fungi, archaea and viruses), and the predominant genes were bacterial genes, which accounted for over 96% of the genes detected by metagenomic taxonomic analysis. The dominant phyla were Proteobacteria and Acid bacteria in bacteria, Ascomycota and Basidiomycota in fungi, and Crenarchaeota in archaea, and their levels

were altered by fertilizer. Moreover, the Proteobacteria, Basidiomycota, Crenarchaeota and Euryarchaeota relative abundances were highest in the NPK treatment and lowest in the organic fertilizer treatment. By contrast, Acid bacteria, Ascomycota and Euryarchaeota were lowest in the NPK treatment. In long-term fertilized soil, the pH decreased significantly with inorganic fertilizer.

Fertilizers influence not only soil chemical properties but also microbiome gene levels. Long-term NPK fertilizer application had a greater effect on microbiome genes than organic fertilizer and organic–inorganic fertilizers. Present study suggested that chemical fertilizer had more effects on nucleic acid transcription and protein transcription than organic fertilizer. This may be related to the significant effects of soil organic carbon on microbial metabolic pathways, which can dissolve organic carbon into CO<sub>2</sub> while providing cells with energy. Chemical fertilizer and organic fertilizer provide different types of nutrition for microorganism activities. Previous studies suggested that fertilizer can improve microbial metabolic activity, increase the number of single organisms, such as microbes, fungi and small animals, and accelerate the decomposition of macromolecular complexes to small complexes. We also found that chemical fertilizer had effects on antioxidant activity, enzyme activity and molecular transducer activity. The ribosome pathway was determined to be significantly enriched in each treatment by KEGG pathway analysis, followed by oxidative photosynthesis and carbon metabolism, possibly because fertilizer application affected cation transport and the biosynthesis of organic and amino acids.

Moreover, nitrogen chemical fertilizer application could increase environmental information processing, possibly because the N fertilizer had an impact on these processes. Organic fertilizer and chemical fertilizer provided different forms of nutrients to the soil and changed the content of soil organic carbon, active nitrogen and C: N ratio. These changes affected the decomposition, synthesis and transformation of microorganisms.

### **10.3 The Soil Microbiome Participating in N Cycling:**

The N-cycle is an important bio-geochemical cycle and is almost entirely performed by microbiome redox reactions. Fertilization can affect the soil N cycle, in which it plays a very important role. Therefore, it is important to understand how fertilizers affect the parts of the microbiome that participate in the N cycle, especially in long-term fertilized soil. Hydroxyl amine oxidoreductase (Hao) catalyzes the oxidation of NH<sub>2</sub>OH to NO<sub>2</sub><sup>-</sup>, and NPK improved this process. Similarly to results reported by Chen et al. [57], it was found that long-term fertilization with nitrogen had significant impacts on the diversity or community of amoA and hao genes. NarG, nirK, norZ, and norB and nosZ genes were used to reveal denitrification, including NO<sub>3</sub><sup>-</sup> to NO<sub>2</sub><sup>-</sup>, NO<sub>2</sub><sup>-</sup> to NO, NO to N<sub>2</sub>O and N<sub>2</sub>O to N<sub>2</sub> transformations. It was discovered that the NPK and NPK and organic fertilizer treatments increased the relative abundance of the narG, nosZ, norZ and norB genes and accelerated denitrification. Meng et al. [58] showed that long-term fertilization significantly influenced soil microbial community, NH<sub>4</sub><sup>+</sup> and NO<sub>3</sub><sup>-</sup> and the emission of N<sub>2</sub>O, and that these changes were due to long-term N fertilizer application. In addition, fertilizer application had a significant influence on microbiome active processes, especially hydrolase activity acting on carbon–nitrogen bonds, nitrogen compound metabolic processes and carbon–nitrogen ligase activity with glutamine as an amido-N donor.

## **10.4 Conclusion:**

Fertilizer application changed soil chemical properties: the organic fertilizer treatment increased soil pH, the NPK inorganic fertilizer decreased either the soil pH or NH<sub>4</sub><sup>+</sup>-N, and the NPK and organic fertilizer treatment also decreased soil pH but increased NH<sub>4</sub><sup>+</sup>-N. The soil microbiome consisted of bacteria, fungi, archaea and viruses, and the bacteria accounted for over 96% of the total genes.

The dominant phyla were Proteobacteria, Acid bacteria, Firmicutes (bacteria), Ascomycota, Basidiomycota (fungi) and Crenarchaeota (archaea), and fertilizer application did not change the soil microbiome composition and dominant phyla but changed the relative abundance of the microbiome components. Inorganic fertilizer-supplemented maize straw had more influence on the soil microbiome than other treatments. The genes that were most differentially expressed were enriched in 48 pathways in no fertilizer treatment vs. NPK, and we found that organic fertilizer and inorganic fertilizer both had a significant influence on metabolic processes, cellular processes, single-organism processes, binding, catalytic activity and structural molecule activity, cell parts, macromolecules and organelles. The NPK treatment rich in nucleic acid binding transcription factor activity, protein binding transcription factor activity, antioxidant activity, enzyme regulator activity, molecular transducer activity (molecular function), nucleoid, and extra cellular region (cellular component). The organic fertilizer and NPK plus organic fertilizer treatments increased microbial N fixation, and the NPK and NPK plus organic fertilizer treatments decreased amoA and amoB and accelerated denitrification.

## **10.5 References:**

1. Zhao, J.; Ni, T.; Xun, W.; Huang, X.; Huang, Q.; Ran, W.; Shen, B.; Zhang, R.; Shen, Q. Influence of straw incorporation with and without straw decomposer on soil bacterial community structure and function in a rice-wheat cropping system. *Appl. Microbiol. Biotechnology*. 2017, 101, 4761–4773.
2. Kalivas, A.; Ganopoulos, I.; Psomopoulos, F.; Grigoriadis, I.; Xanthopoulou, A.; Hatzigiannakis, E.; Osathanukul, M.; Tsafaris, A.; Madesis, P. Comparative metagenomics reveals alterations in the soil bacterial community driven by N-fertilizer and Amino 16(R) application in lettuce. *Genom. Data* 2017, 14, 14–17.
3. Yergeau, E.; Quiza, L.; Tremblay, J. Microbial indicators are better predictors of wheat yield and quality than N fertilization. *FEMS Microbiol. Ecol.* 2020, 96, fuz205.
4. Zhang, Y.; Li, C.; Wang, Y.; Hu, Y.; Li, X. Maize yield and soil fertility with combined use of compost and inorganic fertilizers on a calcareous soil on the North China Plain. *Soil Tillage Res.* 2016, 155, 85–94.
5. Zhang, B.Y.; Chen, T.L.; Wang, B. Effects of Long-term Uses of Chemical Fertilizer on Soil Quality. *Chin. Agric. Ence Bull.* 2010, 26, 182–187.
6. Tayyab, M.; Islam, W.; Arafat, Y.; Pang, Z.; Zhang, C.; Lin, Y.; Waqas, M.; Lin, S.; Lin, W.; Zhang, H. Effect of Sugar cane Straw and Goat Manure on Soil Nutrient Transformation and Bacterial Communities. *Sustainability* 2018, 10, 2361.
7. Hester, E.R.; Harpenslager, S.F.; van Diggelen, J.M.H.; Lamers, L.L.; Jetten, M.S.M.; Luke, C.; Lückner, S.; Welte, C.U. Linking Nitrogen Load to the Structure and Function of Wetland Soil and Rhizosphere Microbial Communities. *M-Systems* 2018, 3, e00214–e00217.

8. Mendes, L.W.; Raaijmakers, J.M.; de Hollander, M.; Mendes, R.; Tsai, S.M. Influence of resistance breeding in common bean on rhizosphere microbiome composition and function. *ISMEJ*. 2017, 12, 212–224.
9. Yang, Y.; Zhou, Z.; Li, X.; Liu, J. Bacterial diversity as affected by application of manure in red soils of subtropical China. *Biol. Fertile. Soils* 2017, 53, 639–649.
10. Shi, Y.; Ziadi, N.; Hamel, C.; Bélanger, G.; Abdi, D.; Lajeunesse, J.; Lafond, J.; Lalonde, R.; Shang, J. Soil microbial biomass, activity and community structure as affected by mineral phosphorus fertilization in grasslands. *Appl. Soil Ecol.* 2020, 146, 103391
11. Gu, S.; Hu, Q.; Cheng, Y.; Bai, L.; Liu, Z.; Xiao, W.; Gong, Z.; Wu, Y.; Feng, K.; Deng, Y.; et al. Application of organic fertilizer improves microbial community diversity and alters microbial network structure in tea (*Camellia sinensis*) plantation soils. *Soil Tillage Res.* 2019, 195, 104356. [Cross Ref]
12. Su, J.Q.; Xia, Y.; Yao, H.Y.; Li, Y.Y.; An, X.L.; Singh, B.K.; Zhang, T.; Zhu, Y.G. Metagenomic assembly unravel microbial response to redox fluctuation in acid sulfate soil. *Soil Biol. Biochem.* 2017, 105, 244–252.
13. Chen, W.; Teng, Y.; Li, Z.; Liu, W.; Ren, W.; Luo, Y.; Christie, P. Mechanisms by which organic fertilizer and effective microbes mitigate peanut continuous cropping yield constraints in a red soil of south China. *Appl. Soil Ecol.* 2018, 128, 23–34.
14. Ahmed, V.; Verma, M.K.; Gupta, S.; Mandhan, V.; Chauhan, N.S. Metagenomic Profiling of Soil Microbes to Mine Salt Stress Tolerance Genes. *Front. Microbiol.* 2018, 9, 159.
15. Das, S.; Gwon, H.S.; Khan, M.I.; Van Nostrand, J. D.; Alam, M. A.; Kim, P. J. Taxonomic and functional responses of soil microbial communities to slag-based fertilizer amendment in rice cropping systems. *Environ. Int.* 2019, 127, 531–539.
16. Gruber, N.; Galloway, J.N. An Earth-system perspective of the global nitrogen cycle. *Nature* 2008, 451, 293–296.
17. Kuypers, M.M.M.; Marchant, H.K.; Kartal, B. The microbial nitrogen-cycling network. *Nat. Rev. Microbiol.* 2018, 16, 263–276.
18. Soni, R.; Kumar, V.; Suyal, D.C.; Goel, R. Metagenomics of Plant Rhizosphere Microbiome. 2017, 978-981-10-5050-3\_12
19. Deng, Y.; Feng, K.; Wei, Z.; Liu, W.; Liang, Y.; Jin, D. Recent studies and applications of metagenomics in environmental engineering. *Chin. J. Environ. Eng.* 2016, 10, 3373–3382.