Eco. Env. & Cons. 29 (May Suppl. Issue) : 2023; pp. (S395-S398)
Copyright@ EM International
ISSN 0971–765X

DOI No.: http://doi.org/10.53550/EEC.2023.v29i03s.068

Sustainable agriculture through enhancement and understanding the micro biomes: A Review

Dilbag Singh[1], Livleen Shukla[1] and Shweta Sharma[2*]

[1]Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India
[2]Department of Zoology, CCS Haryana Agricultural University, Hisar, Haryana, India

(Received 15 December, 2022; Accepted 2 February, 2023)

ABSTRACT

As we all know that the Green Revolution increased the world's crop output via using different varieties of cereal which possess high-yielding capacity but these crops required high fertilizers, water supplies along with synthetic agrochemicals. The positive result of this revolution is the reduction of poverty and hunger but there are a lot of negative effects including increased soil degradation and chemical runoff. The role of microbes in benefit of agriculture is not new it is in use since 19th century which is the role of rhizobia in leguminous crops. Microbes possess various properties e.g. biopesticides, biofertilizers, biocontrol agent. From this information this review is designed to elaborate multiomics techniques for deeper understanding in the plant-microbiome association functionally and structurally also highlight the microbiome research area to improved agricultural outcomes.

Key words: *Biofertilizers, Biopesticides, Green revolution, Multiomics, Plant-Microbiome association.*

Introduction

Multiomics approach is the best way to understand the correlation of plant-microbiomes. This integrated multiomics approaches include the use of amplicon sequencing and metagenomics to reveal the composition of microbiomes followed by evaluation of their function via using meta transcriptomics (which revealed kingdom-level differences in the active rhizosphere microbiome of different cereals; e.g. sorghum under drought stress shows increased transcriptional activity of genes in root-associated micro biome which involved in carbohydrate and amino acid netabolism and their transport which is due to shifting of function and activity of actinobacteria) and metaproteomics (provided direct insights into the molecular phenotypes of microbial communities from therhizosphereand phyllosphere of agricultural plants) (Fig. 1) (Xu *et al.*, 2018; Bona *et al.*, 2019). and lastly with the help of metabolomics one can study the networks of interactions in which microbes participate (Trivedi *et al.*, 2021). Hence a mechanistic view can be provided on how individual microbes and microbial communities drive plant–microbiome interactions towards plant health and resilience to environmental stresses. **Core microbiome (Fig. 2)** are the common microbes

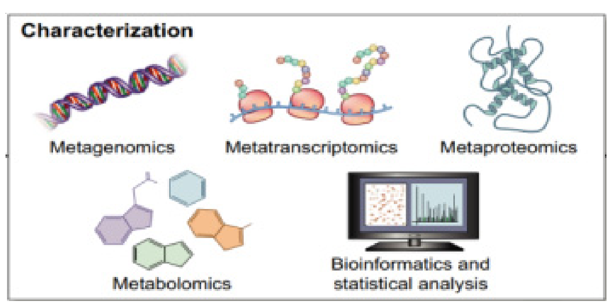

Fig. 1. Characterization of microbes using multiomics approach.

present in the host microbiome and their integration helps in the plant growth at different locations. Phyllogenetically different plants may show overlapping in core microbes showed their long association among plants (Blaustein *et al.*, 2017; Hamonts *et al.*, 2018; Compant *et al.*, 2019). These microbiome helps in plant colonization and their growth. Hence these core microbiota may provide a path to evaluate the plant-microbiome interaction and improve the growth of plants. On the other hand bioinformatics studies revealed other microbes "**Hub microbes**" which connected to other microbes and may control positively as well as negatively the abundance and function of other microbes as shown in attached figure (Hamonts *et al.*, 2018; Roman-Reyna *et al.*, 2019). Many studies revealed positive role of hub microbes hence the mechanistic role of these hub under stress conditions should be evaluated.

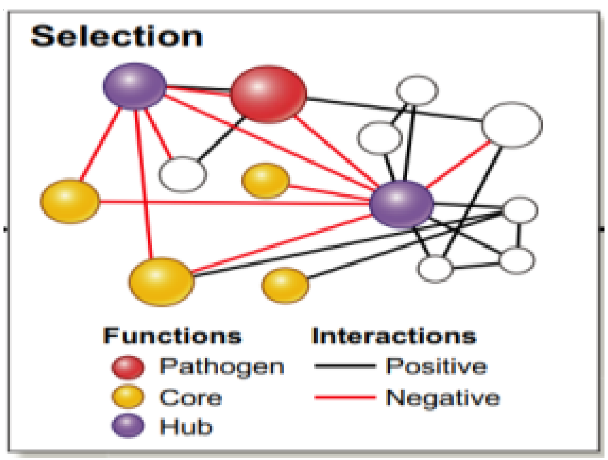

Fig. 2. Core microbiome.

What is the "impact of microbiomes on plant functions"?

Similar to the roles of microbiome in human gut; the microbiome of plant roots provide functional roles e.g. including nutrient uptake, growth promotion and disease suppression in their host (Berendsen *et al.*, 2012). These microbione via providing nutrient mobilization decreased the role of fertilizers; use of fertilizers causes environmental problems. Hence the use of microbes leads to a sustainable approach of agriculture. Also microbes act as *biocontrol agent* (Duran *et al.*, 2018).

Translational Phase: After obtaining huge data from the characterization of microbes we are on a page where microbiome based approaches are the best solution for the in-situ promotion of plant growth under biotic and abiotic stress along with a range of environmental conditions.

How can we achieve this "Phase"

A) Host-mediated microbiome engineering: For this aspect we must choose microbiome which are best adapted to a particular biome, resistant to random invasion, and also provide long-term benefits i.e. for multiple generation. Artificial selection of a particular microbiome for a particular plant during flowering, drought or in salt tolerance condition results in high production and benefits (Morella *et al.*, 2020; Gu *et al.*, 2020).

B) **Plant engineering**: Genes of interest in plants can be modulated (down-regulation/up-regulation) to influence rhizosphere/phyllosphere microbiome. For example mutation in rice nitrate transporter resulted into recruitment of specific microbiota which are responsible for higher NUE (Zhang *et al.*, 2019; Geddes *et al.*, 2019).

C) **Genetically modified microbes**: There are many genes in microbes which are involved in plant-microbe interaction and the modification in these genes may result into disease resistance, N-fixation and more production in plants which is beneficial for us and as well as these modification leads to reduction in the use of fertilizers, hence beneficial for the environment as well (Sheth *et al.*, 2010; Goold *et al.*, 2018).

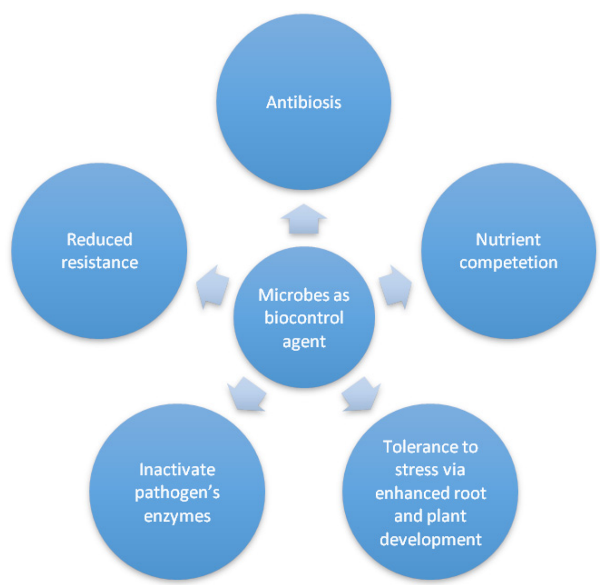

Fig. 3. How does microbes work as biocontrol agent.

D) Management practices to optimize the microbiome: Use of appropriate microbes is must in relation to the spatial, temporal factors e.g. few microbes perform their maximal activity in summer, so modified management practices and microbiome engineering leads to more sustainable agricultural production in the long term (Trivedi *et al.,* 2020).

After getting this much information now the question comes how to **commercialize** the products?

The first basic thing is Feature select (Syn Coms vs individual strains) which states there are more chances that cocktails of more than one beneficial microbe will establish properly and provide beneficial functions as compare to single-strain inoculant (Castrillo *et al.,* 2017; Niu *et al.,* 2017; Carrion *et al.,* 2019). Then comes the formulation (which is critical for successful microbial inoculant which is basically a consortium containing gram-negative, non-spore forming bacteria determining their stability and viability during various stages of production until their appropriate application). Formulation can be of dry or wettable form and they are important for the companies which may develop their own proprietary formulations (Bashan *et al.,* 2014; Jackson, 2017). For example PUSA decomposer in which microbes are formulated in capsule and have the capability to degrade/decompose paddy straw. After formulation we come to delivery part how to deliver these beneficial microbes so that their efficacy is highest with less labour in monitoring. At last question comes how and where to store? The delivery system may vary with respect to the crop some microbe well established when given to the seed stage some on the root part so it basically depends on the plant. Literature shows that the shelf-life of microbial consortium is highest when stored in low temperature and humidity condition. Last but not the least come the role of regulatory agencies which will be involved in proper commercialization of the product designed to establish an early dialogue with the registered agency to facilitate the registration process to prevent patent and IPR issues.

Conclusion

Keeping in mind this scenario, i.e. a microbe or microbial consortia identified by one of the several approaches outlined earlier was successfully formulated, delivered and shown to have field efficacy. These microbial consortium not only enhance the crop productivity but also help the crop to cope up with several stresses including biotic and abiotic, microbes' biocontrol property helps in disaese management of crops. Clearly, a holistic approach towards the use of microbial products, wherein the products are targeted for a specific field environment and cropgenotype.

Future prospective: Before choosing the microbial species, a proper knowledge of the environment, genes of plants and microbes should be known. Then modification should be made in such genes which will lead to reduction in the use of fertilizers, water and results into enhances production and this approach will be environmental friendly. Then the formulation of this consortium should be eco-friendly and economic and lastly it should store microbes so that their efficacy comes out more and we can store them for longer period. This type of approach will be resulted into a sustainable agricultural which means it'll be environment friendly, easy to use and also economic and is in the approach of common farmers. Also the production of crops will be higher and also have no side effects on the health.

References

Bashan, Y., de-Bashan, L. E., Prabhu, S. R. and Hernandez, J. P. 2014. Advances in plant growth-promoting bacterial inoculant technology: formulations and practical perspectives (1998-2013). *Plant and Soil.* 378(1): 1-33.

Berendsen, R. L., Pieterse, C. M. and Bakker, P. A. 2012. The rhizosphere microbiome and plant health. *Trends in Plant Science.* 17(8) : 478-486.

Blaustein, R. A., Lorca, G. L., Meyer, J. L., Gonzalez, C. F. and Teplitski, M. 2017. Defining the core citrus leaf- and root-associated microbiota: Factors associated with community structure and implications for managing huanglongbing (citrus greening) disease. *Applied and Environmental Microbiology.* 83(11): e00210-17.

Bona, E., Massa, N., Novello, G., Boatti, L., Cesaro, P., Todeschini, V.A. and Gamalero, E. 2019. Metaproteomic characterization of the *Vitis vinifera* rhizosphere. *FEMS Microbiology Ecology.* 95(1): fiy204.

Carrión, V. J., Perez-Jaramillo, J., Cordovez, V., Tracanna, V., De Hollander, M., Ruiz-Buck, D. and Raaijmakers, J. M. 2019. Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. *Science.* 366(6465): 606-612.

Castrillo, G., Teixeira, P.J.P.L., Paredes, S. H., Law, T.F., De Lorenzo, L., Feltcher, M.E. and Dangl, J.L. 2017. Root microbiota drive direct integration of phosphate

stress and immunity. *Nature.* 543(7646): 513-518.
Compant, S., Samad, A., Faist, H. and Sessitsch, A. 2019. A review on the plant microbiome: ecology, functions, and emerging trends in microbial application. *Journal of Advanced Research.* 19 : 29-37.
Durán, P., Thiergart, T., Garrido-Oter, R., Agler, M., Kemen, E., Schulze-Lefert, P. and Hacquard, S. 2018. Microbial interkingdom interactions in roots promote Arabidopsis survival. *Cell.* 175(4): 973-983.
Geddes, B.A., Paramasivan, P., Joffrin, A., Thompson, A.L., Christensen, K., Jorrin, B. and Poole, P. S. 2019. Engineering transkingdom signalling in plants to control gene expression in rhizosphere bacteria. *Nature Communications.* 10(1): 1-11.
Goold, H.D., Wright, P. and Hailstones, D. 2018. Emerging opportunities for synthetic biology in agriculture. *Genes.* 9(7): 341.
Gu, Y., Dong, K., Geisen, S., Yang, W., Yan, Y., Gu, D. and Friman, V.P. 2020. The effect of microbial inoculant origin on the rhizosphere bacterial community composition and plant growth-promotion. *Plant and Soil.* 452(1): 105-117.
Hamonts, K., Trivedi, P., Garg, A., Janitz, C., Grinyer, J., Holford, P. and Singh, B. K. 2018. Field study reveals core plant microbiota and relative importance of their drivers. *Environmental Microbiology.* 20(1): 124-140.
Jackson, T. A. 2017. Entomopathogenic bacteria: mass production, formulation, and quality control. In *Microbial Control of Insect and Mite Pests* (pp. 125-139). Academic Press.
Morella, N. M., Weng, F. C. H., Joubert, P. M., Metcalf, C. J. E., Lindow, S. and Koskella, B. 2020. Successive passaging of a plant-associated microbiome reveals robust habitat and host genotype-dependent selection. *Proceedings of the National Academy of Sciences.* 117(2) : 1148-1159.
Niu, B., Paulson, J. N., Zheng, X., and Kolter, R. 2017. Simplified and representative bacterial community of maize roots. *Proceedings of the National Academy of Sciences.* 114(12): E2450-E2459.
Roman-Reyna, V., Pinili, D., Borja, F. N., Quibod, I. L., Groen, S. C., Mulyaningsih, E. S. and Oliva, R. 2019. The rice leaf microbiome has a conserved community structure controlled by complex host-microbe interactions. *Bio. Rxiv.* 615278.
Sheth, R. U., Cabral, V., Chen, S. P. and Wang, H. H. 2016. Manipulating bacterial communities by in situ microbiome engineering. *Trends in Genetics.* 32(4): 189-200.
Trivedi, P., Leach, J. E., Tringe, S. G., Sa, T. and Singh, B. K. 2020. Plant–microbiome interactions: from community assembly to plant health. *Nature Reviews Microbiology.* 18(11): 607-621.
Trivedi, P., Mattupalli, C., Eversole, K. and Leach, J. E. 2021. Enabling sustainable agriculture through understanding and enhancement of microbiomes. *New Phytologist.* 230(6): 2129-2147.
Xu, J., Zhang, Y., Zhang, P., Trivedi, P., Riera, N., Wang, Y. and Wang, N. 2018. The structure and function of the global citrus rhizosphere microbiome. *Nature Communications.* 9(1): 1-10.
Zhang, J., Liu, Y. X., Zhang, N., Hu, B., Jin, T., Xu, H. and Bai, Y. 2019. NRT1. 1B is associated with root microbiota composition and nitrogen use in field-grown rice. *Nature Biotechnology*. 37(6): 676-684.