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Editorial

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Biodiversity and biotechnological applications of novel plant growth promoting methylotrophs

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Editorial

Methylotrophic bacterial community is a very important group of bacteria utilizing reduced carbon compounds. Methylotrophic bacteria are well enough to survive in all types of environmental conditions including acidic/alkaline habitats,[1–3] hyper saline,[4,5] drought,[6–8] low temperature[9–11] and high temperature.[6,12,13] The methylotrophic microbes help plant for adaptation under diverse unfavourable environmental conditions. The pink pigmented facultative methylotrophic (PPFMs) bacteria is abundantly reported as plant microbiomes (epiphytes, endophytes, rhizospheric).[11,13,14] The methylotrophic microbes could be promote the plant growth and soil health for sustainable agriculture directly by N2-fixation fixation; P, K and Zn solubilization; production of Fe-chelating compounds; production of PGP hormones such gibberellic acids, auxin and cytokinin and ACC deaminase activities[6,11,13,15] or by in-directly by production of siderophores, ammonia, HCN, enzymes and secondary metabolites.[16,17] The plant growth promoting methylotrophs as single bioinoculants or with co-inoculated as microbial consortium may be use as bioinoculants/biofertilizers of biocontrol agents for enhanced crops production and soil fertility for sustainable agriculture.[18–21]

The different class α, β and γ–proteobacteria of methylotrophic bacteria communities have been reported worldwide. The class α-proteobacteria has been reported as most dominant followed by β–proteobacteria. The novel methylotrophic microbes have been isolated and characterized from different habitats worldwide including *Methylocella silvestris* BL2T , *Methylocella palustris* KT, *Methyloferula stellata* AR4T and *Methylocapsa acidiphila* B2T from acidic soil;[22–25] Methylobacterium tarhaniae N4211T from arid soil;[26] *Methylobacterium iners* 5317S-33T and *Methylobacterium aerolatum* 5413S-11T from air sample;[27] *Methylobacterium adhaesivum* AR27T and *Methylobacterium isbiliense* AR24T from drinking water;[28,29] Methylobacterium brachiatum B0021T, *Methylobacterium gregans* 002-074T, *Methylobacterium komagatae* 002-079T, *Methylobacterium persicinum* 002-165T and *Methylobacterium tardum* RB677T from freshwater sample;[30] *Methylobacterium organophilum* XX, *Methylotenera versatilis* 301T and *Methylotenera mobilis* JLW8T from lakes;[31–33] *Methylobacterium brachythecii* 99bT, *Methylobacterium cerastii* C44, *Methylobacterium gnaphalii* 23eT, *Methylobacterium gossipiicola* Gh-105T, *Methylobacterium haplocladii* 87eT, *Methylobacterium oxalidis* 35aT, *Methylobacterium phyllosphaerae* B27T, *Methylobacterium phyllostachyos* BL47T, *Methylobacterium platani* PMB02T, *Methylobacterium pseudosasicola* BL36T, *Methylobacterium thuringiense* C34T, *Methylobacterium trifolii* TA73T, from leaf surface of diverse plants;[34–42] *Methylobacterium aminovorans* TH-1, *Methylobacterium goesingense* iEII3, *Methylobacterium soli* YIM 48816T, *Methylobacterium suomiense*, F20T, *Methylobacterium thiocyanatum*, *Methylobacterium variabile* GR3T, *Methylopila capsulata* IM1T, and *Methylopila helvetica* VKMB-189 from soil samples[43–50]

To understand the mechanisms of plant growth promotion and genes involved in plant growth promotion there are many reports on whole genome sequences of methylotrophic bacteria are available at NCBI GenBank database (https://www.ncbi.nlm.nih.gov) *Methylobacterium populi* BJ001, *Methylobacterium extorquens* CM4, *Methylobacterium nodulans* ORS 2060, Methylobacterium aquaticum MA-22A, Methylobacterium radiotolerans JCM 2831, *Methyloferula stellata* AR4, *Methylotenera mobilis* JLW8, *Methylotenera versatilis* 301, *Methylobacterium* sp. AMS5, *Methylotenera versatilis* 301 *Methylotenera mobilis* JLW8, *Methylovorus glucosetrophus* SIP3-4, *Methylovorus glucosetrophus* SIP3-4, *Methylobacterium mesophilicum* SR1.6/6, and *Methylobacterium indicum* SE2.11

Plant-associated methylotrophs produce PGP phytohormones such as auxins, gibberellins and cytokinin by *Methylobacterium extorquens* IIWP-43, *M. extorquens* MP1, *M. mesophilicum* B-2143, *M. mesophilicum* HHS1-36, *M. mesophilicum* IIWP-45, *M. mesophilicum* NIAW1-41, *M. phyllosphaerae* HHS2-67, *M. radiotolerans* HHS1-45, *M. radiotolerans* IHD-35 and *M. zatmanii* MS4. Many methylotrophs has been reported to fix N2 e.g. *Methylobacterium mesophilicum* B-2143, *M. nodulans* 2060T, and Methylobacterium sp. THD-3511,[51–56]. A vast number methylotrophs with P-solubilizing ability have been reported *Methylobacillus arboreus* Iva, M. extorquens G10, M. extorquens IIWP-43, *M. lusitanum* MSF 32, *M. mesophilicum* IIWP-45, *M. mesophilicum* NIAW1-41, M. radiotolerans IHD-35, *Methylopila musalis* MUSA and *Methylovorus menthalis* MM.[2,6,13,57,58]

Conclusion

The methylotrophic microbes from diverse sources have potential applications in agriculture, industry and allied sectors. The methylotrophic bacteria could be used for plant growth and soil health for sustainable agriculture when inoculated as single or as consortium under the natural as well as abiotic stress conditions.

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Conflict of interest

All authors declare that they have no conflicts of interest to this work.

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