Editorial

Impact of global change on the plant microbiome

Plant-associated microorganisms maybe invisible to the naked eye, yet they play a key role in the future sustainability of terrestrial ecosystems – from arable lands to rainforests, through tundra and taiga to deserts. It is now widely recognized that climate change dramatically impacts plant performance and physiology. However, plants are not living alone, they are supra-organisms hosting a wide range of commensal, beneficial and detrimental microbes. The plant with its associated microbiota – the collection of all microorganisms in a location – faces altered environmental conditions as a result of a rapidly changing climate. The signs of climate change are undeniable, and the dramatic impact for plant and microbial inhabitants of our planet is a serious concern. Warming strikingly shifts both the phylogenetic and functional structures of soil microbial communities, which lead to unknown alterations in communities and processes. Similarly, plants and their microbial consortium are directly impacted by changing environmental conditions leading to different plant interaction characteristics, altered ecology, as well as a change in functioning. Most importantly, the plant microbiota might respond to changes in plant physiology, which could affect the microbial diversity and functioning in a poorly known, but critical, feedback loop. Microorganisms might also play an important role for the plant in regard to adaptation to changing conditions. Describing, understanding and predicting the impacts of anthropogenically-driven climate change on plant–microbe interactions and ecosystem functioning is therefore a scientific and societal challenge.

In this *New Phytologist* Special Issue dedicated to the plant microbiota, several experts in the field discuss the microbial contributions to climate change. In so doing they consider the effects of global warming, extreme weather, flooding and other consequences of climate change on microbial communities in terrestrial ecosystems and on host–microbiota interactions. They explore open questions and research needs including: *How do global environmental changes affect the phylogenetic diversity and physiology of the plant-associated microorganisms in the environment? What are the consequences of this change on plant biology and development? How can the effects of global change on microbial communities be mitigated? How can we deal with both the spatial and temporal scales of research questions arising in global change microbiology? What are the current open questions, research needs and priorities?* As a follow-up, this collection of papers describe how climate change affects plant–microbe associations, which mechanisms are involved, and what effects on ecosystem function can be expected in the long term. The authors explore the plant-associated microbiota world across all scales from the genomic to ecosystem level, including above- and below-ground interactions. They address the effects of global environmental changes on the diversity, functioning and evolution of the plant microbiota and how these changes are altering different types of interactions, including symbiotic and endophytic associations, as well as multi-partite interactions. Several studies also investigated how beneficial microorganisms play a role in plant adaptation to stress conditions.

The overarching objective of this collection is to provide a platform for discussion of the most pressing issues influencing microbial communities and their interactions with their host plant and then, to integrate information from different approaches. With this in mind, we aim to create a systematic framework to understand and improve plant–microbe interactions under typical stress conditions (e.g., increase of CO_2, drought, soil warming, salinity), related to global environmental changes. Of note, the articles in this Special Issue discuss the interactions of plants with a wide range of microbes, including bacteria or fungi, beneficial microbes or pathogens and cover molecular approaches to ecosystems implications. Through this collection we hope to obtain and further stimulate a systematic understanding and interest in the interaction between plants, beneficial microorganisms, pathogens and environment.

According to the different original research articles, global change factors are expected to have profound impacts not only on the composition, but also on the function of the plant microbiota. These effects can induce changes in the microbiota either directly, or indirectly via global change-induced modulation of the host and/or the environment (**Fig. 1a**). In particular, drought was found to alter the composition and diversity of arbuscular mycorrhizal (AM) fungal communities (Fu *et al.*, 2022, in this issue pp. 000–000), to induce shifts in aboveground microbial assemblages (Debray *et al.,* 2022, in this issue pp. 000–000) and to trigger transcriptional acclimation in the etomycorrhizal fungus *Suillus pungens* (Erlandson *et al.,* 2022, in this issue pp. 000–000). In addition to water deficits, warming was reported to modulate turnover of mycorrhizal fungal mycelium in peatland via shifts in microbial decomposer assemblages (Maillard *et al.,* 2022, in this issue pp. 000–000) and is predicted to alter the assembly of nitrogen fixing taxa in Sub-Arctic tundra (Klarenberg *et al.,* 2022, in this issue pp. 000–000), (**Fig. 1b**). These data, together with the observation that 1) high nitrogen fertilisation can disrupt normal temporal dynamics of AM fungal communities in an agricultural field (Babalola *et al.,* 2022, in this issue pp. 000–000), and 2) replacement of native birch by fast growing spruce extensively modulate soil bacterial and fungal assemblages in boreal forests (Mundra *et al.,* 2022, in this issue pp. 000–000), illustrate the invisible, yet major, impacts that anthropogenically-driven perturbations have on belowground microbial populations (**Fig. 1b**). Whether these global change-induced perturbations in belowground microbial populations will have major consequences on plant health, plant distribution, and plant adaptation to stress remains a key unanswered question.

Given that microbes have interacted with their host plants for 450 million years combined with reports of evidence for co-evolution (i.e., Abdelfattah *et al.,* 2022, in this issue pp. 000–000), it becomes clear that numerous microbial functions have been co-opted by plants to promote adaptation to environmental constraints. Therefore, the potential to use the plant microbiome to promote host tolerance to global change stressors is high (**Fig. 1b**). Different strategies have been discussed here, including 1) iterative root microbiome selection to alleviate salt stress (King *et al.,* 2022, in this issue pp. 000–000); 2) use of habitat-adapted microbiomes to promote host tolerance to warming (Carell *et al.,* 2022, in this issue pp. 000–000); and 3) utilization of microbes from extreme desert environments (Maldonado *et al.,* 2022, in this issue pp. 000–000). Particularly, the observation that habitat-adapted microbial communities can transmit thermotolerance to *Sphagnum* peatmoss and can promote resilience to warming demonstrates that rapid adaptation to stress in the host can occur via the microbiota (Carell *et al.,* 2022). Taken together, the results suggest that microbial commensals and symbionts might represent key components promoting host survival and rapid adaptation to environmental perturbations.

This collection also includes a number of Tansley reviews and insights, Research reviews and Viewpoints that discuss various aspects including the role of beneficial fungi for promoting stress tolerance (Almario *et al.,* 2022, in this issue pp. 000–000), the potential of root metabolome engineering for modulating beneficial plant–microbe interactions (Hong *et al.,* 2022; in this issue pp. 000–000), the consequences of climate change on phyllosphere/rhizosphere microbiomes and mountain microbial biogeography (Zhu *et al.,* 2022, pp. 000–000; Trivedi *et al.,* 2022, pp. 000–000; Wang *et al.,* 2022, pp. 000–000), as well as the consequences of introducing probiotic microbial taxa in ecosystems (Moore *et al.,* 2022, in this issue pp. 000–000). The articles in the collection also stress the importance of considering host-specificity (Semchenko *et al.,* 2022, in this issue pp. 000–000), eco-evolutionary aspects (Angulo *et al.,* 2022, in this issue pp. 000–000), and belowground–

aboveground diversity linkages (Fei *et al.,* 2022, in this issue pp. 000–000) to understand how microbes affect plant ecological responses to global change.

We hope that this collection of papers will result in a better understanding on how microbial colonization and assemblages, plant–pathogen and plant–beneficial microorganism interactions are affected in altered climate conditions. Additional knowledge should be obtained on the follow-up effects on ecosystem functioning and to which extent beneficial microorganisms may alleviate stress conditions due to climate change. This will rely on developing interdisciplinary research projects that aim to understand how microbial activities and metabolic fluxes alter as climate, precipitation, and temperatures change globally. Shedding light on these questions should include 'genes-to-ecosystems' approaches. The studies presented here are intended to highlight and further stimulate research on the functioning and role of the plant microbiota, and its interaction with plants under stress. Defining the components, dynamics, functions and interactions of the core plant-associated microbiota will assist in developing microbiome-based solutions to create healthy, resilient and sustainable plant ecosystems.

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References

Abdelfattah, A., Tack, A.J.M., Wasserman, B., Liu, J., Berg, G., Norelli, J., Droby, S. and Wisniewski, M. 2021. Evidence for host–microbiome co-evolution in apple. *New Phytologist* https://doi.org/10.1111/nph.17820

Almario, J., Fabiańska, I., Saridis, G. and Bucher, M. 2022. Unearthing the plant–microbe quid pro quo in root associations with beneficial fungi. *New Phytologist* https://doi.org/10.1111/nph.18061

Angulo, V., Beriot, N., Garcia-Hernandez, E., Li, E., Masteling, R. and Lau, J.A. 2022. Plant–microbe eco-evolutionary dynamics in a changing world. *New Phytologist* https://doi.org/10.1111/nph.18015

Babalola, B.J., Li, J., Willing, C.E., Zheng, Y., Wang, Y.-L., Gan, H.-Y., Li, X.-C., Wang, C., Adams, C.A., Gao, C. and Guo, L.-D. 2022. Nitrogen fertilisation disrupts the temporal dynamics of arbuscular mycorrhizal fungal hyphae but not spore density and community composition in a wheat field. *New Phytologist* https://doi.org/10.1111/nph.18043

Carrell, A.A., Lawrence, T.J., Cabugao, K.G.M., Carper, D.L., Pelletier, D.A., Lee, J.H., Jawdy, S.S., Grimwood, J., Schmutz, J., Hanson, P.J., Shaw, A.J. and Weston, D.J. 2022. Habitat-adapted microbial communities mediate Sphagnum peatmoss resilience to warming. *New Phytologist* https://doi.org/10.1111/nph.18072

Debray, R., Socolar, Y., Kaulbach, G., Guzman, A., Hernandez, C.A., Curley, R., Dhond, A., Bowles, T. and Koskella, B. 2022. Water stress and disruption of mycorrhizas induce parallel shifts in phyllosphere microbiome composition. *New Phytologist* https://doi.org/10.1111/nph.17817

Erlandson, S.R., Margis, R., Ramirez, A., Nguyen, N., Lofgren, L.A., Liao, H.-L., Vilgalys, R., Kennedy, P.G. and Peay, K.G. 2022. Transcriptional acclimation and spatial differentiation characterize drought response by the ectomycorrhizal fungus Suillus pungens. *New Phytologist* https://doi.org/10.1111/nph.17816

Fei, S., Kivlin, S.N., Domke, G.M., Jo, I., LaRue, E.A. and Phillips, R.P. 2022. Coupling of plant and mycorrhizal fungal diversity: its occurrence, relevance, and possible implications under global change. *New Phytologist* https://doi.org/10.1111/nph.17954

Fu, W., Chen, B., Rillig, M.C., Jansa, J., Ma, W., Xu, C., Luo, W., Wu, H., Hao, Z., Wu, H., Zhao, A., Yu, Q. and Han, X. 2022. Community response of arbuscular mycorrhizal fungi to extreme drought in a cold-temperate grassland. *New Phytologist* https://doi.org/10.1111/nph.17692

Hong, Y., Zhou, Q., Hao, Y. and Huang, A.C. 2022. Crafting the plant root metabolome for improved microbe-assisted stress resilience. *New Phytologist* https://doi.org/10.1111/nph.17908

King, W.L., Kaminsky, L.M., Gannett, M., Thompson, G.L., Kao-Kniffin, J. and Bell, T.H. 2022. Soil salinization accelerates microbiome stabilization in iterative selections for plant performance. *New Phytologist* https://doi.org/10.1111/nph.17774

Klarenberg, I.J., Keuschnig, C., Russi Colmenares, A.J., Warshan, D., Jungblut, A.D., Jónsdóttir, I.S. and Vilhelmsson, O. 2022. Long-term warming effects on the microbiome and nifH gene abundance of a common moss species in sub-Arctic tundra. *New Phytologist* https://doi.org/10.1111/nph.17837

Maillard, F., Fernandez, C.W., Mundra, S., Heckman, K.A., Kolka, R.K., Kauserud, H. and Kennedy, P.G. 2022. Warming drives a 'hummockification' of microbial communities associated with decomposing mycorrhizal fungal necromass in peatlands. *New Phytologist* https://doi.org/10.1111/nph.17755

Maldonado, J.E., Gaete, A., Mandakovic, D., Aguado-Norese, C., Aguilar, M., Gutiérrez, R.A. and González, M. 2022. Partners to survive: Hoffmannseggia doellii root-associated microbiome at the Atacama Desert. *New Phytologist* https://doi.org/10.1111/nph.18080

Moore, J.A.M., Abraham, P.E., Michener, J.K., Muchero, W. and Cregger, M.A. 2022. Ecosystem consequences of introducing plant growth promoting rhizobacteria to managed systems and potential legacy effects. *New Phytologist* https://doi.org/10.1111/nph.18010

Mundra, S., Kauserud, H., Økland, T., Nordbakken, J.-F., Ransedokken, Y. and Kjønaas, O.J. 2022. Shift in tree species changes the belowground biota of boreal forests. *New Phytologist* https://doi.org/10.1111/nph.18109

Semchenko, M., Barry, K.E., de Vries, F.T., Mommer, L., Moora, M. and Maciá-Vicente, J.G. 2022. Deciphering the role of specialist and generalist plant–microbial interactions as drivers of plant–soil feedback. *New Phytologist* https://doi.org/10.1111/nph.18118

Trivedi, P., Batista, B.D., Bazany, K.E. and Singh, B.K. 2022. Plant–microbiome interactions under a changing world: responses, consequences and perspectives. *New Phytologist* https://doi.org/10.1111/nph.18016

Wang, J., Hu, A., Meng, F., Zhao, W., Yang, Y., Soininen, J., Shen, J. and Zhou, J. 2022. Embracing mountain microbiome and ecosystem functions under global change. *New Phytologist* https://doi.org/10.1111/nph.18051

Zhu, Y.-G., Xiong, C., Wei, Z., Chen, Q.-L., Ma, B., Zhou, S.-Y., Tan, J., Zhang, L.-M., Cui, H.-L. and Duan, G.-L. 2022. Impacts of global change on the phyllosphere microbiome. *New Phytologist* https://doi.org/10.1111/nph.17928

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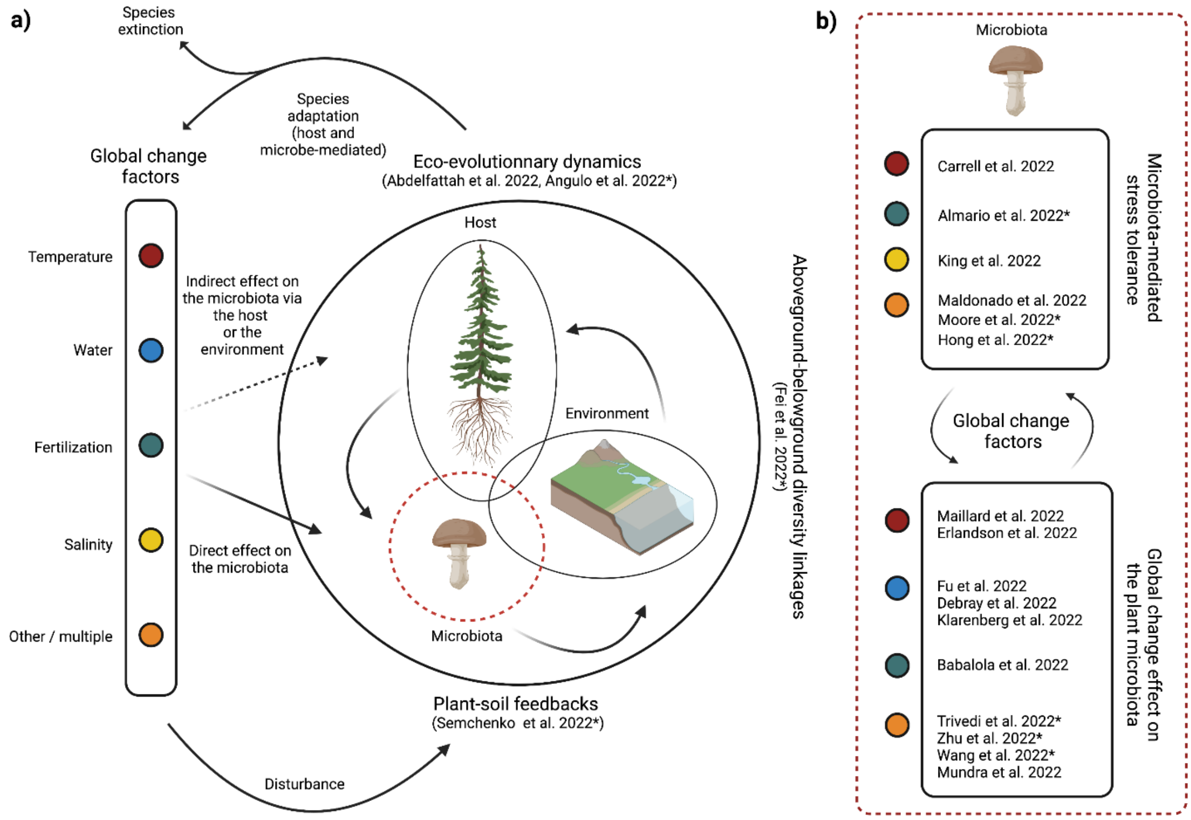

Fig. 1: A collection of articles to understand how global change factors affect plant–microbiota associations. a) Direct and indirect effects of global change factors on the plant microbiota. Indirect effects occur via the host–environment–microbiota triangle. b) Global change factors alter plant microbiota assemblages and modulate beneficial plant–microbe interactions. Plant adaptation to rapid environmental changes is expected to depend on plant–microbiota associations. The 20 articles of this *New Phytologist* Special Issue are highlighted according to the respective themes. Reviews and Viewpoints are indicated by an asterisk.