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DOI

[10.1016/j.copbio.2021.06.016](https://doi.org/10.1016/j.copbio.2021.06.016)

Publication date

2021

Document Version

Final published version

Published in

Current Opinion in Biotechnology

License

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[Link to publication](#)

Citation for published version (APA):

Zancarini, A., Westerhuis, J. A., Smilde, A. K., & Bouwmeester, H. J. (2021). Integration of omics data to unravel root microbiome recruitment. *Current Opinion in Biotechnology*, 70, 255-261. <https://doi.org/10.1016/j.copbio.2021.06.016>

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Integration of omics data to unravel root microbiome recruitment[☆]

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The plant microbiome plays an essential role in supporting plant growth and health, but plant molecular mechanisms underlying its recruitment are still unclear. Multi-omics data integration methods can be used to unravel new signalling relationships. Here, we review the effects of plant genetics and root exudates on root microbiome recruitment, and discuss methodological advances in data integration approaches that can help us to better understand and optimise the crop–microbiome interaction for a more sustainable agriculture.

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Current Opinion in Biotechnology 2021, **70**:255–261

This review comes from a themed issue on **Plant biotechnology**

Edited by **Robert Schuurink** and **Harro Bouwmeester**

For a complete overview see the [Issue](#) and the [Editorial](#)

Available online 6th July 2021

<https://doi.org/10.1016/j.copbio.2021.06.016>

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Introduction

The current challenge in agriculture is to be able to increase crop yield under sustainable conditions to feed the growing world population without harming the environment. The plant microbiome could play an essential role in achieving this challenge, as it is becoming increasingly clear that it plays an essential role in supporting plant growth and health. Advances in data analysis – such as multivariate analyses, differential abundance testing methods and machine learning methods – now enable us to link candidate microbes to a phenotype of interest (e.g. plant growth, yield, nutrient uptake efficiency, tolerance to disease) [1–3]. However, to be able to select plants that recruit these beneficial microbes, it is essential that the

molecular mechanisms underlying microbiome recruitment are unravelled. With the advent of the omics technologies, we can characterise plants in great detail using (epi-)genomics, transcriptomics, proteomics and metabolomics. Through the development of new data analysis paradigms, in principle, these omics data could be related to the associated microbiome (Figure 1). In this review we will discuss the different advanced statistical approaches that have been developed to analyse and integrate plant omics with microbiome data to propose new mechanistic hypotheses for root microbiome recruitment and its effect on plant phenotype.

Plant genetics underlying plant microbiome recruitment

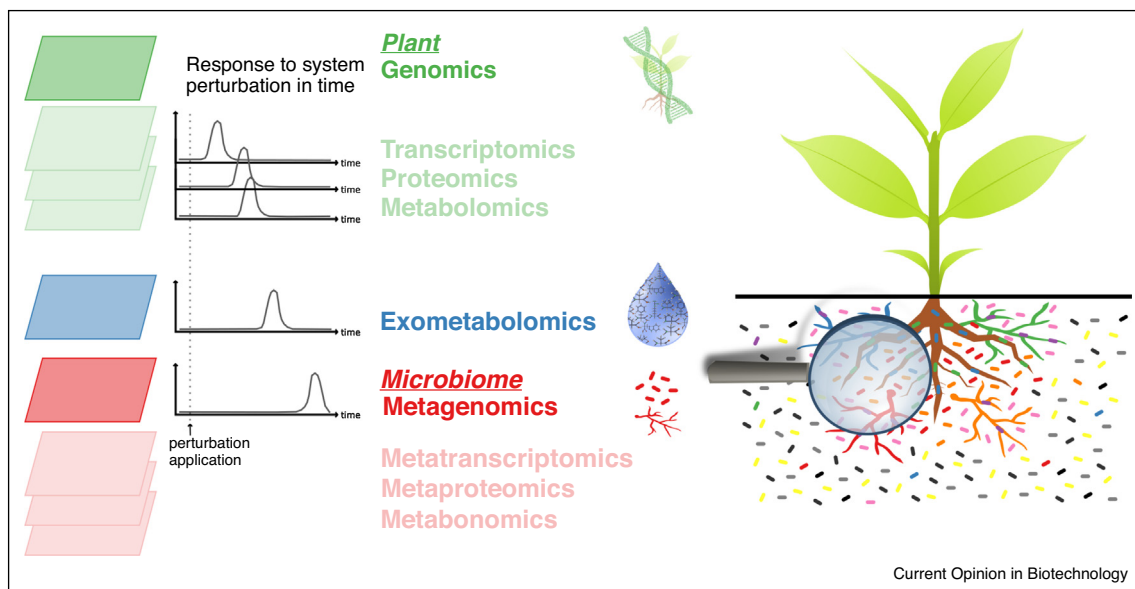
Traditional Genome Wide Association Studies (GWAS)

Development of the next-generation sequencing technologies and their decreasing costs have allowed high-throughput plant genotyping using large numbers of single nucleotide polymorphisms (SNPs). This has enabled the use of mapping approaches to identify genes underlying plant traits of interest, through QTL mapping and GWAS [4–6]. Since a number of years, also the plant microbiome is being used as a quantitative plant trait in GWAS to find plant genes underlying microbiome recruitment using mixed linear models [1,7,8^{*},9,10]. This confirmed the notion that the plant genotype drives its associated microbial communities, and linked plant genes involved in stress response, kinase activity, cell wall integrity, root development and carbohydrate metabolism to the occurrence of specific taxa [7,8^{*},9,10]. Interestingly, in maize, the predicted bacterial metabolic functions displayed a higher and more significant heritability than the diversity and relative abundance of individual taxa [1]. In future studies, the use of shotgun metagenomics data will further improve the mapping of microbial functions, as was recently demonstrated for the rice phyllosphere microbiome [10].

Nevertheless, identifying the underlying plant loci involved in the microbiome recruitment remains challenging. First, only a small percentage of the variation in the microbiome is generally explained by the plant genotype and just few microbiome traits are usually heritable. Moreover, microbiome recruitment seems to mostly be a

[☆] Given his role as Guest Editor, Harro Bouwmeester had no involvement in the peer-review of this article and has no access to information regarding its peer-review. Full responsibility for the editorial process for this article was delegated to Rob Schuurink.

Figure 1



Use of omics data to unravel plant microbiome recruitment.

Integration of multiple omics data sets, such as genomics, epigenetics, transcriptomics, proteomics, metabolomics (defined here as the metabolite profile in an organism), exometabolomics (defined here as the metabolite profile secreted by an organism), metagenomics, metatranscriptomics, metaproteomics and metabonomics (defined here as the metabolite profile from complex systems, such as microbial communities) to unravel the plant-microbiome interaction.

polygenic trait. So, the current GWAS models, even with enough power, often fail to detect the microbiome recruitment loci, as discussed elsewhere in this issue [11]. If candidate genes are identified, reproducibility and validation of these candidates using plant mutants and synthetic communities are challenging. In human-microbiome GWAS, results are often difficult to compare between studies [12,13]. For plants, Beilsmith *et al.* proposed a workflow, including thorough quantification and standardized protocols [14]. Also, as environmental conditions are a major component of the variability, GWAS will need to be done across different environmental conditions to test the effect of the environment on candidate genes. Recently, Brachi *et al.* were able to identify heritable microbial hubs that are affected by plant genomics traits across different environmental conditions [15].

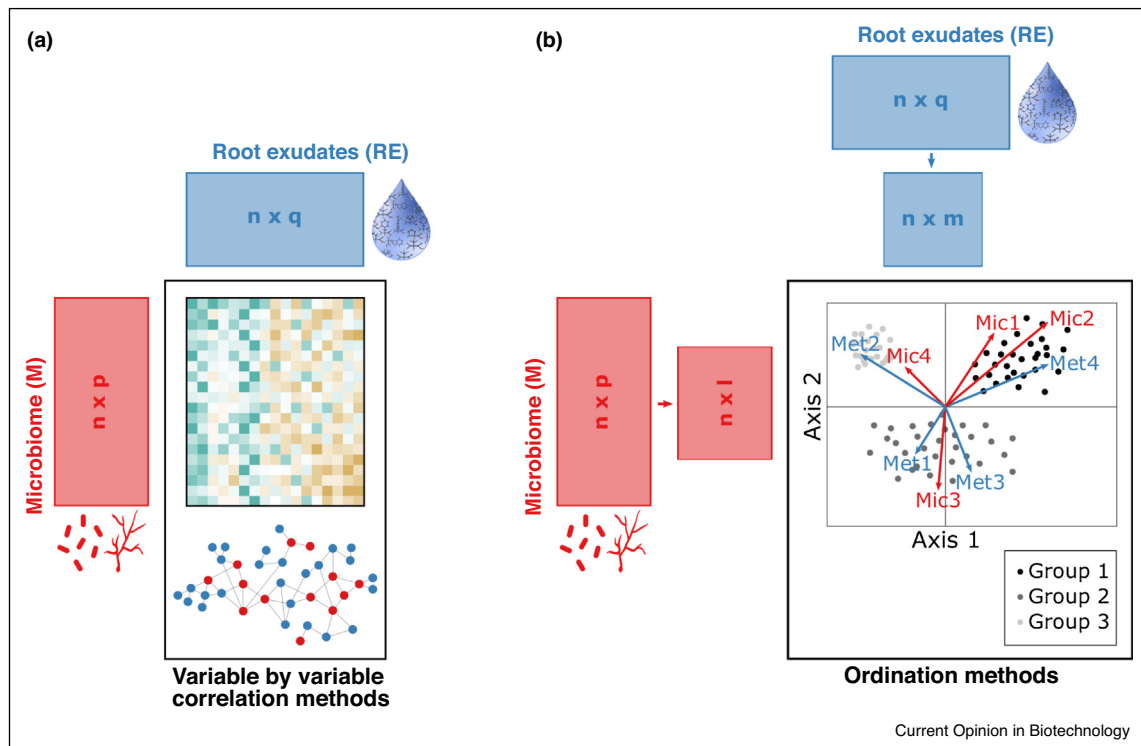
Perspectives

There are several recent methodological advances in association studies. First, the use of *k*-mers instead of the commonly used SNPs confirmed associations previously found, but also pinpointed new associations with gene variants missing from reference genomes [16**]. Second, to increase the mapping power, Beilsmith *et al.* proposed using multi-traits GWAS modelling SNP associations with many traits rather than with each trait

individually, although these models are computationally challenging [14]. Third, to overcome the difficulties of experimental validation, causal inference methods [17], such as genetic structural equation model (GSEM), were proposed, which might be applied as covariance models in multi-traits GWAS to improve power [18**].

Finally, a recent promising method development in plant-microbe interaction association studies is the addition of the plant phenotype. Since the microbiome can be considered as a host phenotype but also contribute to the host phenotype, Oyserman *et al.* recently proposed an extended model that includes the microbiome into the traditional GE model, that is, GEM [19**]. While the traditional GE model considers the effect of the genotype (G), the environment (E) and their interaction (G:E) on the phenotype (Y or here M for the microbiome), that is, $M = G + E + G:E + e$, the new GEM model considers the effect of the genotype, the microbiome, the environment and their interaction to determine the plant phenotype (Y), that is, $Y = G + E + M + G:E + G:M + E:M + G:E:M + e$. A future challenge will be to apply this model to complex natural communities, consisting of hundreds to thousands of species, and taking into consideration also covariance between host genotype, environment and microbiome. Finally, a method called SICOMORE (Selection of Interaction

Figure 2



Metabolomics and metagenomics data integration approaches.

A graphical summary of the main approaches for metabolomics and metagenomics data integration, including: **(a)** variable-by-variable analyses, such as Pearson, Spearman correlations, sparCC, or neural network approaches, where the outputs can be represented as heatmap and/or networks; **(b)** supervised and unsupervised ordination methods, for which an ordination plot can be rendered and/or features explaining variance extracted.

Abbreviations: n, number of samples; p, number of microbiome variables; q, number of root exudate variables; l, number of latent variables for the microbiome data; m, number of latent variables for the root exudates data; Mic: microbe; Met: root exudate metabolite.

effects in COmpressed Multiple Omics REpresentations) was recently developed and applied in a plant–microbiome study. The authors detected interactions between plant genomic markers (SNPs) in *Medicago truncatula* and rhizosphere bacterial genera that are linked to a plant phenotype (e.g. specific nitrogen uptake) [20].

Root exudates shape the root and rhizosphere microbiome

In a number of studies, it was shown that metabolites in the root exudate play a role in shaping the composition of the root and rhizosphere microbiome [21–28]. We postulate that the discovered relationships between root exudates and the microbiome represent just the tip of the iceberg and propose that data integration methods can be used to unravel new signalling relationships. Pang *et al.* reviewed the integration of plant specialized metabolites and microbiome data [29]. Many methods have been suggested, but most do not take into account the zero-

inflated count distribution nor the compositional aspect of these microbiome data. Solutions for these problems include using transformation, imputation and normalization of the data, or using distance-based models. M2IA (automated microbiome and metabolome integrative analysis pipeline), a web-based application combines such pre-processing with standard data integration methods [30].

Figure 2 illustrates two different integration approaches of which one uses a variable-by-variable analysis, in which correlations between variables of both data sets are compared for their linear (Pearson), rank (Spearman), or other types of correlations or co-occurrence. As an example, calculating Pearson correlations, Huang *et al.* [31] identified and linked rhizosphere bacterial OTUs and flavonoids that could explain bitterness in sugarcane. Using Pearson correlation on log transformed data sets, Chaparro *et al.* found that root exudates phenolics and amino acids correlated to bacterial communities composition

g. one block of microbiome data and one block of metabolomics data) into latent variables. These latent variables are now connected through an assumed pathway defining their connectivity. This part of the model is called the inner model, and the part describing the manifest variables in terms of their latent variables is called the outer model. The elegance of SEMs is that they can distinguish direct from indirect effects. **Figure 3** shows that there is a direct effect from PG to Phe, but also an indirect effect through the path PG, RE, M and Phe. SEMs are capable of disentangling these effects. Such SEMs can also be extended to deal with genetic effects [18**]. Special versions of SEMs (called Structural Causal Models) are used in causal analysis [49]. SEMs are starting to be used in microbiome research, for example, in ecological applications [50–53]. In some cases, summaries of the microbiome (e.g. alpha-diversity measures) can be used as the outer model, i.e. they are used as latent variables in the SEM model. These examples show that SEMs are indeed powerful models to study complex systems.

The real challenge of the use of SEMs in microbiome research is in keeping the notion of latent variables since that allows for modelling simultaneously multiple blocks of multivariate (manifest) variables. This may encompass, for example, many SNPs for the PG, many OTUs/ASVs (amplicon sequence variants) for the microbiome, and many metabolites for the RE. There are (at least) three challenges to overcome. The first is to extend the traditional SEMs to handle more than one latent variable per block. This is not trivial, but some ideas on how to do this are available, for example, using sequential and orthogonalized partial least square regression for path analysis (SO-PLS-Path) models [54,55]. Another challenge is to extend the SEMs to handle data of different measurement types. In the example above, SNPs and OTUs/ASVs consist of (limited) count data, while RE consists of quantitative data. One avenue to explore may be the use of nonlinear generalized structured component analysis, which can handle both quantitative and qualitative data [56] or extensions of generalized simultaneous component analysis [45]. Although both extensions can handle high-dimensional blocks in the SEM models, in each block there may still be variables/features that are not important but may obscure the relations. Hence, the final challenge is to select variables to overcome this problem. This may be done in each block before any SEM modelling using techniques from machine learning [57]. Alternatively, this can be done by carefully studying the outcome of a SEM model and interrogating the model for variable importance, for example, by studying the loadings of the variables in the outer relationships. If these challenges are tackled then the rewards are high: a full description of the system on the level of the measured variables relevant to the biological system.

Conclusions and outlook

By now there is substantial evidence that plant genetics affects the root microbiome although it often explains just a small part of the total variation. It is becoming clear that, to really expand our knowledge on the plant microbiome interaction, the microbiome should not only be considered as a phenotype but should also be part of the explanatory variables that predict the plant phenotype. Moreover, there are many indications that specific metabolites in the root exudate drive microbiome selection and/or assembly. Multi-omics data integration could help to identify the molecular mechanisms underlying microbiome recruitment also considering metabolite–metabolite, microbe–microbe, and metabolite–microbe interactions. Furthermore, modelling, using SEM, could help us to go beyond finding more associations and causation, integrating all the drivers, including plant genetics, root exudates and the microbiome to predict the plant phenotype, and identify direct and indirect effects among the drivers. This knowledge will allow us to shape the microbiome through breeding, possibly through changes in the root exudate, and optimise plant/crop growth under the desired conditions.

Conflict of interest statement

Nothing declared.

CRedit authorship contribution statement

Anouk Zancarini: Writing - original draft. **Johan A Westerhuis:** Writing - original draft. **Age K Smilde:** Writing - original draft. **Harro J Bouwmeester:** Writing - original draft.

Acknowledgements

The authors acknowledge funding by the University of Amsterdam, especially through the Research Priority Area Systems Biology program, the Dutch Research Council (NWO/OCW) for the MiCRop Consortium programme Harnessing the second genome of plants (to HB; Grant number 024.004.014) and funding by the European Research Council through ERC Advanced grant CHEMCOMRHIZO (to HB; 670211).

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