

The promise of the plant's second genome

Editorial

With the increasing need to produce more food to address global hunger, we need integrated, cross-functional approaches for crop improvement. The developments in genomics have provided scientists with several tools that can enable a greater understanding of the plant's genome. This knowledge in turn helps scientists to develop crops that yield more and endure biotic and abiotic stresses. Metagenomics approaches are also helping us to study microbes in their native ecological states, thus unraveling the role of microbiomes in our lives. Microbes play a significant role in many environments related to human lives. Significant progress in understanding the diversity and roles of the microbiome in human health and disease has been made since the first large-scale study in 2006¹ which introduced the overwhelming presence of microbial organisms in the human gut. Since then, the diversity and importance of microbiomes have been studied in several environments. As with humans, plants have their own microbiomes and studies have shown the rhizosphere to have tremendous microbial density and diversity with almost 1011 microbial cells per gram of soil represented by >30,000 prokaryotic species.²

New genomics technologies are enabling large-scale characterization of microbial diversity in plants and studies aiming to exploit the microbiomes are underway in plant model systems. Using a 16s pyrosequencing approach on several maize inbred lines across multiple environments, Peiffer et al.³ have shown the presence of substantial bacterial diversity in the maize rhizosphere compared to the bulk soil indicating a preferential recruitment of specialized bacteria by corn plants. They also indicated a hint of genotype-specific microbiota and a small but significant heritable variation in total bacterial diversity in different fields. Similarly, an exploration of microbiome in the Arabidopsis rhizosphere also indicated preferential colonization by some bacterial phylum.^{4,5} A few focused studies have shown the utility of plant-microbial association to abiotic and biotic stress tolerance through the modulation of plant exudates to either recruit beneficial microbes or drive away harmful microbes. Some of these examples clearly indicate the role that microbiomes may play in plant health and crop improvement.⁶ However, given the dynamic nature of plants and their environmental interactions, a comprehensive understanding of the interplay of genetics, environment and the plant microbiome is important to fully harness the microbiome for crop improvement. A first step to fully harness the microbiome for crop improvement is to gain a complete understanding of the diversity and functional capacity of the plant microbiome, its constituent genetic elements and their complex interactions. Efforts are currently underway to foster coordinated efforts among scientific community to understand the diversity of plant related microbes and their interactions with other plants and animals under the umbrella of phytobiomes initiative (www.phytobiomes.org). A second step would be to use this understanding to modulate either the plant machinery or

Volume 2 Issue 4 - 2015

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Received: August 26, 2015 | **Published:** August 29, 2015

the phytobiome for desired outcomes. Although the complex nature of the interaction of plants with the microenvironments that they grow in make this a daunting task, the availability of new technologies make it more possible now than ever before. Concerted, collaborative, cross-functional approaches involving scientists from diverse fields including but not limited to genetics, physiology, genomics, chemistry, computer sciences and plant breeding are needed to tackle the identification, understanding and application of microbiomes for sustained crop improvement.

Acknowledgements

None.

Conflict of interest

Author declares that there is no conflict of interest.

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