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Jason G. Wallace, Alonso Favela, and Sierra Raglin

Cold Spring Harb Protoc; 2025; 10.1101/pdb.top108463

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Alonso Favela, Sierra Raglin, and Jason G. Wallace

Cold Spring Harb Protoc; 2025; 10.1101/pdb.prot108580

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Jason G. Wallace

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Jason G. Wallace and Daniel Laspisa

Cold Spring Harb Protoc; 2025; 10.1101/pdb.prot108582

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Jason G. Wallace and Holly Griffis

Cold Spring Harb Protoc; 2025; 10.1101/pdb.prot108583

Manipulating the Maize (*Zea mays*) Microbiome

Sierra S. Raglin, Alonso Favela, Daniel Laspisa, and Jason G. Wallace

Cold Spring Harb Protoc; 2025; 10.1101/pdb.prot108584

Cover Illustration: Plants host an incredible diversity of microorganisms—the plant’s microbiome—that colonize every accessible plant tissue and interact with each other and their plant host. In maize, the microbiome has been greatly studied, and it has been shown to play a role in plant productivity, stress tolerance, disease susceptibility, and agricultural sustainability. Despite this, there is still much to discover about the maize microbiome, especially with regard to how it can be harnessed for more productive and sustainable agriculture. The maize microbiome, however, can be difficult to study, and characterizing and experimenting on these communities require specialized techniques that many researchers may not be familiar with. In this issue, Wallace et al. provide an overview of recent progress in the field of maize microbiome research. The authors discuss the major microbiome compartments, review the methods currently available to study the maize microbiome and its functions, and discuss how to carry out maize microbiome experiments (doi:10.1101/pdb.top108463). The cover image shows part of a mosaic made of different colors of maize kernels, depicting DNA. Most kernels were grown in a Cornell research field in the summer of 2012, and they represent some of the natural color variation of maize kernels. In the image, the color code used is green for guanine (G), orange for cytosine (C), blue for thymine (T), and white for adenine (A); starting at the *top left*, the sequence shown is thus GCTTCA, which is part of exon 6 of the maize *r1* gene, which is one of the genes that controls maize kernel color. Image provided by the authors; the full mosaic is available at [https://commons.wikimedia.org/wiki/File:Maize_DNA_mosaic_\(full\)_01.jpg](https://commons.wikimedia.org/wiki/File:Maize_DNA_mosaic_(full)_01.jpg).

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