

US tallgrass prairie's microbial past revealed

Efforts to restore the prairie ecosystem might need to look below ground as well.

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Tallgrass prairie once dominated the US Midwest, but nearly all of it has been tilled and farmed since settlers moved into the region in the mid-nineteenth century. New research suggests that one of the most dramatic aspects of that landscape transformation was the loss of microbial diversity in prairie soils.

A study published today in *Science* uses genetic sequencing to reconstruct the microscopic community of the tallgrass prairie¹, including a group of poorly understood bacteria that was once especially abundant. Noah Fierer, a microbial ecologist at the University of Colorado Boulder, and his colleagues collected soil samples from 31 cemeteries and natural preserves where the prairie has remained undisturbed.

The researchers used two different approaches to examine the microbiota contained in the samples. They first sequenced a common gene from each microbe to understand the taxonomic diversity of the soil communities. Then they conducted a metagenomic analysis of known protein-coding genes to learn more about the roles of bacteria in the prairie ecosystem.

Using data on climate variations across the Midwest, the authors extended their findings to predict the historical composition of the soil microbiota across the entire region once covered by tallgrass prairie, which at one time extended over 10% of the contiguous United States. A group of bacteria from the phylum Verrucomicrobia was especially abundant in the soil samples that Fierer's team analysed, and the distribution of specific species seemed to correlate with climatic variations in the prairie region, the scientists found.

The presence of Verrucomicrobia bacteria also correlated with the presence of genes for breaking down carbohydrates, suggesting a possible role for the bacteria. They seem to thrive in soil with poor nutrients, which might explain why they are less common on land that has been farmed and fertilized. Previous work by Fierer's group suggested that the abundance of Verrucomicrobia in soil had been underestimated in earlier studies because of bias in the way that samples are usually sequenced². Much is still unknown about the bacteria, which are hard to study because they grow slowly in the wild and not at all in the laboratory. "It opens a whole research area," says Charles Rice, a soil microbiologist at Kansas State University in Manhattan, about the study's finding on Verrucomicrobia.

James Tiedje, a microbial ecologist at Michigan State University in East Lansing, says the paper outlines a valuable new approach for understanding complex soil communities. He adds, however, that the model could be strengthened by taking soil characteristics into account, although the study's authors say that historical data are unavailable.

Meanwhile, Fierer says that his results suggest that prairie restoration efforts might need to go beyond — or rather, below — animals and plants to consider transplanting soil microbes as well.

With sequencing becoming cheaper and easier — a study on this scale would not have been feasible even five years ago — scientists are just beginning to characterize the diversity of soil microbes in prairies and elsewhere. As Fierer notes: "The frustrating thing but also good thing is there's all sorts of novel diversity in soil."

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References



T.Bannon/CustomMedical Stock/Newscom

Farming has destroyed most of the US tallgrass prairie, which once covered 10% of the lower 48 states.

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1. Fierer, N. *et al.* *Science* **342**, 621–624 (2013).
 2. Bergmann, G. T. *et al.* *Soil Biol. Biochem.* **43**, 1450–1455 (2011).