

## Population genomics of the maize pathogen *Ustilago maydis*

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The maize pathogen *Ustilago maydis* was a pioneer model species for the study of the molecular mechanisms of meiotic recombination. Its efficient recombination system permits transgenics studies and turned it into a powerful model for studying the molecular biology of plant-pathogen interactions. The sequencing of its genome revealed a globally compact genome with a low frequency of transposable elements, as well as a singular architecture where effector genes, playing a direct role in the interaction with the host, are gathered into so-called "virulence clusters." Despite its fundamental importance as a model species, we know little about the natural history of *Ustilago maydis*. We analyzed the genomes of 22 individuals sampled in the supposed center of origin of the species, in Mexico. We find that geography explains little of the contemporary variation. The sampled individuals were shown to consist of two genetics components, possibly resulting from two ancestral subpopulations that split at the time of Maize domestication and are connected by gene flow, and that both underwent a strong genetic bottleneck at the time of domestication. We find that genetic diversity, GC-content, and background recombination rate are remarkably constant along the genome. Contrasting patterns of polymorphism and divergence with the outgroup species *Sporisorium reilianum*, we report that more than 40% of substitutions have been adaptive on average, and the rate of adaptive substitutions was four times higher in so-called virulence clusters, highlighting the role that these compartments played in the evolution of this species.