

Wielding the subtle weapons of a fungus

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Maize as a fungal host: *Ustilago maydis* causes maize smut. An international research team working with biologists at the Max Planck Institute for Terrestrial Microbiology has now identified genes of the fungus implicated in the infection of the plant. Image: Christoph Basse

It doesn't look appetizing: when *Ustilago maydis* attacks a maize plant, its cobs bear hideous tumours rather than crunchy niblets. So far, no effective means of combating the maize smut pathogen has been found. However, an international team has now made significant progress in the search for a solution.

Led by researchers from the Max Planck Institute for Terrestrial

Microbiology in Marburg, the scientists have analysed the *U. maydis* genome. Among the 7,000 genes of the fungus, they have found some with which the fungus lives at the expense of its host plant - without killing it. These genes probably also help the fungus to circumvent the plant's defences. Researchers are now hoping to apply these findings to other fungi, which like *Ustilago maydis* depend on living plants (*Nature*, November 2, 2006).

In Mexico the galls of *Ustilago maydis* are considered to be a delicacy. To farmers in most other countries however, the tumours that develop on the maize cob are regarded as a nuisance. The fungus is certainly not poisonous, which means that infected maize plants can easily be used as cattle fodder, but are not suitable for maize meal or popcorn. The US agricultural authorities in particular have been trying to combat the fungus for a long time, so far to no avail.

A team of almost 80 scientists from all over the world has now made significant headway. The researchers investigated the genome of the fungus to discover how it damages the plant. In the process they identified many genes which contain blueprints for secreted proteins. The fungus expels these proteins. Some of these genes are located adjacent to each other in the genome, forming clusters. This indicates that they might be involved in one and the same process. "If they hadn't been present in clusters, we would probably not have discovered them," says Jörg Kämper, the scientific officer at the Max Planck Institute for Terrestrial Microbiology responsible for coordinating the researchers' work. "It's like a cornfield in which 200 cornflowers are growing. If they are scattered over the field, you don't notice them. But if they're close together, they are easy to spot."

"Our work was made possible by three very good sequencings," says Jörg Kämper. Both Bayer CropScience and Exelixis (USA) had ascertained how the DNA components in the *Ustilago* genotype are arranged. The

Broad Institute (USA) has also sequenced *Ustilago* as part of the Fungal Genome Initiative. "In order to analyse the genome sequence, we brought together the whole *Ustilago* community," explains Kämper. "Each of us concentrated on genes for specific cellular processes."

The Marburg scientists focused on genes which might play a part in infecting the plant and found them in the clusters of secreted proteins. The activity of the genes increases as soon as the fungus infects a plant. "This indicates that the secreted proteins could be effectors, which control the interaction of the fungus with the plant," says Regine Kahmann, Director at the Max Planck Institute in Marburg. In order to confirm this suspicion, her working group performed various experiments, in each case removing one of these twelve clusters from the genome. This revealed that four of the clusters are essential in order for the fungus to develop its full damaging effect. One of the gene clusters, however, clearly helps *Ustilago* to curb its own aggressiveness: the fungus caused even greater damage to its host when the scientists switched off this ensemble of genes. Refraining from causing too much damage to its host also makes sense for the fungus, because *Ustilago maydis* relies on the living plant in order to propagate. The fact that *Ustilago maydis* spares its host as much as possible is also indicated by the number of fungal enzymes that can destroy the cell wall of the plant: *Ustilago* has just 33; fungi which simply eat their hosts have well over 100.

Ustilago maydis certainly does not present a serious problem to maize farmers, but in recent years it has become a model for other biotrophic fungi, many of which are related to *Ustilago maydis*. This group of fungi, which also includes rust fungus, causes a lot of trouble for farmers worldwide. However, biologists cannot specifically alter the genes of most of these fungi in the laboratory. "Hopefully our findings on *Ustilago maydis* can be transferred to this group of fungi," says Kämper.

The scientists now hope to find out what function the secreted proteins perform. "Surprisingly, hardly any of these proteins resemble a known protein from a different organism," says Kahmann. She and her colleagues suspect that the fungus uses these proteins to outsmart the defence mechanisms of the plant. In so doing, the proteins might form a biochemical cover which serves as camouflage in order to slip by the plant's defences unnoticed. Alternatively, the secreted proteins might actively suppress the defences. What is certain is that the gene clusters play a crucial role in this and now the researchers hope to discover precisely what that role is.

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