Background
During the past decade, the basidiomycete *Ustilago maydis* has become one of the prime model systems to study plant/pathogenic interactions. In contrast to various other phytopathogenic fungi, *U. maydis* can be easily propagated on artificial media and is amendable to various molecular techniques, comparable to the yeast *Saccharomyces cerevisiae*. Similar to other pathogens of plants and humans, *U. maydis* is a dimorphic fungus, with haploid yeast like cells, called sporidia, that grow strictly saprophytic, and a filamentous growing pathogenic dikaryon that is dependent on the host plant corn for its development. After infection of its host plant maize, *U. maydis* induces the formation of tumors in which the fungal hyphae differentiate and generate diploid spores. The outstanding feature of the *U. maydis* system is that the change from saprophytic growth to the biotrophic stage is controlled by a single genetic switch, namely the bE and bW homeodomain proteins that are encoded by the multiallelic b-mating type locus. After fusion of two haploid sporidia, the bE and bW proteins form a heterodimer when the two proteins originate from different b-alleles. The heterodimeric bE/bW complex regulates b-dependent processes via its function as a transcriptional regulator (Reviewed in Kahmann and Kämper, 2004).

Aims
The major interest of our group is the elucidation of the regulatory processes that lead to the establishment of the pathogenic stage and the subsequently to colonization of the host plant. During the last year, we have established Affymetrix DNA-arrays for *U. maydis* that allow the parallel detection of 6200 from the estimated 7000 genes. We have used the gene chip technology to monitor the changes in gene expression after b-induction in a 12 hours time course, and by this means have identified 248 b-responsive genes. Although we are currently analyzing various genes from these different functional categories, our main interest is to identify genes with a function during pathogenesis. Since the deletion of single genes only in very limited cases have been shown to influence pathogenic development, we have focused on the systematic deletion analysis of b-regulated genes encoding proteins with potential regulatory functions. Following this strategy, we have identified various novel pathogenicity factors for *U. maydis*:

1) The b-regulated zinc-finger transcription factor Rbf1 is required for both filamentous growth as well as pathogenic development. Microarray experiments revealed that this transcription factor plays a crucial role for the expression of b-dependently regulated genes, by that assigning a central role within the b-regulatory network. Deletion of *rbf1* leads to a drastic deregulation of b-dependent genes; from a total of 134 genes induced 3 h after formation of a compatible bE/bW heterodimer, 110 are drastically reduced in expression or not expressed at all. The presence of such a central regulatory protein has been postulated for years by our group; using the microarray technology, we were able to verify its existence.

2) The b-dependently expressed homeodomain transcription factor Hdp2 is also essential for pathogenic development; in contrast to Rbf1, however, filamentous growth is not affected.

3) The b-dependent gene *umclp1* encodes a protein with unknown function; formally, the protein functions as repressor for the filamentous growth on the plant surface. The finding that the protein interacts with bW in a yeast two hybrid screen makes it likely that that Umclp1 might
modify or alter the specificity of the bE/bW complex. In the same screen, also Rbf1 was identified as a potential interacting partner for Umclp1.

4) The b-dependent transcription factor Riz1 appears to be instrumental for the expression of specific genes during the initial growth on the plant surface. Array experiments with cells harvested from the plant surface revealed a set of genes that is specifically expressed in dependency of the presence of an active bE/bW; in the respective Δriz1 mutant strains, a substantial fraction of these genes is either not expressed or significantly reduced in expression. Interestingly, the induced expression of riz1 in axenic culture also leads to the induction of these “plant surface specific” genes.

Our aim is to evaluate the regulatory network between these different transcription factors, with the aim to understand the specific input/output signals and their connection to the establishment of the pathogenic program. In particular, the project within the graduate school will deal with the functional interactions of bE/bW, Rbf1 and Umclp1. The particular questions that we will addressed are:

1) Is Umclp1 modulating the function for the bE/bW heterodimer? Is it competing for the same promoter elements? The overexpression of Umclp1 leads to a loss of filamentation and pathogenicity, a phenotype that can be explained by both models.

2) Is there an additional modulation of Rbf1 by Umclp1? Are Rbf1, bE/bW and Umclp1 eventually forming a complex?

3) How are b-dependent genes regulated by bE/bW and Rbf1? Are bE/bW competing for the same promoter elements? Are there composite elements that require the binding of both proteins? The promoter of the b-dependent gene dik6 harbours a bbs (b-binding site) that was shown to be involved in b-dependent regulation; however, induction of Rbf1 leads also the induction of dik6 independently from b. Preliminary experiments place the Rbf1 responsive promoter-element a region close to (or identical to) the bbs site. On the other hand, the expression of Umclp1 is strictly b-dependent; Rbf1 is not required for the regulation.

Own publications (last five years)
Eichhorn, H., Lessing, F., Kämper, J., Müller, P., Kahmann, R. A high affinity iron permease is required for virulence in Ustilago maydis. under revision
Kämper, J., Friedrich, M., Kahmann, R., Creating diversity in self-nonself recognition loci by homologous recombination. prepared for resubmission to PNAS