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## **GEMO: an innovative project on Evolutionary Genomics of Magnaporthe oryzae**

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**GEMO: an innovative project on Evolutionary Genomics of *Magnaporthe oryzae*.**

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Developing integrated control methods against pests of cultivated plants can significantly contribute to increasing food production while reducing inputs threatening the environment. The durability of a control method can be improved by a better knowledge of the pathogen's genetic determinants that are responsible for this adaptation. We were granted by the French National Research Agency for a project that aims at sequencing the genomes of several strains of the phytopathogenic model species *Magnaporthe oryzae* and at exploiting these complete sequences to characterize the repertoire of genes involved in pathogenicity and host specificity, and study their evolution. We will sequence 7 strains of the species *M. oryzae* representing different genetic groups pathogenic of different species of Poaceae and one strain of the sister species *M. grisea*. ESTs produced during the infection by two strains pathogenic of rice and wheat on their respective host will also be sequenced. Different available annotation pipelines will permit to list and do comparative analyses of different gene families known or speculated to be involved in pathogenicity. Transcriptomic data of the two strains with different host specificities will be compared to identify key genes in specialization to the host. Genome fluidity will be characterized by synteny analyses and by the identification and localization of repeated elements. The impact of these rearrangements on pathogenicity genes and host specificity genes will be tested. Molecular signatures of positive or purifying selection in coding and regulatory sequences will be searched for by different methods. The whole set of data will be integrated in a database that will be designed to be accessible publicly.

*Keywords:* *Magnaporthe*, génome, effecteur, séquençage