

ISOLATING RESISTANCE GENES AGAINST *FUSARIUM* EAR ROT IN MAIZE

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We investigated global gene expression in maize ears at several time points after infection with *Fusarium verticillioides*. In kernels at 48 h post infection with a fumonisin-producing strain, about 800 differentially expressed sequences were identified and nearly 10% assigned to the category cell rescue, defence and virulence. The expression analysis was extended to early (12, 24 h) and late (72, 96 h) phases after infection with a fumonisin-nonproducing strain. The mutant strain was able to activate host defence genes later than the wild type strain. When resistant and susceptible maize genotypes were compared, in the resistant lines the expression of defence genes were induced upon infection, indicative of a basal defence response against the fungus. In the susceptible genotypes defence genes were induced specifically after pathogen infection. The basal defence response was also active against several fungal species invading maize kernels. The differentially expressed genes were selected as candidate genes for mapping. SNP markers were developed for resistant and susceptible maize lines. SSR markers were selected according to their chromosomal positions on the maize reference map with the aim to test the polymorphisms in the two parental lines and in a segregating F₂ population. The molecular markers associated to resistance will be localized on a high density molecular map and exploited to detect quantitative trait loci (QTLs).