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STUDY OF *FUSARIUM*-INDUCED BIOSYNTHETIC PATHWAY SHIFTS IN *ZEA MAYS* L.

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During the summer of 2009, 36 maize inbred lines together with 6 reference lines were tested for their tolerance towards Fusarium infection, by means of a *Kernel Inoculation Assay*. Primary open pollinated cobs were infected 15 days after silk emersion with a spore suspension (10^6 spores/ml) obtained from a mix of two *Fusarium verticillioides* strains isolated in Northern Italy. Inoculation with sterile water was used as a negative control. Subsequently, the number of infected kernels near the inoculation site was counted using the following scale and expressing the surface area of the cob covered with mycelium: 1 = 0% (no infection); 2 = 1-3%; 3 = 4-10%; 4 = 11-25%; 5 = 26-50%, 6 = 51-75%; 7 = 76-100%.

Based on these results, two genotypes were selected with diversified responses to Fusarium infection: Lo186, exhibiting a clear infection pattern with abundant mycelium growth and Lo435 with a far more resistant phenotype. Both accessions were subsequently inoculated as described previously, either with spore suspension or with sterile water, and kernel material was collected around the infection sites. Material was collected at two time points after inoculation (1 day and 5 days) from 5 independent cobs from each of the two genotypes. Total RNA was then isolated from each of the collected samples. Total RNA was, moreover, extracted at the two time points from non-inoculated cobs.

Three independently isolated RNA samples obtained from Lo186 after a 5 day infection period with Fusarium, three RNA samples isolated from identical material but obtained through inoculation with water, and three RNA samples again obtained from identical material, but collected from non-inoculated cobs, were used to prepare hybridization probes, which were subsequently used to hybridize an Affymetrix maize array. The comparison of the expression profiles obtained with non-inoculated, water-inoculated, and Fusarium-inoculated kernel material allowed identifying numerous genes exhibiting differential expression patterns across the series assayed. The genes identified, their putative functions with respect to fungal infection, and the biosynthetic pathways involved will be discussed.