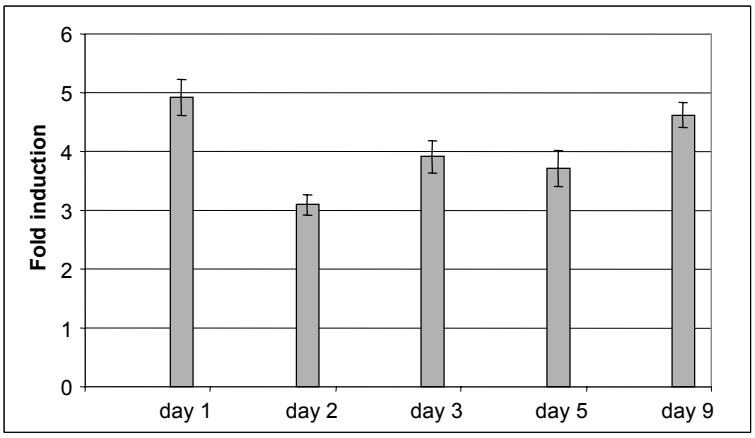
Fold induction
6
5
4
3
2
1
0
day 1
day 2
day 3
day 5
day 9

Supplemental Figure 1. Kinetics of expression of *gas1* during the biotrophic phase of *U. maydis* by real-time PCR.

Six-day old maize seedlings were infected with a mixture of the compatible *U. maydis* wild type strains FB1 and FB2. At the time points indicated the third leaves of the infected maize plants were collected and used for total RNA isolation. Real time RT-PCR was used to assay the expression levels of *gas1* using the constitutively expressed peptidylprolylisomerase gene *ppi1* as control. First strand cDNAs were synthesized from 5 µg of total RNA using the ThermoScript RT-PCR System (Invitrogen life technologies) following the manufacturer's instructions. Quantitative real-time PCRs were performed using the Roche LightCycler and SYBR Green PCR Master Mix (Roche Biochemicals) and primers ffgasq (AAACCGCGTCGACCCTTT) and revgasq (ATGGCGCCGTACTTTTGG) for detection of *gas1* and ffppiq (CGAGAACGAGGGCACCAA) and revppiq (GCGAAAAAGCGTTTAAAGAACAC) for detection of *ppi1*. Gene-specific primers were designed using Primer Express software (Applied Biosystems) to amplify a 70 bp product representing the 3' end of the corresponding cDNA. The PCR conditions consisted of denaturation at 95°C for 10 min, followed by 40 cycles of denaturation at 95°C for 15 s, annealing at 60°C for 30 s and extension at 70°C for 30 s. Expression levels are presented as values relative to that of *gas1* during growth in culture, after normalization to *ppi1* levels. Six independent amplifications were performed, and the average of the results retained. The error bar indicates the standard deviation.