Supporting information

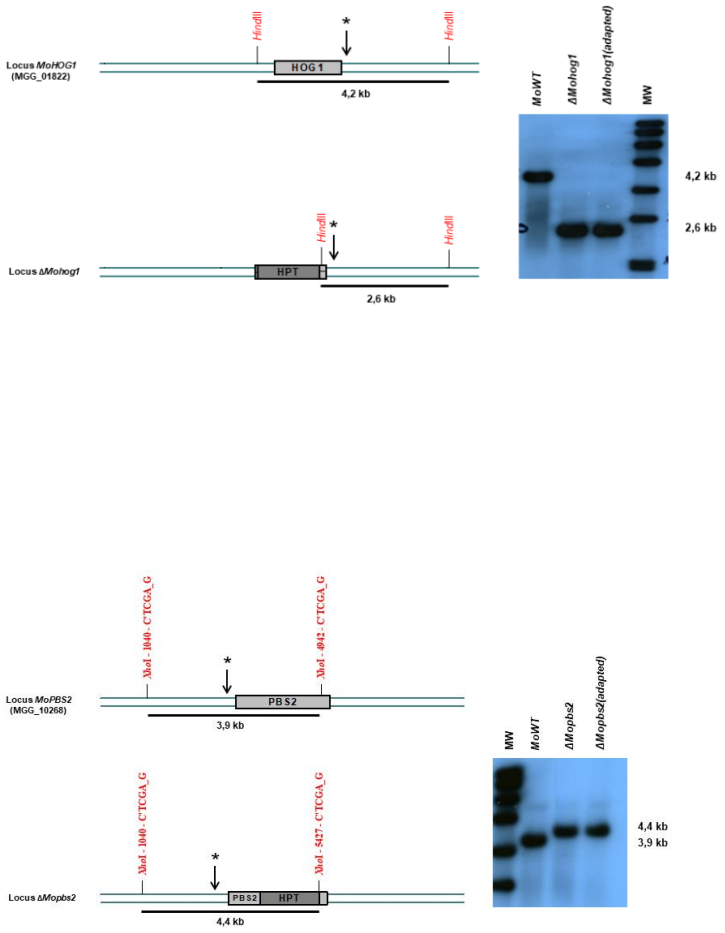

Figure S1: **Schematic presentation and verification of the *MoWT*, the lof-mutants and the adapted strains by southern hybridization within the *Magnaporthe oryzae* genome.** Southern blot analysis of gene deletion/disruption mutants in *M. oryzae* with gene specific probes. Genomic DNA of *M. oryzae* strain 70-15 and the mutants was isolated and restricted with restriction enzymes. The probes which we used for hybridization with the genomic DNA of the wildtype strain and the corresponding mutant strains were always identical.

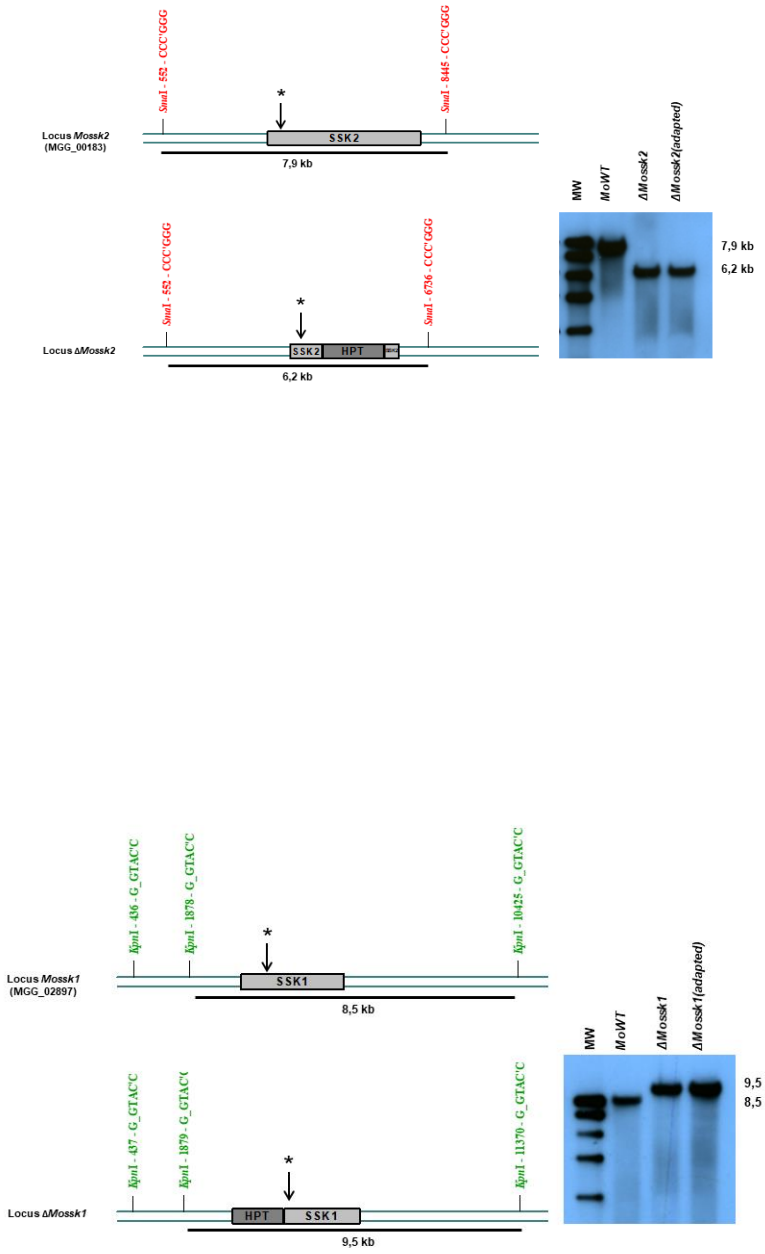

Figure S1 (continued): **Schematic presentation and verification of the *MoWT*, the lof-mutants and the adapted strains by southern hybridization within the *Magnaporthe oryzae* genome.**

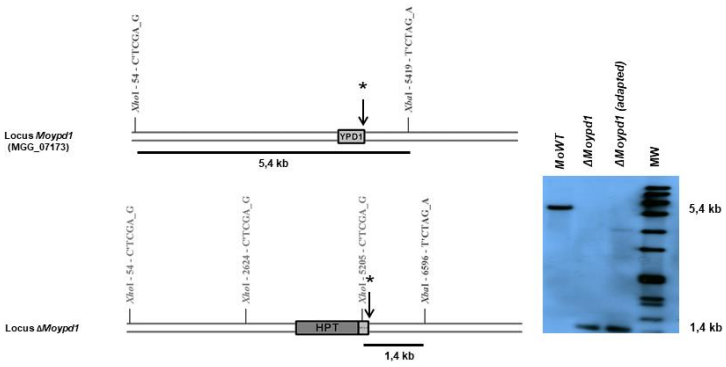

Figure S1 (continued): **Schematic presentation and verification of the *MoWT*, the lof-mutants and the adapted strains by southern hybridization within the *Magnaporthe oryzae* genome.**

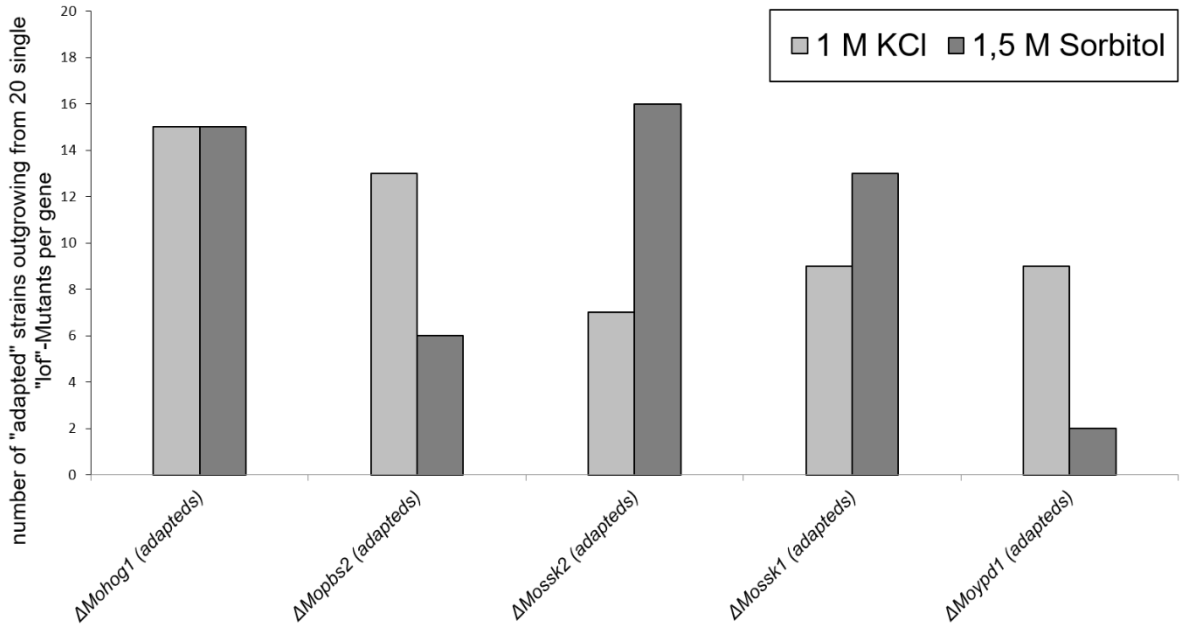

Figure S2: **Investigation of the "adaptation-frequency" in *Magnaporthe oryzae* mutants with inactivated components of the HOG signaling cascade.**

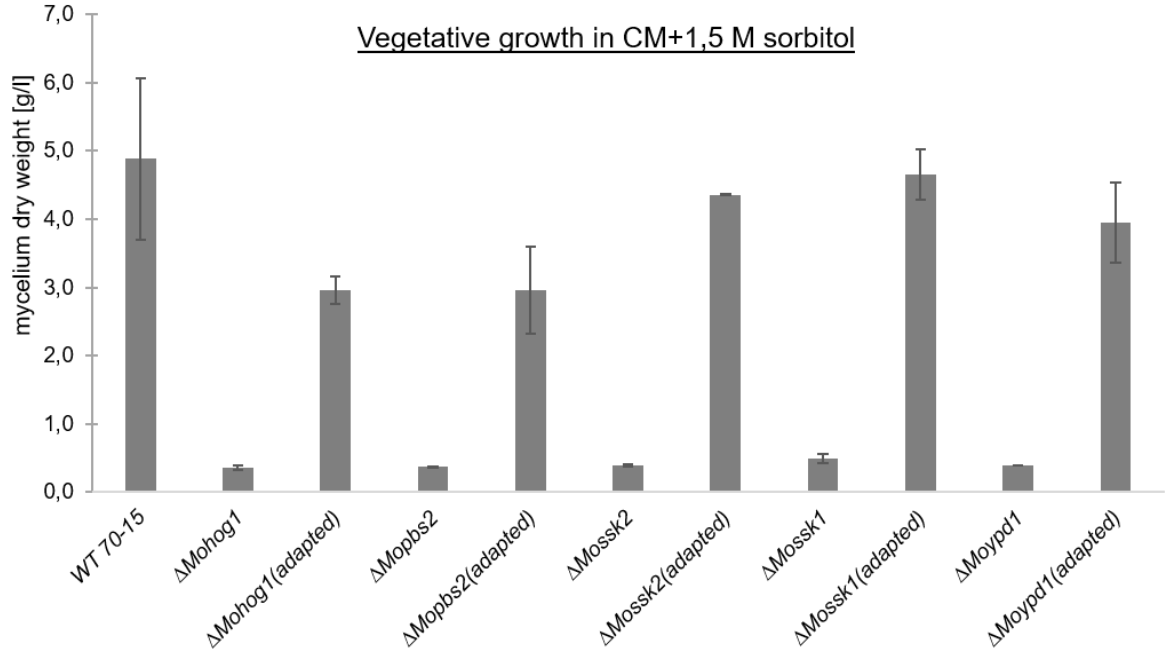

Figure S3: **Mycelium dry weight of the *Magnaporthe oryzae* wildtype strain, mutants with inactivated components of the HOG signaling cascade and the "adapted" strains after growth in liquid culture upon sorbitol-stress.** The fungal colonies were grown in 250 ml complete medium inclusive 1,5 M sorbitol for 6 d at 26 °C and 120 rpm. Error bars represent the standard deviation of three biological replicates of each strain.

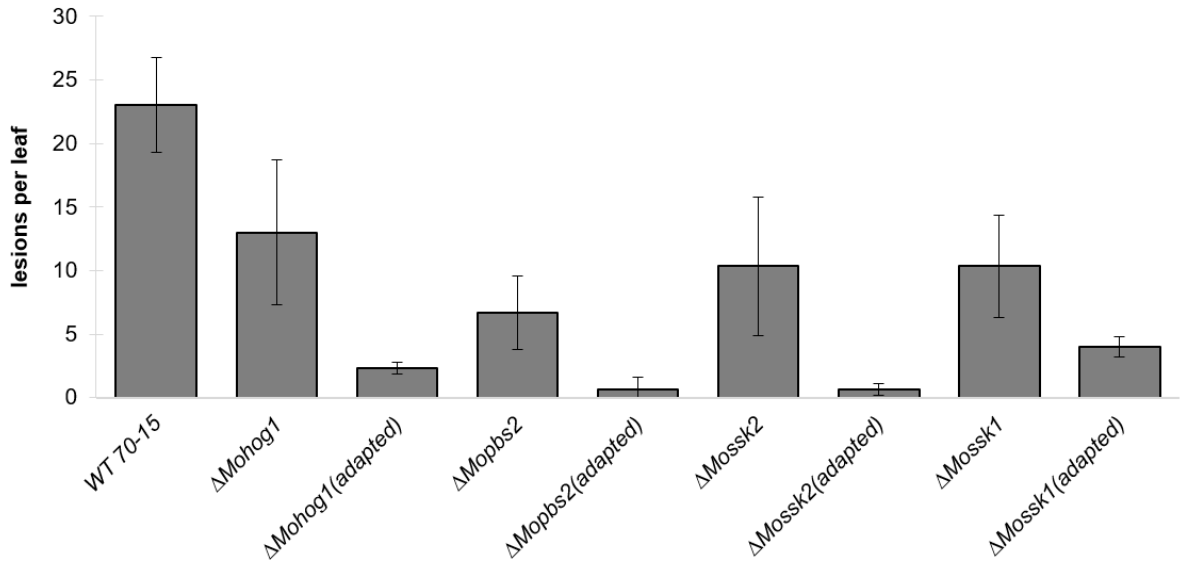

Fig.S4: Pathogenicity assay of the *MoWT*, the lof mutants and the "adapted" strains. The plant infection assays were carried out as described in experimental procedures. The error bars represent the standard deviation of three experiments with three replicates each.

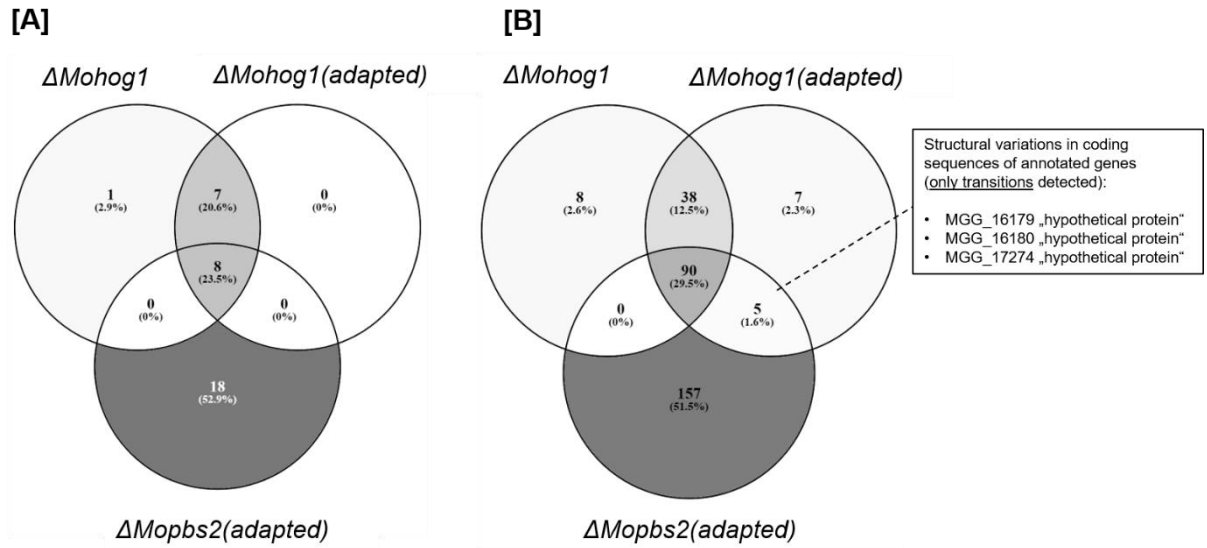

Fig.S5: VENN diagram of putative structural variations in promotor [A] and in coding sequences (CDS) [B] within the genome of *ΔMohog1*, *ΔMohog1(adapted)* and *ΔMopbs2(adapted)*. Numbers in the intersection regions represent overlapping SNPs among the strains. Numbers in parentheses show the corresponding relative percentage of genes harbouring the SNPs.

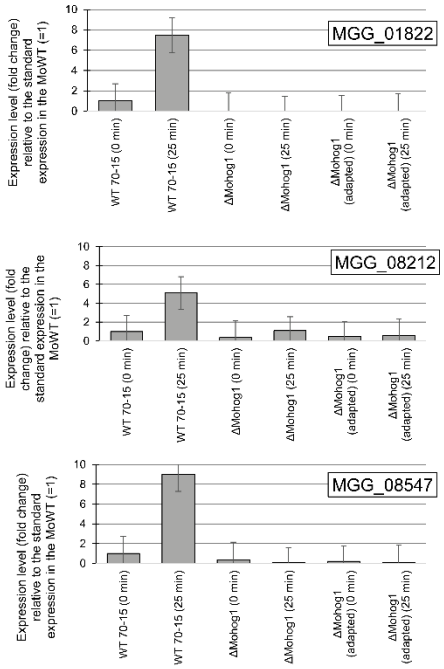

Fig.S6: **qPCR results of selected genes**. qRT-PCR analysis of putative genes in MoWT, the "lof" mutants ΔMohog1 and ΔMohog1(adapted). The M. oryzae cultures were grown for 96 h in CM at 26 °C and 100 rpm. Each of the cultures was separated into two samples, one mixed with 0.5 M KCl and one untreated control further grown in CM at 26 °C and 100 rpm). Samples were taken after 25 min. The RNA was isolated from the mycelium samples and the results of transcript abundance given relative to quantification in the MoWT untreated control. Three biological replicates were used of each.