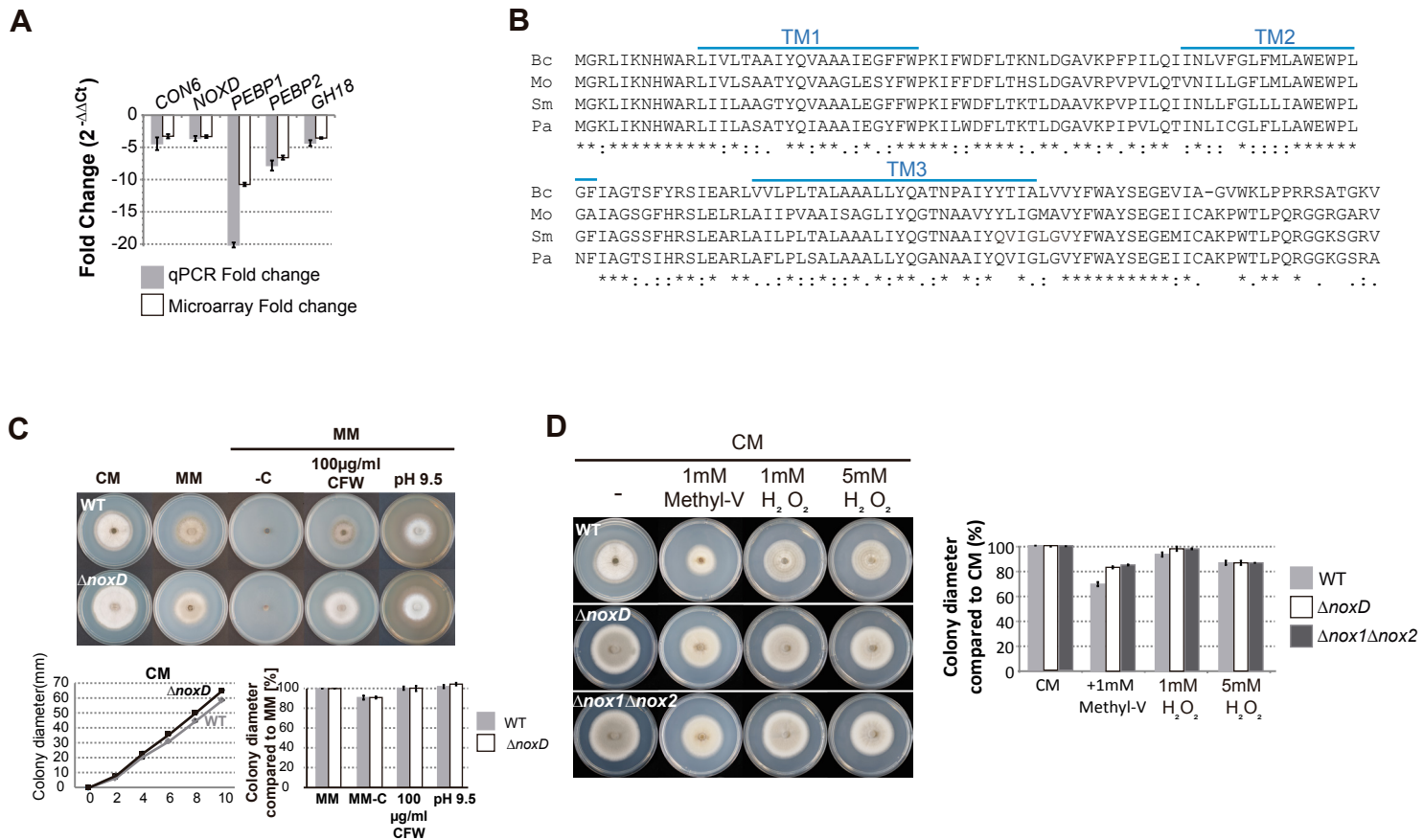


# S8 Figure



**S8 Fig. NoxD is not involved in *M. oryzae* response to stress conditions.** (A) Comparison of expression levels of five Tpc1-dependent genes. qPCR experiments confirmed microarray expression changes for selected genes. qPCR data were normalized against actin and wild type (WT) expression of the gene. (B) Fungal NoxD proteins were aligned using CLUSTAL Omega (EMBL-EBI server). Bc, *Botrytis cinerea* (EMR81583); Pa, *Podospira anserina* (CDP23073); Sm, *Sordaria macrospora* (CAL68654); Mo, *Magnaporthe oryzae* (MGG\_09956.8). TM, transmembrane regions predicted using *M. oryzae* NoxD and TMHMM Server v. 2.0 (<http://www.cbs.dtu.dk/services/TMHMM/>). TargetP 1.1 localizes *M. oryzae* NoxD in the secretory pathway although lacks a clear signal peptide prediction. (C) Growth tests on CM and MM. The  $\Delta noxD$  mutant grows slightly faster on CM while no differential growth of  $\Delta noxD$  is observed upon exposure to carbon starvation, calcofluor white and pH 9.5. (D) Effect of different oxidative stresses in WT,  $\Delta noxD$  and  $\Delta nox1\Delta nox2$  strains. Both mutants were more resistant than WT on complete medium (CM) supplemented with 1mM Methyl-V and 1mM  $H_2O_2$  but not on CM with 5 mM  $H_2O_2$ . Growth was monitored at 8 dpi. CM is taken as reference for each strain.