Characterization and transcriptional regulation of *Stachybotrys elegans* Mitogen-Activated-Protein Kinase gene, *smkA*, following mycoparasitism and starvation conditions

Current Genetics

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Liquid chromatography-mass spectrometry/mass spectrometry analysis

For LC-MS/MS analyses, during the first 12 min, 5 µL of sample were loaded on column at a flow rate of 600 nL/min of buffer A and, subsequently, the separation was done using a gradient from 2–80% buffer B over 110 min at a flow rate of 250 nL/min and then 2% buffer B for 10 min at a flow rate of 600 nL/min. Full scans were acquired in the mass range between 360 and 1800 Da. Data dependent MS/MS scans were performed in the LTQ for the top ten most abundant masses with intensity higher than 10000 counts. Target ions already selected for MS/MS were dynamically excluded for 25 s. Nanospray and S-lens voltages were set to 0.9–1.8 kV and 50 V, respectively. Capillary temperature was set to 225°C. Collision induced
dissociation (CID) was used with a collision energy of 35%, activation Q setting of 0.25 and 10 ms activation time for MS.

**Protein identification**

For the construction of the target in-house-built protein library, data were retrieved from the National Center for Biotechnology Information (NCBI, http://www.ncbi.nlm.nih.gov/) and the Gene Ontology database (http://www.geneontology.org/). For Proteome Discoverer searches, trypsin was selected as the digestion enzyme allowing for 2 missed internal cleavage sites per peptide. Deamidation (N and Q) and oxidation (M) were selected as dynamic modifications, and carbamidomethyl (C) as static. The mass tolerance for the precursor and fragment ions was set to 15 and 0.6 ppm, respectively.