**Supplementary Text 1: List of the main findings of previous transcriptional profiling studies using caspofungin**

**Reference:** Valero C, Colabardini AC, Chiaratto J, et al. Aspergillus fumigatus Transcription Factors Involved in the Caspofungin Paradoxical Effect. *mBio*. 2020;11(3):e00816-20. Published 2020 Jun 16. doi:10.1128/mBio.00816-20

**Experiment:** RNA-seq Postexposure to 2 μg/ml caspofungin for 48 h

**Main Findings:** Enrichment analyses performed for the wild-type (CEA17) strain demonstrated a transcriptional upregulation of genes coding for proteins involved in C-compound and carbohydrate metabolism; sugar, glucoside, polyol, and carboxylate catabolism; lipid, fatty acid, and isoprenoid metabolism; secondary metabolism; flavin adenine dinucleotide/flavin mononucleotide (FAD/FMN) and NAD/NADP binding; and electron transport. On the other hand, there was a downregulation of genes coding for proteins involved in rRNA processing, tRNA processing, RNA binding, ribosome biogenesis, secondary metabolism, and degradation of serine.

**Reference:** Aruanno M, Bachmann D, Sanglard D, Lamoth F. Link between Heat Shock Protein 90 and the Mitochondrial Respiratory Chain in the Caspofungin Stress Response of Aspergillus fumigatus. Antimicrob Agents Chemother. 2019 Jun 24;63(7):e00208-19. doi: 10.1128/AAC.00208-19. PMID: 31061164; PMCID: PMC6591604

**Experiment:** Transcriptomic analyses (RNA sequencing [RNA-seq]) were performed in three biological replicates of whole-RNA extracts of KU80 under basal conditions and after 2 h of exposure to caspofungin at 2 μg/ml (i.e., the concentration required to induce the paradoxical effect of caspofungin).

**Main Findings:** The mitochondrion-carried genes of the mitochondrial respiratory chain (MRC) were strongly induced by caspofungin in KU80 strain.

**Reference:** Cagas SE, Jain MR, Li H, Perlin DS. Profiling the Aspergillus fumigatus proteome in response to caspofungin. Antimicrob Agents Chemother. 2011 Jan;55(1):146-54. doi: 10.1128/AAC.00884-10. Epub 2010 Oct 25. PMID: 20974863; PMCID: PMC3019664.

**Experiment:** The isolates used in this work were grown with shaking (225 rpm) at 37°C in 50 ml of YPD broth containing 0.12 μg/ml of caspofungin. A whole-genome array was evaluated.

**Main Findings:** At 24 h, 18 genes were downregulated, and 59 genes were upregulated. Of the 59 upregulated genes, 51 (86.4%) were ribosomal genes. The 18 downregulated proteins include stress response genes such as Mn-superoxide dismutase and mitochondrial hypoxia response domain protein along with several transporter proteins (e.g., plasma membrane H+-ATPase and siderochrome-iron transporter).

**Reference:** Conrad T, Kniemeyer O, Henkel SG, Krüger T, Mattern DJ, Valiante V, Guthke R, Jacobsen ID, Brakhage AA, Vlaic S, Linde J. Module-detection approaches for the integration of multilevel omics data highlight the comprehensive response of Aspergillus fumigatus to caspofungin. BMC Syst Biol. 2018 Oct 20;12(1):88. doi: 10.1186/s12918-018-0620-8. PMID: 30342519; PMCID: PMC6195963.

**Experiment:** Mycelia of the *Aspergillus fumigatus* strain CEA17 Δ*akuB* were pre-cultured for 16 h in *Aspergillus* minimal medium and then stressed with a sub-inhibitory concentration of caspofungin (100 ng/ml). Samples were taken at different time points (0.5 h, 1 h, 4 h and 8 h after treatment).

**Main Findings:** The differentially expressed genes were related to (1,3)-alpha-D-glucan biosynthesis and carbohydrate metabolic processes, actin filament-based processes, activation of protein kinase activity, response to oxidative stress, cell wall assembly and remodeling, cytoskeletal organization, signaling and oxidative stress response, electron transport chain, amino acid metabolic process, mitogen-activated kinases (MAPK) and secondary metabolite fumagillin biosynthesis.

**Reference:** Altwasser R, Baldin C, Weber J, Guthke R, Kniemeyer O, Brakhage AA, Linde J, Valiante V. Network Modeling Reveals Cross Talk of MAP Kinases during Adaptation to Caspofungin Stress in Aspergillus fumigatus. PLoS One. 2015 Sep 10;10(9):e0136932. doi: 10.1371/journal.pone.0136932. PMID: 26356475; PMCID: PMC4565559.

**Experiment:** RNA samples for sequence analyses (RNA-seq) were obtained by growing mycelia for 16 h in *Aspergillus* Minimal Medium (AMM), and then addition of caspofungin (0.1 μg ml-1). Samples were taken at different time points (0.5 h, 1 h, 4 h and 8 h after treatment).

**Main Findings:** Genes involved in carbohydrate metabolism (FunCat ID 01.05) were differentially expressed in response to caspofungin during all time points (*e*.*g*. β-glucosidases, exo- and endo-β-1,3(4)-D-glucanases).