



Exploring Protein Expression in *Exophiala dermatitidis* to Identify Biological Mechanisms of Radioprotection

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Abstract:

Exophiala dermatitidis (*E. dermatitidis*) is a melanized polymorphic fungus that displays a moderate resistance to ionizing radiation that allows it to survive under conditions that are normally prohibitive to the survival of multi and single- cellular organisms. Because the individual sequence of DNA does not notably change across organisms, repair or protection pathways must be present within an organism to ensure survival, and, in select circumstances, resists damage induced by ionizing high levels of radiation, and recent studies show increased growth rates are induced under low-level radiation. Understanding the changes in the proteome induced by both high-level radiation and low-level radiation on this model fungus could help to identify the molecular mechanisms of melanin in protecting melanized cells and organisms.

Here initial comparisons are made between the proteomes of *E. dermatitidis* and the non-melanized *wpdks* variant. Proteins of note are described, particularly proteins involved in DNA repair, melanin production, ribosomal production, and ROS repair. Statistical comparisons between the two strains are highlighted. In particular, while delta variant produced 50% more protein families than the WT, both produced the same number of protein families related to the aromatic amino acid family biosynthetic process.

With this baseline established between the wild-type and mutant strains, future work will probe radiatively stressed cell lines, proteome responses to ROSs and RNSs, impacts of variable radiation sources, alternative protein extraction methods, and DDA proteomics. Additional studies will be conducted on other melanized fungi in collaboration with PNNL