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Genome Sequence Is Not a Predictor of Radiation Resistance

Bethesda, Md. – For the last two decades, researchers worldwide have been using whole genome sequencing to understand what makes cells radiation-resistant, hoping to solve an old biological mystery: why is it that one of the most radiation-resistant organisms, *Deinococcus radiodurans*, aka “Conan the bacterium,” can survive hundreds of times more DNA damage caused by gamma rays than most other organisms? According to a study published recently in *Standards of Genomic Sciences* by researchers at the Uniformed Services University (USU), the amount of radiation a *Deinococcus* cell can survive in fact has little to do with the number and types of its DNA repair proteins.

The study, “High-quality genome sequence of the radioresistant bacterium *Deinococcus ficus* KS 0460,” was published July 28 in *Standards of Genomic Sciences*, and was led by Dr. Michael J. Daly, professor of Pathology at USU, and Drs. Vera Y. Matrosova and Elena K. Gaidamakova, USU staff scientists.

Researchers have known for years that DNA repair enzymes are required to survive chromosome damage caused by radiation. The unanswered question has remained: why do ordinary repair enzymes work so much better in *Deinococcus* bacteria than in other cells? In 1997, “Conan the bacterium” became one of the first organisms ever to be subjected to whole genome sequencing. Back then, it took two years to sequence and decipher a bacterium, which takes just days now. The research team at USU compared *Deinococcus ficus* with dozens of its closest relatives including “Conan.” In the end, there was nothing special about DNA repair machinery in *Deinococcus*. Instead, the metabolic configuration of cells – in other words, how they eat and process food – appears more important to understanding radiation resistance. This fresh insight points to new ways to help cancer patients survive radiation therapy, and to develop countermeasures against growing nuclear threats.

“Despite the very best genomic efforts to understand radiation resistance, a sequence simply cannot predict whether a cell is resistant or not. And, this is now forcing scientists to consider other ways to gauge radiation resistance,” Daly said.

This project was supported by a Defense Threat Reduction Agency grant HDTRA-18774-M, and the team of researchers working at USU also included Olga Grichenko, Rok Tkavc, Gözen Ertem, Isabel Conze, Polina Klimenkova, Robert Volpe, Cene Gostincar, Tine Grebenc, and Michael Woolbert. Additional support was provided by the Department of Energy’s Joint Genome Institute, in Walnut Creek,

California, the Los Alamos National Laboratory, in Los Alamos, New Mexico, the Leibniz Institute DSMZ, German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany, the University of Ljubljana and Slovenian Forestry Institute, both in Slovenia, as well as the National Institutes of Health, National Center for Biotechnology Information, and National Library of Medicine, in Bethesda, Md.

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