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# Personalized gene therapies may increase survival in brain cancer patients

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Personalized prognostic tools and gene-based therapies may improve the survival and quality of life of patients suffering from glioblastoma, an aggressive and deadly form of brain cancer, reports a new University of Illinois study funded by the NIH National Cancer Institute.

"We confirmed known biomarkers of glioblastoma survival and discovered new general and clinical-dependent gene profiles," said Nicola Serao, a U of I Ph.D. candidate in animal sciences with a focus in statistical genomics. "We were able to compare biomarkers across three glioblastoma phases that helped us gain insight into the roles of genes associated with cancer survival."

Glioblastoma is a complex, multifactorial disease that has swift and devastating consequences, Serao said. Although some genes have been associated with the presence of glioblastoma, few have been identified as prognostic biomarkers of glioblastoma survival and fewer have been confirmed in independent reports.

"You can't just find one gene that is related to this cancer and fix it," he said. "This is one of the aspects of our research that makes it unique. We were able to look at several genes at the same time and relate our findings to this cancer."

Using genomic information from more than 22,000 genes, Serao took this huge piece of information and began slicing away at it, one gene at a time, until he ended up with a group of genes related to brain cancer.

He studied different survival variables, including length of survival from birth to death, from diagnosis to death, and from diagnosis to progression of the cancer.

"We studied different variables, but they were complementary, and allowed us to learn more about those genes," he said. "We understand that some genes have much more impact in cancer than others. And we also discovered that some genes only appeared in one variable, so they were specific for a given phase of cancer."

This study not only evaluated genes influencing survival, but also took into consideration clinical factors such as age, race and gender.

"Our research suggests you can't treat all patients the same," Serao said. "For example, we found gene expression patterns that have different, and sometimes opposite, relationships with survival in males and females and concluded that treatments affecting these genes will not be equally effective. Personalized therapy dependent on gender, race and age is something that is possible today with our advanced genomic tools."

Recognizing that genes seldom act alone, this team of researchers took several genes into consideration at the same time and uncovered networks of genes related to glioblastoma survival.

Sandra Rodriguez Zas, co-researcher and U of I professor of animal science and bioinformatics, said they looked at commonalities between the genes linked to glioblastoma survival and progression, too.

"If a large number of genes linked to survival belong to a particular pathway, this pathway is considered enriched," Rodriguez Zas said. "Depending on whether the pathway and genes have tumor suppressor or oncogenic characteristics, we should be able to use that information to support or attack that pathway with targeted therapies."

Gaining a deeper understanding of the biological meaning, or roles, for these genes will provide researchers with even more ammunition to fight this deadly form of brain cancer.

"Because of the innovative approach we used, we believe we can more confidently predict whether a patient will have a shorter or longer survival rate and select the most adequate therapies," she said.

This study, "Cell cycle and aging, morphogenesis, and response to stimuli genes are individualized biomarkers of glioblastoma progression and survival," was published in *BMC Medical Genomics*. Researchers include Nicola Serao, Kristin Delfino, Bruce Southey, Jonathan Beever and Sandra Rodriguez Zas of the University of Illinois.

Provided by University of Illinois at Urbana-Champaign