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OU researchers learning more about human cancer through genetic analysis of corn

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The genetic information in a kernel of corn could be a key to better understandin how normal cells become cancerous in humans, according to a recent collaborat study conducted by a team of Oakland University researchers including (from left Catalina Kenney, Dr. Gerard Madlambayan, J. Paige Gronevelt, Dr. Randal Westric Dr. Shailesh Lal, and Amy Siebert-McKenzie.

“This is an exciting development as it suggests we can use plants as model systems to better understand human disease,” said **Dr. Gerard Madlambayan**, an associate professor with the **Department of Biological Sciences** who specializes in cancer research.

According to Madlambayan, the link was discovered when **Dr. Shailesh Lal**, a professor of biological sciences at Oakland University who specializes in the molecular and genetic analysis of plants, identified a “regulatory” gene while studying the corn genome.

“It turns out that if you destroy this gene, instead of being plump the kernel becomes totally shriveled,” Lal said. “Intriguingly, we found that if you take this mutant kernel and grow it in tissue culture, it proliferates, just like the growth of a tumor.”

Because the corn gene is “46 percent similar” to a human gene with unknown function, Lal partnered with Madlambayan to determine whether suppressing the gene would have an effect on human cancer cells as well. The study is also being conducted with **Dr. Randy Westrick**, an assistant professor of biological sciences, whose research focuses on the genetic determinants of thrombosis (abnormal blood clot formation) and who has expertise in mammalian genome-editing technology. OU students involved in the project include Amy Siebert-McKenzie (Ph.D. candidate) of St. Clair Shores, J. Paige Gronevelt (M.Sc. candidate) of Lake Orion, and Catalina Kenney, an undergraduate student from White Lake.

“Our team took cancer cell lines and suppressed the gene using CRISPR/Cas9, which is a cutting-edge tool used to edit genes,” Madlambayan said. “When we decreased expression in our leukemia cells, we found that it had a significant effect on the expression of many other genes known to be involved in cancer.”

This led the research team to suspect that this gene is a “master regulator gene,” or one that controls the expression of many other genes.

“We think our data is showing very clearly that this is a master gene that can control the expression of many genes,” Lal said. “We looked at the genes it affects and controls, and it tu out that a number of these genes have been reported to be involved in promoting the proliferation of cancer cells.”

With additional work from collaborators at the University of Florida (Dr. Brad Barbazuk and Dr. Mark Settles), the group is now starting to identify genes that are affected by the “maste gene.

“We’ve been doing this kind of genetic analysis in humans for a long time, but sometimes it just takes another way of thinking to lead you down a different path,” Madlambayan said. “ entire project started from analysis of corn genetics. We’re starting to show that you can learn a lot about human disorders by analyzing the plant genome, in this case corn.”

“Working on this collaborative project has been an amazing training experience” said Siebert-McKenzie. “It has broadened my knowledge of topics in my field to include not only blee and blood clotting disorders but also blood cell formation and blood cancer development.”

It is Lal’s hope that others learn from their discovery.

“We’re hoping that others will start to use plants as a model system to better understand human disease. That’s the path we’re on,” he said. “We’ve taken the expertise of plant and

The work was supported by external grants from the National Science Foundation (NSF) and the National Institutes of Health(NIH) as well as support from the Center for Biomedi Research at Oakland University.