

1-24-2012

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Recommended Citation

"Social Networks in our DNA" (2012). *News Releases*. 734.
https://ecommons.udayton.edu/news_rls/734

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Social Networks in our DNA

01.24.2012 | Research, Faculty, Science Sharing on social networks has become a part of everyday life — and it may even be part of our DNA, according to a University of Dayton biologist.

The National Science Foundation this month awarded University of Dayton biology assistant professor Thomas Williams a three-year, \$450,000 grant to study networks of genes and how these "social networks" evolve by establishing, changing or losing connections between them.

"From an evolutionary perspective, networks of genes have been cobbled together, sort of haphazardly," Williams said. "New connections are formed, existing connections are lost. The goal is to tease apart how genes communicate within these networks to understand which connections matter."

He will study differences in the abdominal pigmentation of male and female fruit flies of different species for clues on how evolution used the same genes differently to develop diversity.

Although his research focuses on fruit flies, the findings could have applications for human health and commercial endeavors.

"Like other organisms, humans have natural variation in our genes, but some of these variations are buffered because of the structure of genetic networks, and others aren't," Williams said. "My research may help us understand why."

"Genetic engineering is also widely used in commercial products, and an understanding of how one change will affect the whole organism is critical."

Williams said scientists have traditionally conceptualized trait development as the result of a linear pathway of genes. For example, he said, human gender is determined by the presence or absence of a specific Y chromosome gene, which then affects the activity of another gene and so on.

"But when you consider that male traits can differ not only in type but also in where and when they develop, you find pathways are insufficient to explain these profound differences," he said. "Researchers are only recently exploring traits not as the result of pathways but as the result of larger networks — an assembly of multiple pathways working together."

Williams' research is rooted in discoveries in the 1980s that found radically different organisms have a similar set of genes, suggesting much of the Earth's biological diversity comes not from new genes but on how the same genes are used differently.

A major factor in how organisms use the same genes differently is cis-regulatory elements or enhancers — what Williams calls "genetic switches." These switches send signals to genes that instruct them when and where in an organism to "turn on" — that is, make a protein. Recent studies have shown mutations in these switches can affect cholesterol levels, heart attack risk, developmental disorders and various disease susceptibilities.

This NSF grant is Williams' second national funding award. In 2011, he received \$132,000 from the American Heart Association to support research on fruit flies that may lead to an understanding of how seemingly obscure changes in our genetic code can lead to increased heart disease risk and even lactose intolerance.

He has published research on topics in evolutionary biology in *Nature*, *Nature Reviews Genetics* and *Cell*. His research focuses on understanding why members of the same and different species look and behave differently.

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