

# Between the genes -- a making sense of genomic 'dark matter'

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A group of University of Toronto scientists have uncovered some of the secrets behind what molecular biologists call "dark matter" transcripts. The findings will be published next week in the online, open access journal *PLoS Biology*.

The term "dark matter" refers to the genomic output that does not originate from known [genes](#), arising instead from regions that were once thought of as nothing more than "[junk DNA](#)." When genetic signals, namely RNA transcripts, were discovered coming from these areas, many believed there was a whole new mystery to solve, and that much more was going on than originally expected.

However, a new study, led by Postdoctoral Fellow Harm van Bakel and Prof. Timothy Hughes from the Banting and Best Department of Medical Research and the Terrence Donnelly Centre for Cellular and Biomolecular Research, indicates that most of these signals are likely to be by-products of signals from already known genes. Most of the other signals, the research indicates, are more consistent with background noise than meaningful signals.

Part of the mystery came from the methodology used. Many original reports of dark matter signals used "tiling microarrays," which these researchers determined was creating many false positives. By using a recently available method of sequencing very large numbers of transcripts, they were able to determine that unexplained dark matter only accounts for 2% of the total transcripts, much less than originally

believed. Of that 2%, most are very close to known genes, indicating that they are likely to be part of the gene itself.

"The fact that most dark matter transcripts could be linked to known genes suggests that they are not signals emerging from a hidden universe within the genome," says van Bakel. "Though it is too early to exclude some functional role, the dark matter transcripts may primarily be by-products of normal [gene expression](#)."

"Given the size of the human [genome](#), it's important to know where to focus our attention," says van Bakel. "Up until now, we had no way of knowing if we were missing out on some key biological information. This discovery allows us to zero in on what is really important."

**More information:** van Bakel H, Nislow C, Blencowe BJ, Hughes TR (2010) Most "Dark Matter" Transcripts Are Associated With Known Genes. PLoS Biol 8(5): e1000371. [doi:10.1371/journal.pbio.1000371](https://doi.org/10.1371/journal.pbio.1000371)

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