Exploring lincRNA's role in breast cancer

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Once considered part of the "junk" of our genome, much of the DNA between protein-coding genes is now known to be transcribed. New findings by scientists at Fox Chase Cancer Center have identified several dozen transcripts known as lincRNAs, or long intergenic non-coding RNAs, that are dysregulated in breast cancer. The results, to be presented at the AACR Annual Meeting 2013 on Monday, April 8, offer both a new research path for better understanding of how breast cancer works and a new method for identifying lincRNAs that may contribute to tumorigenesis or regulation of other cancers.

"This is a very preliminary result," says study author Xiaowei Chen, PhD, assistant professor at Fox Chase, "because we spent most of our time trying to define how to pull out the useful information" from the region of the genome between protein-coding genes. Even though "the overall concept is new," says Chen, in the end the team settled on standard methods for each step of the genome-wide approach for identifying lincRNA-coding regions.

In the study, researchers conducted pairwise comparisons of genomic information between five tumor samples and the adjacent normal cells. That comparison yielded 47 lincRNA transcripts, of which the team selected the most prevalent 14. They then checked how these lincRNAs were expressed by 12 established breast cancer cell lines and four non-cancerous cell lines. The team found that expression varied widely, indicating that lincRNAs are differentially regulated within breast cancer cell lines.

"We wanted to identify the changes in order to find some candidates," says Chen, rather than identify all candidates; "there are many more, I believe." The next step will be to conduct a functional analysis of these 14 most prevalent transcripts to see if the expression has any biological meaning. Already, the team has identified one lincRNA gene that Chen says "looks pretty promising," but full results will come later.

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