

Study links long non-coding RNAs with the timing of gene expression

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(Phys.org) —Yeast can quickly adapt to changes in its environment with the help of molecules known as long non-coding RNAs, a Purdue study shows.

Elizabeth Tran, assistant professor of biochemistry, and her fellow researchers found that long non-coding RNAs prepare metabolic genes to be activated swiftly when baker's yeast needs to switch its source of energy from glucose - its main sugar source - to an alternative sugar, galactose.

The study is the first to link long non-coding RNAs with the timing of [gene expression](#).

"The fact that long non-coding RNAs are involved in the timing of gene expression was totally unexpected," Tran said. "This opens up new and exciting challenges for the future of genomic research."

Long non-coding RNAs - ribonucleic acids that are longer than 200 nucleotides - are molecules that influence the expression of protein-coding genes in yeast, plants and mammals. They were first described in 2007, and the functions of the vast majority of these molecules remain unknown.

One suggested role of long non-coding RNAs in yeast was [gene repression](#), but Tran's study showed the opposite is true: Long non-coding RNAs accelerate the activation of genes involved in galactose

digestion when glucose is lacking in the environment.

Yeast with long non-coding RNA begin metabolizing galactose about 30 minutes quicker than yeast without - a significant time difference in an organism that replicates every 90 minutes.

"That quick shift could make the difference in survival," Tran said.

Over time, the level of galactose enzyme gene expression in [yeast](#) with and without long non-coding RNAs becomes the same, but "it's that initial burst of gene expression in response to the environment that may provide a significant evolutionary advantage," said Tran. She likened it to the edge a sprinter would gain over his opponents by propelling himself out of the starting block ahead of them.

"One reason the runner Usain Bolt is so fast is that he developed a technique of getting out of the block really quickly," she said. "Being able to do that means you can spread out your energy during the race - all because you started faster at the beginning."

Tran said that similar long non-coding RNAs might play a role in the timing of gene expression in humans as well. In mammals, they are often associated with genes that control growth and organ development, which require tight control of initiation timing.

"When a growing embryo has to make an arm, for example, that timing has to be incredibly precise," she said.

Humans contain upwards of 8,000 long non-coding RNAs, some of which have been linked to cancer, developmental diseases and cardiomyopathy and other non-DNA mutations in the genome. Tran said the chances are high that long non-coding RNAs play a role in human diseases, developmental defects and delays.

"Now the question becomes why long non-coding RNAs are so closely associated with development," Tran said. "Having opened up the possibility that they're linked to timing and not end level of gene expression is really key."

More information: Cloutier SC, Wang S, Ma WK, Petell CJ, Tran EJ (2013) Long Noncoding RNAs Promote Transcriptional Poising of Inducible Genes. *PLoS Biol* 11(11): e1001715. [DOI: 10.1371/journal.pbio.1001715](https://doi.org/10.1371/journal.pbio.1001715)

Provided by Purdue University

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