



# HARVARD MEDICAL SCHOOL

## NEWS ALERT

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### Newly discovered RNA steers brain development

#### FINDINGS:

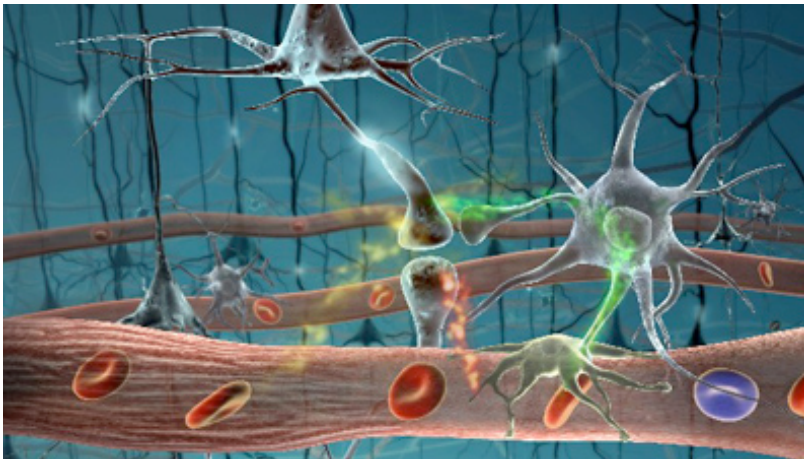
A newly discovered class of RNA molecules helps elucidate the long-standing scientific question of how a person's external experiences turn on the genes that over time help shape the connections among cells that make up the human brain. Called enhancer RNAs, these molecules operate globally throughout the genome within neurons.

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#### RELEVANCE:

These findings reveal a new and foundational way that neurons regulate gene activity in response to external stimuli. There is mounting evidence that this particular process of regulation is at the heart of many disorders of cognition, such as autism spectrum disorders.



Amid a network of blood vessels and star-shaped support cells, neurons in the brain signal each other and form synaptic connections.

Image courtesy of National Institute of General Medical Sciences.

BOSTON, Mass. (April 14, 2010) — How does the brain work? This question is one of the greatest scientific mysteries, and neurobiologists have only recently begun to piece together the molecular building blocks that enable human beings to be “thinking” animals.

One fundamental property of the mammalian brain is that it continues to develop after birth,

and one of the biggest drivers of the formation of new links between neurons is experience. Every time a baby sticks her finger on a pin or laughs in response to an adult's embellished gestures, a cascade of genetic activity is triggered in her brain that results in new, and perhaps even lifelong, synaptic connections.

New research from the lab of [Michael Greenberg](#), Nathan Marsh Pusey professor and chair of neurobiology at HMS, in collaboration with bioinformatics specialist and neuroscientist [Gabriel Kreiman](#), assistant professor of ophthalmology at Children's Hospital Boston, has found that a particular set of RNA molecules widely considered to be no more than a genomic oddity are actually major players in brain development—and are essential for regulating the process by which neurons absorb the outside world

into their genetic machinery.

“This discovery may inform disorders of cognition such as autism spectrum disorders,” says Greenberg. “It’s incredibly important to know all about the brain’s genetic regulatory mechanisms in order to think more deeply about how to develop therapies for treating these sorts of conditions.”

This research will be published online April 15 in the journal *Nature*.

For over 25 years, Greenberg and his lab have been unraveling the mechanisms that enable the outside world to have a profound and lasting effect on neuronal genes. Broadly speaking, when a neuron is stimulated by an external excitation (the pin, the gesture), it releases chemicals called neurotransmitters (the most common one is glutamate). This neurotransmitter binds to a receptor on the neuron surface and then sets in motion a chain of events that affects the genetic activity of the cell. This in turn helps to modify the synaptic connections between neurons, which are the basis of learning and memory.

But what exactly happens inside of a cell after it is activated by neurotransmitter release?

To get closer to the cellular action, Tae-Kyung Kim and Jesse Gray of the Greenberg lab, in collaboration with Martin Hemberg from the Kreiman lab at Children’s, used two kinds of high-throughput, next-generation sequencing technologies, RNA-Seq and CHIP-Seq.

Working with mouse brain cells in culture, the researchers used RNA-Seq to identify, with great sensitivity, the RNA sequences that are newly synthesized when a neuron is stimulated in a manner that mimics the effect of a neurotransmitter, and which in turn touches off a domino-like cascade of intracellular signals. The researchers were then able to identify, sequence and—using CHIP-Seq—establish the genomic “address” and the regulatory factors that control the expression of all the genes switched on in these brain cells by the stimulus.

They discovered that there were individual and disparate stretches of DNA that appeared to be amplifying the genes’ activity, escalating the process of messenger RNA and protein production. These bits of DNA, called “enhancer regions,” were more often than not targeting their genes over vast genomic distances, like a computer dictating orders to a global digital network via satellite.

Most important, however, was the discovery that these enhancer regions accomplished this phenomenon by producing their own RNA molecules, and that these enhancer RNAs, or eRNAs, were intensifying the enzymatic processes that are essential for a gene’s ability to create protein.

“Biologists have known about enhancers since 1980, and there has even been a paper or two describing RNA produced at enhancer regions, but it was largely considered an isolated curiosity,” says Greenberg. “What we’ve discovered here is how widespread this phenomenon is. We’ve found that there are thousands of these enhancers, that they’re spread throughout the genome, and that they are essential to the process in which experience results in new synaptic connections. What’s more, we suspect that they’re active in many other mammalian cell types, not just neurons.”

It isn’t clear yet precisely how these eRNAs accomplish their synaptic-building tasks, or even where they travel to within the neuron once they are produced. These are questions for further study. Still, the researchers believe there is a likelihood that these finding may eventually prove relevant to, and cast light on, our understanding of certain neurological and psychiatric disorders in which the regulation of gene activity plays a critical role.

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Written by David Cameron

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“Widespread transcription at neuronal activity-regulated enhancers”

Tae-Kyung Kim(1\* ^), Martin Hemberg(2\*), Jesse M. Gray(1\*), Allen M. Costa<sup>1</sup>, Daniel M. Bear(1), Jing Wu(3), David A. Harmin(1,4), Mike Laptewicz(1), Kellie Barbara-Haley(5), Scott Kuersten(6), Eirene Markenscoff-Papadimitriou(1^), Dietmar Kuhl(7), Haruhiko Bito(8), Paul F. Worley(3), Gabriel Kreiman(2) & Michael E. Greenberg(1)

(1) Department of Neurobiology, Harvard Medical School, 220 Longwood Avenue, Boston, Massachusetts 02115, USA.

(2) Department of Ophthalmology, Children’s Hospital Boston, Center for Brain Science and Swartz Center for Theoretical Neuroscience, Harvard University, 300 Longwood Avenue, Boston, Massachusetts 02115, USA.

(3) The Solomon H. Snyder Department of Neuroscience, Johns Hopkins University School of Medicine, 725 North Wolfe Street, Baltimore, Maryland 21205, USA.

(4) Children’s Hospital Informatics Program at the Harvard-MIT Division of Health Sciences and Technology, 300 Longwood Avenue, Boston, Massachusetts 02115, USA.

(5) Molecular Genetics Core facility, Children’s Hospital Boston, 300 Longwood Avenue, Boston, Massachusetts 02115, USA.

(6) Epicentre Biotechnologies, 726 Post Road, Madison, Wisconsin 53713, USA.

(7) Institute for Molecular and Cellular Cognition (IMCC), Center for Molecular Neurobiology (ZMNH), University Medical Center Hamburg-Eppendorf (UKE), Falkenried 94, 20251 Hamburg, Germany.

(8) Department of Neurochemistry, Graduate School of Medicine, University of Tokyo, Bunkyo-ku, Tokyo 113-0033, Japan.

^ Present addresses: University of Texas Southwestern Medical Center, Department of Neuroscience, 5323 Harry Hines Blvd, Dallas, Texas 75390-9111, USA (T.-K.K.); Graduate Program in Neuroscience, University of California San Francisco, 513 Parnassus Avenue, San Francisco, California 94123, USA (E.M.-P.).

\* These authors contributed equally to this work.

**HARVARD MEDICAL SCHOOL CONTACT:**

David Cameron

[david\\_cameron@hms.harvard.edu](mailto:david_cameron@hms.harvard.edu)

617.432.0441

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