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Contact: James Devitt
212.998.6808
james.devitt@nyu.edu

RESEARCHERS FIND NEW GENES NECESSARY TO MAKE EMBRYO

Researchers at New York University and the medical schools at Harvard and Yale universities have identified new genes necessary for embryonic development, according to findings published in the latest issue of *Genome Research*. This discovery is an important step toward a complete mapping of which parts of the genome are required for embryonic development. The new findings also probe into how genetic networks are built and how they could evolve.

The team, headed by biologists at NYU, is studying the genome of the *Caenorhabditis elegans* (*C. elegans*), the first animal species whose genome was completely sequenced and a model organism to study how embryos develop. Using RNA interference (RNAi), a method for identifying the function of genes, the researchers almost double previous estimates of how many genes are required to make an embryo. Their study focused on the genes expressed by the mother and imparted to the egg, ready to be used during the earliest stages after fertilization. They discovered over 150 additional genes required to make an embryo beyond what was previously known, leading them to conclude that many more genes will be found in the future. The researchers estimate that at least 2,600 genes are required for embryonic development in *C. elegans*, of which about 70% are currently known.

The majority of genes required for embryogenesis in *C. elegans* have counterparts in humans whose roles are often unknown. For example, human counterparts of four of the newly identified genes are known to be associated somehow with disease, and mutations in two of these are associated with tumors. The *C. elegans* study suggests specific cellular roles for these genes, thus providing important clues to how these genes work in humans.

The new data also asked allowed the researchers to have a first genome-wide look at a classic genetic phenomenon called "partial penetrance" – whereby the same genetic mutations may elicit different results in different individuals.

"The results from the analyses of genes showing partial penetrance suggest the possibility of a general architectural motif in genetic networks," said Fabio Piano, an NYU biologist and lead author of the study, "in which genes in critical positions consist largely of older components while new functions added later provide additional layers of regulation to lend adaptive functions to these core networks."

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