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## **NYU BIOLOGISTS MAP OUT EARLY STAGES OF EMBRYO FORMATION**

A team of genomic researchers headed by biologists at New York University's Center for Comparative Functional Genomics, in collaboration with researchers at Harvard University, the Max Planck Institute, and Cenix Biosciences, has mapped out a preliminary molecular diagram of the early stages of embryo formation, offering for the first time a global look at how a single cell begins its path into a multi-cellular organism. The findings are reported in the August 11 issue of the journal *Nature*.

The team is studying the function of the genome of *Caenorhabditis elegans* (*C. elegans*), the first animal species whose genome was completely sequenced and a model organism to study how embryos develop.

With the complete genome sequence of *C. elegans*, the researchers sought to comprehend how the parts encoded by the genome are used to build complex dynamical biological systems—in this case, an engineering diagram for embryo formation. Using a new way to combine results from different functional genomic approaches including RNA interference (RNAi), a method for studying the function of genes *in vivo*, the researchers were able to develop a first-draft diagram for the early embryo at the molecular level, describing how its components fit together both physically and logically.

“These results point to a high level of coordination among a relatively small number of molecular machines required for proper early embryonic development in *C. elegans*,” said Fabio Piano, an assistant professor in NYU's Department of Biology, who headed the research team. “This may also be the case for human embryogenesis. The diagrams linking all these genes reveal discrete patterns of interconnections, allowing us to begin to visualize the molecular network underlying a complex process like early embryogenesis as a whole.”

These analyses suggest that out of the almost 20,000 genes in *C. elegans*, the embryo requires a core set of less than 1,000 genes to coordinate the early events that guide the development of the animal. The results further suggest specific roles for new genes that had not been studied before, and functional tests of a subset of these supported the predictions.

Describing how embryos function at the molecular level may help understand how human embryos develop, and may also provide new insights for cancer research since genes acting in early embryogenesis are often erroneously reactivated in cancer cells.

The research is the latest in a series of studies conducted at NYU's Center for Comparative Functional Genomics in collaboration with researchers at Harvard and Yale Universities, which set the stage for these most recent findings. An essential aspect of these studies was the coordination between experts in cell and molecular biology and those with computational and mathematical backgrounds.

At the NYU Center for Comparative Functional Genomics, this research program work has been supported by grants from the National Institute of Child Health and Human Development to Piano and NSF's ADVANCE Fellows program to Kristin Gunsalus, assistant research professor in NYU's Department of Biology and a first author of the study published in *Nature*.

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