How Maternal Transcription Factors Shape Early Embryonic Chromatin Landscape in Time and Space

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Ken Cho
Professor, Developmental and Cell Biology
University of California, Irvine

For more information, contact: Nestor Oviedo
noviedo2@ucmerced.edu

Abstract
After fertilization, the embryonic genome is inactive until transcription is initiated during the maternal-to-zygotic transition, known as zygotic genome activation (ZGA). At present, the functional relationships between transcription factors (TFs), co-regulators and the epigenetic landscape around ZGA, and subsequent germ layer specification, are still not well understood. Our current model is that maternally expressed TFs collectively function at the top of a hierarchy of TF interactions to not only mark developmental genes for activation prior to the onset of zygotic gene expression, but also coordinate major reorganization of the epigenetic landscape during ZGA.

About the Speaker
Grinnell College, Grinnell, IA B.S 1980 Chemistry
University of Pennsylvania, Philadelphia, PA Ph.D. 1985 Molecular Biology

1986-1991 Postdoctoral Fellow, Biological Chemistry, UCLA, CA
1991-1997 Assistant Professor, Developmental & Cell Biology, UCI CA
1997-2000 Associate Professor, Developmental & Cell Biology, UCI, CA
2000-present Professor, Developmental & Cell Biology, University UCI, CA
2005-2007 Vice-chair, Developmental & Cell Biology, UCI, CA
2007-2012 Chair, Developmental and Cell Biology, UCI, CA

2005-2010 Editorial Board, Cell Research
2012-2020 Advisory Board Member, Development, Growth and Differentiation
2011-present Editorial Board, Developmental Biology
2014-present Editorial Board, JoVE
2020-present Deputy Editor, Development, Growth and Differentiation

Honors
1992-1994 Basil O’Connor Research Scholar
1993-1995 American Cancer Society Junior Faculty Research Award
1994-1998 Pew Scholar in Biomedical Sciences
1996-2001 NIH Research Career Development Award
2012 AAAS fellow, elected