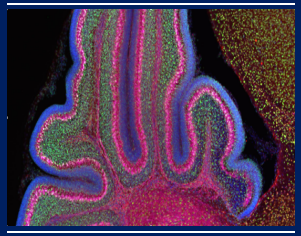
QUANTITATIVE & SYSTEMS BIOLOGY COLLOQUIUM: Chromatin Regulation of Neuronal Maturation

Anne West
Duke University



Date:
02/26/2026

Time:
10:30 AM – 11:45 AM

Location:
SSM 116

About The Speaker:

Anne E. West is the George Barth Geller Distinguished Professor of Neurobiology, Professor of Cell Biology, and the Associate Director of the Medical Sciences Training Program (MSTP) in the Duke University School of Medicine. She is a member of the Duke Institute for Brain Sciences, the Center for Advanced Genomic Technologies, and the Duke Cancer Institute.

Dr. West is a molecular geneticist whose research focuses on identifying the regulatory mechanisms that control the development and plasticity of the brain. She seeks to discover how environmental experiences are transduced into changes in brain function via epigenetic modification of the genome. Her lab uses transgenic mice, behavioral analyses, biochemical and cell biological methods, human neurons, and high-throughput sequencing to elucidate the mechanisms by which chromatin regulatory proteins promote adaptations in neuronal function. In addition to enhancing understanding of normal brain development and plasticity, her studies are revealing how dysregulation of neuronal gene transcription contributes to cognitive impairment, substance use, and neurodevelopmental disorders including autism.

Dr. West obtained her B.A. in 1989 from Cornell University, where she did undergraduate research in chemical ecology. She received her M.D. and Ph.D. degrees in 1998 from Harvard Medical School, with research in neuronal cell biology. She then did postdoctoral research at Children's Hospital in Boston, studying signal transduction and activity-dependent plasticity in neurons. She came to Duke as an Assistant Professor in 2005.

Dr. West is highly involved in graduate education at Duke, and she is a past winner of the Gordon G. Hammes faculty teaching award from the School of Medicine. She is also a 2025 recipient of the Landis Award from NINDS for outstanding mentoring. She has been active in university governance, serving on the Academic Council as well as its executive committee, the University Priorities Committee, and the External Engagement committee of the Board of Trustees. Outside of Duke, she serves on the Board of Reviewing Editors at eLife and she is a frequent grant reviewer and study section chair for the National Institutes of Health, as well as a reviewer for the Simons Foundation Autism Research Initiative (SFARI).

Abstract:

Neurons are remarkably long-lived cells that are born early in development and maintained over the lifespan of an organism. In the developing brain, neurogenesis is followed by a prolonged period of transcriptional maturation, during which neurons acquire the functional capacity to participate in CNS circuitry. This postmitotic phase of neuronal maturation is mediated at least in part by regulators of chromatin biology; mutations in chromatin regulators are implicated in neurodevelopmental disorders, showing the importance of this process for cognition.

To discover how transcriptional regulatory networks evolve over neuronal maturation, we used a novel low-input sequencing method called 'HiCAR' or (HiC on accessible regulatory DNA) to profile dynamics in regulatory chromatin loop formation in maturing cerebellar granule neurons (CGNs) as a function of time and in response regulatory perturbations. We observe that as CGNs mature, they show bidirectional changes in cis-regulatory loop formation at genes that turn on early versus late in differentiation. By 7 days-in-vitro (DIV7), CGNs gain about four-times as many regulatory loops compared to granule neuron precursors (GNPs), over half of which are anchored at least at one promoter and concentrated within topologically associating domains (TADs). We also find these interactions to be potentially poised by an architectural role for the repressive chromatin modification H3K27me3. Taken together, we show that the transcriptional maturation of CGNs occurs in concert with the maturation of their gene-regulatory topology.

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