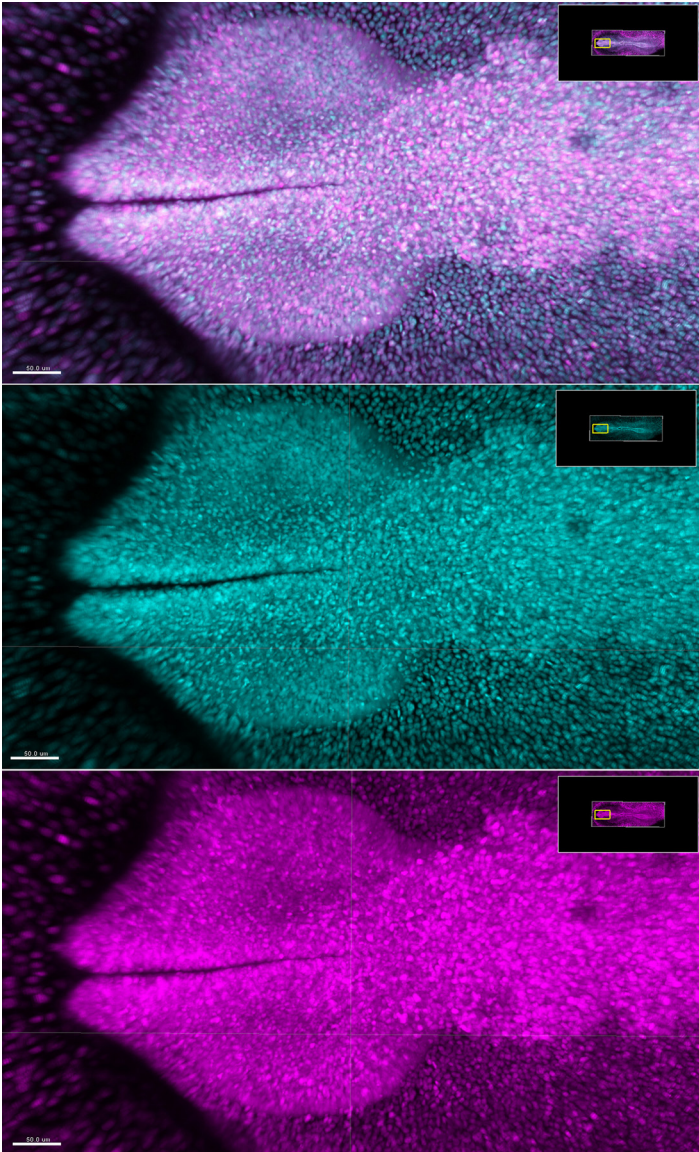


Abstracts of papers presented  
at the 2014 meeting on

# AVIAN MODEL SYSTEMS

March 5–March 8, 2014



Cold Spring Harbor Laboratory  
Cold Spring Harbor, New York

Abstracts of papers presented  
at the 2014 meeting on

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# AVIAN MODEL SYSTEMS

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March 5–March 8, 2014

Arranged by

David Clayton, *Queen Mary University of London, UK*

Rusty Lansford, *Children's Hospital Los Angeles/  
University of Southern California*

Andrea Streit, *Kings College London, UK*

Cold Spring Harbor Laboratory  
Cold Spring Harbor, New York

This meeting was funded in part by the **University of Arizona; Developmental Dynamics, Elsevier/*Mechanisms of Development* and International Society of Developmental Biologists;** and the **Society for Developmental Biology and *Developmental Biology*.**



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*Front Cover:* Stage 9 Tg(PGK:H2B-mChFP) quail embryos showing H2B-chFP+ cell nuclei; DAPI stained nuclei; and merged images of H2B-chFP+ & DAPI stained nuclei. Image by David Huss\_Lansford lab.

*Back Cover (top):* Zebra finches. Image by David Clayton.

*Back Cover (bottom):* Multiplexed amplification with orthogonal hybridization chain reactions in a quail embryo. Image by David Huss\_Lansford lab.

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**The neural crest cell cycle is related to phases of migration in the head**

Dennis A. Ridenour, Rebecca McLennan, Jessica M. Teddy, Craig L. Semerad, Jeffrey S. Haug, Paul M. Kulesa.

Presenter affiliation: Stowers Institute for Medical Research, Kansas City, Missouri.

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**Novel tools for characterising inter- and intra-chromosomal rearrangements in avian microchromosomes**

Pamela E. Lithgow, Rebecca O'Connor, Deborah Smith, Gothami Fonseka, Claudia Rathje, Richard Frodsham, Patricia C. O'Brien, Malcolm A. Ferguson-Smith, Benjamin M. Skinner, Darren K. Griffin, Michael N. Romanov.

Presenter affiliation: University of Kent, Canterbury, United Kingdom.

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**Origin of the avian adenohipophyseal placode and its relationship with other rostral placodes**

Luisa Sanchez-Arrones, Marcos Cardozo-Ruiz, Africa Sardonis, Jose Luis Ferran, Matias Hidalgo-Sanchez, Luis Puelles, Paola Bovolenta.

Presenter affiliation: Centro de Biología Molecular Severo Ochoa, Madrid, Spain; CIBER de Enfermedades Raras, Madrid, Spain.

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**Transcriptional profiling to characterize tissues and pathways in the chicken**

Carl J. Schmidt, Colin Kern, Allison G. Rogers, Chris M. Ashwell, Michael E. Persia, Max F. Rothschild, Robert L. Alphin, Eric Benson, Susan J. Lamont.

Presenter affiliation: University of Delaware, Newark, Delaware.

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**Characterization of primary cilia extension during cranial neural crest cell ontogeny**

Elizabeth N. Schock, Ching-Fang Chang, Jaime N. Struve, Samantha A. Brugmann.

Presenter affiliation: Cincinnati Children's Hospital Medical Center, Cincinnati, Ohio.

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**Specification of the podocyte and tubular components of the avian mesonephric kidney**

Mor Grinstein, Ronit Yelin, Doris Herzlinger, Thomas M. Schultheiss.

Presenter affiliation: Technion-Israel Institute of Technology, Haifa, Israel.

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## NOVEL TOOLS FOR CHARACTERISING INTER- AND INTRA- CHROMOSOMAL REARRANGEMENTS IN AVIAN MICROCHROMOSOMES

Pamela E Lithgow<sup>1</sup>, Rebecca O'Connor<sup>1</sup>, Deborah Smith<sup>1</sup>, Gothami Fonseka<sup>1</sup>, Claudia Rathje<sup>1</sup>, Richard Frodsham<sup>2</sup>, Patricia C O'Brien<sup>3</sup>, Malcolm A Ferguson-Smith<sup>3</sup>, Benjamin M Skinner<sup>1,4</sup>, Darren K Griffin<sup>1</sup>, Michael N Romanov<sup>1</sup>

<sup>1</sup>University of Kent, School of Biosciences, Canterbury, United Kingdom, <sup>2</sup>Cytocell Ltd, Newmarket Road, Cambridge, United Kingdom, <sup>3</sup>University of Cambridge, Department of Veterinary Medicine, Cambridge, United Kingdom, <sup>4</sup>University of Cambridge, Department of Pathology, Cambridge, United Kingdom

Avian genome organization is characterized, in part, by a set of microchromosomes that are unusually small in size and unusually large in number. Although occupying about a quarter of the genome, they contain around half the genes and three quarters of the chromosome count. Nonetheless, they continue to belie analysis by cytogenetic means. Chromosomal rearrangements play a key role in genome evolution, fertility and genetic disease and, thus, tools for the microchromosomes are essential to analyze such phenomena in birds. Here we report the development of chicken microchromosomal paint pools, generation of pairs of specific microchromosome BAC clones in chicken, and tools for *in-silico* genomic comparison of microchromosomes. We demonstrate the application of these tools cross-species, which can, in principle, be used in combination to generate a clear picture of microchromosomal rearrangements for numerous avian species. With increasing numbers of avian genome sequences being generated, tools such as these will find great utility in assembling genomes *de-novo* and asking fundamental questions about genome evolution from a chromosome perspective.

