

Andrew R. Gehrke
Curriculum Vitae

Current Address

The University of Chicago, Shubin Lab
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EDUCATION

- 2010-Current **The University of Chicago**
Ph.D Candidate
Department of Organismal Biology and Anatomy
- 2008-2010 **Harvard University (Cambridge, MA)**
Master of Liberal Arts in Extension Studies
Concentration in Biology, September 2010
- 2001-2005 **Boston University (Boston, MA)**
B.A. Philosophy, May 2005

LABORATORY EXPERIENCE

- 2010-Present **Graduate Student, Ph.D Candidate**
The University of Chicago Dept. of Organismal Biology and Anatomy
Laboratory of Prof. Neil Shubin
Gene regulation, genomics, evolution and development of fins and limbs
- 2008-2010 **Graduate Student, ALM Program**
Harvard University Dept. of Organismal and Evolutionary Biology
Laboratory of Prof. Arkhat Abzhanov
Developmental genetics, craniofacial evolution and development.
Thesis Project: Recently, the Abzhanov lab has identified a positive correlation between levels of bone morphogenetic protein 4 (BMP4) and beak depth and width in Darwin's finches. The coding region of BMP4 is nearly 100% conserved throughout these birds, leading us to believe that changes in *cis*-regulatory elements are responsible for generating species-specific beak morphology. To identify regulatory elements of BMP4 that drive expression in the developing beak, we have created lentiviral constructs containing areas of conservation between the chicken and mouse

genomes upstream of GFP. By using this method we hope to identify *cis*-regulatory elements that control BMP4 expression in the beak of the chicken, which we can then line up to the orthologous enhancer in Darwin's finches to probe for potential differences in transcription factor binding sites between species.

2005-2008

Technical Research Assistant

Brigham and Women's Hospital/Harvard Medical School

Laboratory of Prof. Martha L. Bulyk

Functional genomics, identification of transcription factor binding sites and *cis*-regulatory elements.

Project: The DNA binding preferences for most transcription factors (TFs) remain unknown, or poorly annotated. In order to identify and understand genomic regulatory elements, high quality binding site data are needed for a large amount of TFs. We determined the binding preferences for 168 mouse homeodomains as well as 104 additional TFs from a variety of structural classes using a novel design of a protein binding microarray which covers all possible binding variants of up to 10 base pairs. We hope that these data will enhance the ability to identify genomic *cis*-regulatory elements.

2003-2005

Undergraduate Volunteer

Boston University, Department of Biology

Laboratory of Dr. Karen Warkentin

Phenotypic plasticity of the neotropical red-eyed tree frog

Agalychnis callidryas in response to predation

Project: Many neotropical tadpole embryos have the ability to hatch early in response to predation. We attempted to describe a development series of early-hatched tadpoles of the tree frog *Agalychnis saltador* in order to investigate cost/benefit analysis of early hatching.

FIELD EXPERIENCE

October 2004 La Selva Biological Research Station, Costa Rica.

In conjunction with Dr. Ivan Gomez-Mestre of Boston University. Conducted independent nighttime amphibian collection in remote rainforest area, prepared a developmental series of the tree frog *Agalychnis saltador* by extracting tadpoles from eggs at different times during development to analyze the morphological and

developmental effects of premature hatching due to vibrational cues of predators.

PUBLICATIONS

2011

Schneider I, Aneas I, **Gehrke AR**, Dahn RD, Nobrega MA, and Shubin NH. (2011) Appendage expression driven by the Hoxd Global Control Region is an ancient gnathostome feature. *PNAS*. July 15, 2011.

Helfer A, Nusinow DA, Chow BY, **Gehrke AR**, Bulyk ML, Kay SA. (2011) LUX ARRHYTHMO encodes a nighttime repressor of circadian gene expression in the Arabidopsis core clock. *Curr Biol*. 2011 Jan 25;21(2): 126-33

2010

Santos MA, Turinsky AL, Ong S, Tsai J, Berger MF, Badis G, Talukder S, **Gehrke AR**, Bulyk ML, Hughes TR, and Wodak SJ (2010). Objective sequence-based subfamily classification of mouse homeodomains reflect their in vitro DNA-binding preferences. *Nucleic Acids Res*. Dec 1; 38(22):7927-42

Wei GH, Badis G, Berger MF, Kivioja T, Palin K, Enge M, Bonke M, Jolma A, Varjosalo M, **Gehrke AR**, Yan J, Talukder S, Turunen M, Taipale M, Stunnenberg GH, Ukkonen E, Hughes TR, Bulyk ML, and Taipale J (2010). Genome-wide analysis of ETS-family DNA-binding in vitro and in vivo. *EMBO J*. Jul 7;29(13):2147-60

2009

Badis G*, Berger MF*, Philippakis AA*, Talukder S*, **Gehrke AR***, Jaeger SA*, Chan ET*, Metzler G, Vedenko A, Chen X, Kuznetsov H, Wang CF, Coburn D, Newburger DE, Morris Q, Hughes TR, Bulyk ML. (2009) Diversity and complexity in DNA recognition by transcription factors. *Science*. Jun 26;324(5935):1720-3.

* designates co-1st authors

Lesch BJ, **Gehrke AR**, Bulyk ML, Bargmann CI. (2009) Transcriptional regulation and stabilization of left-right neuronal identity in *C. elegans*. *Genes Dev*. Feb 1;23(3):345-58.

Alleyne TM, Peña-Castillo L, Badis G, Talukder S, Berger MF, **Gehrke AR**, Philippakis AA, Bulyk ML, Morris QD, Hughes TR. (2009) Predicting the binding preference

of transcription factors to individual DNA k-mers. *Bioinformatics*. Apr 15;25(8):1012-8.

2008

Berger MF*, Badis G*, **Gehrke AR***, Talukder S*, Philippakis AA, Peña-Castillo L, Alleyne TM, Mnaimneh S, Botvinnik OB, Chan ET, Khalid F, Zhang W, Newburger D, Jaeger SA, Morris QD, Bulyk ML, Hughes TR. (2008) Variation in homeodomain DNA binding revealed by high-resolution analysis of sequence preferences. *Cell*. Jun 27;133(7):1266-76.

* designates co-1st authors

De Silva EK, **Gehrke AR**, Olszewski K, León I, Chahal JS, Bulyk ML, Llinás M. (2008) Specific DNA-binding by apicomplexan AP2 transcription factors. *PNAS*. Jun 17;105(24):8393-8.

PRESENTATIONS

Poster: “*Identification of mammalian transcription factor binding sites using protein binding microarrays*” Systems Biology: Global Regulation of Gene Expression. (March 2007) Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

Poster: “*Determination of mouse transcription factor DNA binding specificities using a compact, universal protein binding microarray*” ORFeome meeting: Orfeomes and Systems (October 2006) Boston MA

Poster: “*Identification of mammalian transcription factor binding sites using protein binding microarrays*”
Harvard Medical School Genetics Retreat (May 2007) Salve Regina University, RI

Poster: “*Determination of mouse transcription factor DNA binding specificities using a compact, universal protein binding microarray*”
Harvard Medical School Genetics Retreat (May 2006) Salve Regina University, RI

Talk: “*How to make an animal: identifying genomic regulatory elements and the making of the metazoan body plan*”
Quincy House Senior Common Room (December 2006) Harvard University, Cambridge, MA