

# Adam R. Boyko

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## Professional Experience

### **Cornell University College of Veterinary Medicine, Ithaca, NY**

Assistant Professor, Biomedical Sciences (2011–present)

### **Embark Veterinary, Inc., Ithaca, NY**

Co-founder and Chief Science Officer (2015–present)

### **Stanford University School of Medicine, Stanford, CA**

Research Associate, Genetics (2009–2011)

### **Cornell University, Ithaca, NY**

Research Associate, Biological Statistics & Computational Biology (2008–2009)

Postdoctoral Researcher, Biological Statistics & Computational Biology (2005–2008)

## Education

### **Purdue University, West Lafayette, IN**

Ph.D., Biology, 2005

M.S., Computer Science, 2004

### **University of Illinois at Urbana-Champaign**

B.S., Ecology, Ethology & Evolution, 1999

B.S., Computer Science, 1999

## Publications

### *Journal Articles*

1. Adam H. Freedman, AH, RM Schweizer, DO Vecchyo, E Han, B Davis, I Gronau, PM Silva, M Galaverni, Z Fan, P Marx, B Lorente-Galdos, O Ramirez, F Hormozdiari, C Alkan, C Vilà, K Squire, E Geffen, J Kusak, **AR Boyko**, HG Parker, C Lee, V Tadigotla, A Siepel, CD Bustamante, TT Harkins, SF Nelson, T Marques-Bonet, EA Ostrander, RK Wayne and J Novembre. **2016** Demographically-based evaluation of genomic regions under selection in domestic dogs. *PLOS Genet*, 12, e1005851.
2. Hayward, JJ, MG Castelhana, KC Oliveira, E Corey, C Balkman, TL Baxter, ML Casal, SA Center, M Fang, SJ Garrison, SE Kalla, P Korniliev, MI Kotlikoff, NS Moise, LM Shannon, KW Simpson, NB Sutter, RJ Todhunter and **AR Boyko**. **2016**. Complex disease and phenotype mapping in the domestic dog. *Nat Comm*, 7, 10460.

3. Schlamp, F, J van der Made, R Stambler, L Chesebrough, **AR Boyko\*** and PW Messer\*. **2016**. Evaluating the performance of selection scans to detect selective sweeps in domestic dogs. *Mol Ecol*, 25, 342–356.
4. White, ME, JJ Hayward, T Stokol, **AR Boyko**. **2015** Genetic mapping of novel loci affecting canine blood phenotypes. *PLOS One*, 10, e0145199.
5. Shannon, LM, RH Boyko, MG Castelhana, E Corey, JJ Hayward, C McLean, ME White, M Abi Said, BA Anita, NB Ikombe, J Calero, A Galov, M Hedimbi, B Imam, R Khalap, D Lally, A Masta, KC Oliveira, J Randall, NM Tam, C Valeriano, FJT Cornejo, L Pérez, NB Sutter, RJ Todhunter, CD Bustamante and **AR Boyko**. **2015**. Genetic structure in village dogs reveals a Central Asian domestication origin. *Proc Natl Acad Sci U S A*, 112, 13639–13644.
6. Li, Y, D Wu, **AR Boyko**, G Wang, S Wu, DM Irwin and Y-P Zhang. **2014**. Population variation revealed high altitude adaptation of Tibetan Mastiffs. *Mol Biol Evol*, 31, 1200–1205.
7. **Boyko, AR**, SA Brooks, AL Behan, E Corey, KC Oliveira, RJ Todhunter, Z Zhang, MG Castelhana, DM Ainsworth and NE Robinson. **2014**. Genomic analysis establishes correlation between growth and laryngeal neuropathy in Thoroughbreds. *BMC Genom*, 15, 259.
8. Freedman, HA, RM Schweizer, I Gronau, E Han, DO Vecchyo, PM Silva, M Galavemi, Z Fan, P Marx, B Lorente-Galdos, H Beale, O Ramierz, F Hormozdiari, C Alkan, C Vilà, K Squire, E Geffen, J Kusak, **AR Boyko**, H Parker, C Lee, V Tadigotla, A Siepel, CD Bustamante, TT Harkins, SF Nelson, EA Ostrander, T Marques-Bonet, RK Wayne and J Novembre. **2014**. Genome sequencing highlights the dynamic early history of dogs. *PLOS Genet*, 10, e1004016.
9. Tang, R, HJ Noh, D Wang, S Sigurdsson, R Swofford, M Perloski, M Duxbury, EE Pettersson, J Albright, M Castelhana, A Auton, **AR Boyko**, G Feng, K Lindblad-Toh and EK Karlsson. **2014**. Candidate genes and functional noncoding variants identified in a canine model of obsessive-compulsive disorder. *Genom Biol*, 15, R25.
10. Auton, A, Y Rui Li, J Kidd, K Oliveira, J Nadel, JK Holloway, JJ Hayward, PE Cohen, JM Grealley, J Wang, CD Bustamante and **AR Boyko**. **2013**. Genetic recombination is targeted towards gene promoter regions in dogs. *PLOS Genet*, 9, e1003984.
11. Goldstein, O, J Mezey, P Schweitzer, **AR Boyko**, C Gao, C Bustamante, J Jordan, G Aguirre and G Acland. **2013**. *IQCB1* and *PDE6B* mutations cause similar early onset retinal degenerations in two closely related terrier dog breeds. *Invest Ophthalmol Vis Sci*, 54, 7005–7019.
12. Li, Y, BM vonHoldt, G Wang, A Reynolds, **AR Boyko**, RK Wayne, D Wu and Y Zhang. **2013**. Artificial selection on brain expressed genes during the domestication of dog. *Mol Biol Evol*, 30, 1867–1876.
13. Schoenebeck, JJ, SA Hutchinson, A Byers, HC Beale, B Carrington, DL Faden, M Rimbault, B Decker, JM Kidd, R Sood, **AR Boyko**, JW Fondon III, RK Wayne, CD Bustamante, B Ciruna and EA Ostrander. **2012**. Variation of *BMP3* contributes to dog breed skull diversity. *PLOS Genet*, 8, e1002849.
14. Xie, X, J Molina, R Hernandez, A Reynolds, **AR Boyko**, CD Bustamante and MD Purugganan. **2011**. Levels and patterns of nucleotide variation in domestication QTL regions on rice chromosome 3 suggest lineage-specific selection. *PLOS One*, 6, e20670.
15. Molina, J, M Sikora, N Garud, JM Flowers, S Rubinstein, A Reynolds, P Huang, SA Jackson, BA Schaal, CD Bustamante, **AR Boyko** and MD Purugganan. **2011**. Reply to Ge and Sang: A single origin of domesticated rice. *Proc Natl Acad Sci U S A*, 108, e756.

16. vonHoldt, BM, JP Pollinger, DA Earl, JC Knowles, **AR Boyko**, H Parker, E Geffen, M Pilot, W Jedrzejewski, B Jedrzejewska, V Sidorovich, C Greco, E Randi, M Musiani, R Kays, CD Bustamante, EA Ostrander, J Novembre and RK Wayne. **2011**. A genome-wide perspective on the evolutionary history of enigmatic wolf-like canids. *Genom Res*, 21, 1294–1305.
17. Molina, J, M Sikora, N Garud, JM Flowers, S Rubinstein, A Reynolds, P Huang, SA Jackson, BA Schaal, CD Bustamante, **AR Boyko** and MD Purugganan. **2011**. Molecular evidence for a single origin of rice. *Proc Natl Acad Sci U S A*, 108, 8351–8356.
18. **Boyko, AR. 2011**. The domestic dog: man’s best friend in the genomic era. *Genom Biol*, 12, 216.
19. Myers, RA, F Casals, J Gauthier, FF Hamdan, J Keebler, **AR Boyko**, CD Bustamante, AM Piton, D Spiegelman, E Henrion, M Zilversmit, J Hussin, J Quinlan, Y Yang, RG Lafrenière, AR Griffing, EA Stone, GA Rouleau and P Awadalla. **2011**. A population genetic approach to mapping neurological disorder genes using deep resequencing. *PLOS Genetics*, 7, e1001318.
20. Myles, S, **AR Boyko**, C Owens, PJ Brown, F Grassi, MK Aradhya, B Prins, A Reynolds, J Chia, D Ware, CD Bustamante and ES Buckler. **2011**. Genetic structure and domestication history of the grape. *Proc Natl Acad Sci U S A*, 108, 3530–3535.
21. **Boyko, AR\***, P Quignon\*, L Li\*, JJ Schoenebeck, JD Degenhardt, KE Lohmueller, K Zhao, A Brisbin, HG Parker, BM vonHoldt, M Cargill, A Auton, A Reynolds, AG Elkahoun, M Castelhana, DS Mosher, NB Sutter, GS Johnson, J Novembre, MJ Hubisz, A Siepel, RK Wayne, CD Bustamante and EA Ostrander. **2010**. A simple genetic architecture underlies morphological variation in dogs. *PLOS Biol*, 8, e1000451.
22. Awadalla, P, J Gauthier, RA Myers, F Casals, FF Hamdan, AR Griffing, M Côté, E Henrion, D Spiegelman, J Tarabeux, A Piton, Y Yang, **AR Boyko**, CD Bustamante, L Xiong, É Fombonne, L Mottron, M Zilversmit, J Keebler, H Daoud, C Marineau, MH Roy-Gagnon, MP Dubé, A Eyre-Walker, P Drapeau, EA Stone, RG Lafrenière, GA Rouleau. **2010**. Direct measure of the *de novo* mutation rate in autism and schizophrenia cohorts. *Amer J Hum Genet*, 87, 316–324.
23. Goldstein, O, JG Mezey, **AR Boyko**, C Gao, W Wang, CD Bustamante, LJ Anguish, JA Jordan, SE Pearce-Kelling, GD Aguirre and GM Acland. **2010**. An *ADAM9* mutation in canine cone-rod dystrophy 3 establishes homology with human cone-rod dystrophy 9. *Mol Vision*, 16, 1549–1569.
24. Williams, LM, X Ma, **AR Boyko**, CD Bustamante and MF Oleksiak. **2010**. SNP identification, verification, and utility for population genetics in a non-model genus. *BMC Genet*, 11, 32.
25. vonHoldt, BM, JP Pollinger, KE Lohmueller, E Han, HG Parker, P Quignon, JD Degenhardt, **AR Boyko**, DA Earl, A Auton, A Reynolds, K Bryc, A Brisbin, JC Knowles, DS Mosher, TC Spady, A Elkahoun, E Geffen, M Pilot, W Jedrzejewski, C Greco, E Randi, D Bannasch, A Wilton, J Shearman, M Musiani, M Cargill, PG Jones, Z Qian, W Huang, Z Ding, Y Zhang, CD Bustamante, EA Ostrander, J Novembre and RK Wayne. **2010**. Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. *Nature*, 464, 898–902.
26. Andrés, AM, MJ Hubisz, A Indap, DG Torgerson, JD Degenhardt, **AR Boyko**, RN Gutenkunst, TJ White, ED Green, CD Bustamante, AG Clark and R Nielsen. **2009**. Targets of balancing selection in the human genome. *Mol Biol Evol*, 26, 2755–2764.
27. Cadieu, E, M Neff, P Quignon, K Walsh, K Chase, HG Parker, BM vonHoldt, A Rhue, **AR Boyko**, A Byers, A Wong, DS Mosher, A Elkahoun, TC Spady, C André, KG Lark, M Cargill, CD Bustamante, RK Wayne and EA Ostrander. **2009**. Coat variation in the domestic dog is governed by variants in three genes. *Science*, 326, 150–153.

28. Torgerson, DG, **AR Boyko**, RD Hernandez, A Indap, X Hu, TJ White, JJ Sninsky, M Cargill, CD Bustamante and AG Clark. **2009**. Evolutionary processes acting on candidate cis-regulatory regions in humans inferred from patterns of polymorphism and divergence. *PLOS Genet*, 5, e1000592.
29. **Boyko, AR**, RH Boyko, CM Boyko, P Jones, HG Parker, M Castelhana, L Corey, J Degenhardt, A Auton, M Hedimbi, R Kityo, EA Ostrander, J Schoenebeck, RJ Todhunter and CD Bustamante. **2009**. Complex population structure in African village dogs and its implications for inferring dog domestication history. *Proc Natl Acad Sci U S A*, 106, 13903–13908.
30. Gray, MM, JM Granka, CD Bustamante, NB Sutter, **AR Boyko**, L Zhu, EA Ostrander and RK Wayne. **2009**. Linkage disequilibrium and demographic history of wild and domestic canids. *Genetics*, 181, 1493–1505.
31. Auton, A, K Bryc, **AR Boyko**, KE Lohmueller, J Novembre, A Reynolds, A Indap, MH Wright, J Degenhardt, RN Gutenkunst, KS King, MR Nelson and CD Bustamante. **2009**. Global distribution of genomic diversity underscores rich complex history of continental human populations. *Genom Res*, 19, 795–803.
32. Nielsen, R, MJ Hubisz, I Hellmann, D Torgerson, AM Andrés, A Albrechtsen, R Gutenkunst, MD Adams, M Cargill, **AR Boyko**, A Indap, CD Bustamante and AG Clark. **2009**. Darwinian and demographic forces affecting human protein coding genes. *Genom Res*, 19, 838–849.
33. Novembre, J, T Johnson, K Bryc, Z Kutalik, **AR Boyko**, A Auton, A Indap, KS King, S Bergmann, MR Nelson, M Stephens and CD Bustamante. **2008**. Genes mirror geography within Europe. *Nature*, 456, 98–101.
34. Nelson, MR, K Bryc, KS King, A Indap, **AR Boyko**, J Novembre, LP Briley, Y Maruyama, DM Waterworth, G Waeber, P Vollenweider, JR Oksenberg, SL Hauser, HA Stirnadel, JS Kooner, JC Chambers, B Jones, V Mooser, CD Bustamante, AD Roses, DK Burns, MG Ehm and EH Lai. **2008**. The population reference sample (POPRES): a resource for population, disease, and pharmacological genetics research. *Amer J Hum Genet*, 83, 347–358.
35. Blekhman, R, M Oma, L Hermann, **AR Boyko**, A Indap, C Koisol, CD Bustamante, KM Teshima and M Przeworski. **2008**. Natural selection on genes that underlie human disease susceptibility. *Curr Biol*, 18, 883–889.
36. **Boyko, AR**, SH Williamson, AR Indap, JD Degenhardt, RD Hernandez, KE Lohmueller, MD Adams, S Schmidt, JJ Sninsky, SR Sunyaev, TJ White, R Nielsen, AG Clark and CD Bustamante. **2008**. Assessing the evolutionary impact of amino acid mutations in the human genome. *PLOS Genet*, 4, e1000083.
37. Lohmueller, KE, AR Indap, S Schmidt, **AR Boyko**, RD Hernandez, MJ Hubisz, JJ Sninsky, TJ White, SR Sunyaev, R Nielsen, AG Clark and CD Bustamante. **2008**. Proportionally more deleterious genetic variation in European than in African populations. *Nature*, 451, 994–998.
38. **Boyko, AR**. **2008**. Optimal age difference cannot differ between monogamous males and females: a comment on Fieder and Huber. *Biol Lett*, 4, 82.
39. Caicedo, AL, SH Williamson, RD Hernandez, **AR Boyko**, A Fledel-Anon, TL York, NR Polato, KM Olsen, R Nielsen, SR McCouch, CD Bustamante and MD Purugganan. **2007**. Genome-wide patterns of nucleotide polymorphism in domesticated rice. *PLOS Genet*, 3, 1745–1756.
40. Boyko, RH, **AR Boyko** and MG Boyko. **2007**. Referee bias contributes to home-field advantage in English premiership football. *J Sports Sci*, 25, 1185–1194.
41. **Boyko, AR**, RM Gibson and JR Lucas. **2004**. How predation risk affects the temporal dynamics of avian leks: sage grouse vs. golden eagles. *Am Nat*, 163, 154–165.

### *Book chapters*

Boyko, RH and **AR Boyko**. 2013. Dog conservation and the population genetic structure of dogs. In *Free-Ranging Dogs and Wildlife Conservation*, ME Gompper (ed), pp. 185–210. Oxford University Press, USA.

## Research Support

### *Ongoing Research Support*

“Comprehensive Characterization of Canine Genomic Structural Diversity.” (JM Kidd and **AR Boyko**, PIs). NIH NIGMS, R01GM103961, 2013–2017.

“The domestic dog as a model system for aging research.” (DEL Promislow, PI; **AR Boyko**, K Creevy and K Greer, co-PIs). NIH NIA, R24 AG044284-01, 2013–2016.

“Developing genomic approaches for using mixed-breed dogs to accelerate canine genetic research.” (JJ Hayward; **AR Boyko**, PI/mentor). Stanton Foundation, 2015.

“Hereditary deafness in dogs—genomic studies in Australian Cattle Dogs and Dalmatians using full sibling pairs.” (GM Strain and **AR Boyko**, PI), AKC Canine Health Foundation, 2015–2017.

“Granulomatous colitis in Boxer dogs and French Bulldogs: Fine mapping of disease-associated loci, evaluation of bacterial killing and transcriptional analysis.” (KW Simpson, PI; **AR Boyko** and NB Sutter, co-PIs). American Kennel Club Canine Health Foundation, #23405, 2014–2015.

“Mitral valve leaflet strain in dog breeds at risk for Myxomatous Mitral Valve Degeneration.” (NS Moise, PI; **AR Boyko** and JT Butcher, coPIs). American Kennel Club Canine Health Foundation, 2014–2015.

“Gene expression profiling of canine brain development.” (**AR Boyko**, PI). Cornell Center for Comparative and Population Genomics, 2013–2015.

“Expansion of genetic mapping and genomic resources for the cat.” (RJ Todhunter, PI; **AR Boyko** and M Castelhana, co-PIs). Feline Health Center, 2015–2016.

“Identification of an ancient mutation associated with XX disorder of sexual development (DSD), an inherited cause of female infertility and sterility in 28 breeds.” (V Meyers-Wallen, PI; **AR Boyko**, co-PI), AKC Canine Health Foundation, 2014–2015.

### *Completed Research Support*

“Tracking the descendants of ancient Pacific Island dogs.” (**AR Boyko**, PI). National Geographic Society, 2014.

“Fine mapping of candidate genes contributing to equine left recurrent laryngeal neuropathy (RLN).” (DM Ainsworth, PI; SA Brooks, DF Antczak, **AR Boyko**, NE Robinson, RJ Todhunter, co-PIs), Zweig Memorial Fund for Equine Research, 2013–2014.

“Genetic and genomic resources for the cat.” (RJ Todhunter, PI; **AR Boyko** and M Castelhana, co-PIs). Feline Health Center, 2013–2014.

“Variation discovery towards fine-mapping dog disease traits.” (NB Sutter, PI; RJ Todhunter and **AR Boyko**, co-PIs). Cornell Center for Advanced Technology (CAT), 2012–2013.

"Tracking ancient dog populations in Africa." (RH Boyko and **AR Boyko**). Petridish.org, 2012.

**AR Boyko** (PI). "Genomic signatures of altitude adaptation in Andean village dogs." Cornell Center for Vertebrate Genomics, 2012–2013.

**AR Boyko** (PI). "Tracking down the descendants of early Native American dogs." National Geographic Society, 2011–2013.

"Genome-wide diversity in village dogs: uncovering the history of dog domestication, the genetics of natural dog populations, and consequences of artificial selection in breed dogs." (**AR Boyko**, PI; CD Bustamante, co-PI), National Science Foundation, Early Concept Grant for Exploratory Research (EAGER), DEB-0948510, 2009–2011.

"The history and biology of dog domestication: a genomic study using a global survey of non-breed affiliated village dogs." (CD Bustamante, PI); **AR Boyko**, co-PI), Cornell Center for Vertebrate Genomics, 2007–2009.

"The evolution of warning coloration in *Heliconius* butterflies." National Science Foundation, Dissertation Improvement Grant, 2003.

"Wright's shifting balance and warning coloration in *Heliconius* butterflies." Organization for Tropical Studies, Graduate Fellowship, 2003.

"Sexual selection and coloration in *Heliconius* butterflies: can mating systems influence the evolution of aposematism and mimicry?" Indiana Academy of Science, 2001.

## Honors

Zoetis Award for Veterinary Research Excellence (2015)

Genome Technology magazine Young Investigator award (2010)

Walter M. Fitch finalist, Society for Molecular Biology and Evolution (2006)

H. E. Umberger Outstanding Graduate Student in Research, Purdue University (2005)

Graduate Student Award for Outstanding Teaching, Purdue University (2005)

Andrews Fellowship, Purdue University (1999)

Chancellor's Scholar, Campus Honor Program, University of Illinois (1995–1999)

James Scholar, College of Engineering, University of Illinois (1995–1999)

## Selected presentations

### 2016

Can your dog's DNA transform human health and aging? SXSW Interactive, Austin, TX.

Evolution unleashed: the making of the dog and its use as a model in biomedicine. Invited talk, Biomedicum Helsinki Seminar Series, University of Helsinki, Finland.

The patterning of phenotypic diversity and genetic variation in purebred and village dogs. Invited talk, Louisiana State University, Baton Rouge, LA.

Shedding light on canine genomics with high-throughput genotyping and imputation of 5,000 dogs. Invited talk, Illumina Workshop, Plant and Animal Genome XXIV Conference, San Diego, CA.

Evolution unleashed: the making of the dog. Invited talk, Five Points lecture series, New York Genome Center, New York, NY.

## 2015

Evolution unleashed: the making of the dog. Invited talk, Center for Computational Biology and Bioinformatics, University of Texas, Austin, TX.

Patterns of genetic diversity in purebred dogs and natural village dog populations. Invited talk, National Animal Interest Alliance annual meeting, Orlando, FL.

Evolution unleashed: the making of the dog. Invited talk, Bell Museum Cafe Scientifique Series, University of Minnesota, Minneapolis.

The 5000 genomes project and the incredible journey of canine genomics. Invited talk, Department of Biomedical Sciences seminar series, Cornell University, Ithaca, NY.

Population genetic signatures of domestication and artificial selection in purebred and village dogs. Invited talk, 7th Tufts' Canine & Feline Breeding & Genetics Conference, Boston, MA.

Evolution unleashed: the patterning of phenotypic diversity and genetic variation in purebred and village dogs. Invited talk, Cornell Center for Vertebrate Genomics (CVG) annual retreat. Ithaca, NY.

Global patterns of genetic structure in village dogs. Advances in Canine and Feline Genomics (8th International Meeting), Cambridge, UK.

Invited speaker/panelist, The Genomic Revolution: How DNA information is changing our lives. Cornell University, Ithaca, NY.

Contrasting patterns of genetic diversity between village dogs and purebred dogs. Invited talk, 4th Annual Cornell University Plant Breeding Symposium, Ithaca, NY.

Signatures of positive selection in the dog genome. Invited talk, Cat and Dog Workshop, Plant and Animal Genome XXIII Conference, San Diego, CA.

## 2014

Complex disease mapping in dogs. Invited talk, City University of Hong Kong, Kowloon, Hong Kong.

The genetic basis of phenotypic variation in purebred and free-ranging dogs. Plenary talk, Merial-NIH National Veterinary Scholars Symposium, Cornell University, Ithaca, NY.

The genetic basis of phenotypic variation in purebred and free-ranging dogs. Invited talk, Michigan State University College of Veterinary Medicine, East Lansing, MI.

Mapping the genetic basis of phenotypic variation in purebred and free-ranging dogs. Invited talk, University of Virginia, Charlottesville, VA.

Mapping the genetic basis of morphological variation and disease in domestic dog. Invited talk, Stony Brook University, NY.

Approaches for complex trait mapping in domestic dogs. Invited talk, Canine Longitudinal Aging Study workshop, Seattle, WA.

Mapping the genetic basis of phenotypic variation in purebred and free-ranging dogs. Invited talk, University of Binghamton, NY.

Impact of domestication and artificial selection on the genetic architecture of canine phenotypic diversity. Invited talk, Domestication Genomics Workshop, Plant and Animal Genome XXII Conference, San Diego, CA.

**2013**

101 Genomes: Studying dogs in the genomic era. Invited talk, 39th Annual Hefner Lecture, Miami University, Oxford, OH.

Comparative genetics of purebred and village dogs. Invited talk, 6th Annual New York State Veterinary Conference, Ithaca, NY.

Haplotype structure reveals population history and selection in modern dogs. Advances in Canine and Feline Genomics (7th International Meeting), Boston, MA.

Semi-custom genotyping array accelerates canine disease and trait mapping. Invited talk, Upstate NY Illumina User Group Meeting, Ithaca, NY.

Genetics and the evolution of village and purebred dogs. Invited talk, Genes to Genomes symposium, American Veterinary Medical Association Conference, Chicago, IL.

Semi-custom genotyping array accelerates canine disease and trait mapping. Invited talk, Genes to Genomes symposium, American Veterinary Medical Association Conference, Chicago, IL.

Genetics and the evolution of village and purebred dogs. Invited talk, Bard College, Annandale-on-Hudson, NY.

From Westies to Wolfhounds: The genetic roots of canine phenotypic diversity. Department of Clinical Sciences seminar series, Cornell University College of Veterinary Medicine.

Comparative population genomics of village and purebred dogs. Invited talk, 3rd Annual NY Conference on Genomics and Systems Biology, NYU Abu Dhabi, UAE.

**2012**

Thinking outside the boxer: free-range dogs and the evolution of canine genomics. Molecular Biology and Genetics Seminar Series, Cornell University.

Free-range dogs and the evolution of canine genomics. Finger Lakes Kennel Club, Ithaca, NY.

Thinking outside the boxer: free-range dogs and the evolution of canine genomics. Molecular and Integrative Physiology Work-In-Progress Seminar, Cornell University College of Veterinary Medicine.

Village dogs reveal domestication origins and genetics of complex traits in domestic dogs. Advances in Canine and Feline Genomics (6th International Meeting), Visby, Sweden.

Comparative genetics of purebred and village dogs. Invited talk, Cornell University College of Veterinary Medicine Open House.

Thinking outside the boxer: Dog genomics and strategies for canine disease mapping. Invited talk, Einstein University.

**2011**

Genetic signatures of local adaptation and population structure in village dogs. Baker Institute Seminar Series, Cornell University.

Genetic diversity in village dog populations. Invited talk, UCLA Center for Society and Genetics annual symposium, University of California, Los Angeles.

Comparative population genomics of village and purebred dogs. Invited seminar, Cornell Center for Comparative and Population Genomics, Ithaca, NY.

Comparative population genomics of village and purebred dogs. Invited talk, Arizona State University, Tempe, AZ.

Comparative population genomics of village and purebred dogs. Invited talk, Cornell University College of Veterinary Medicine, Ithaca, NY.

Comparative analysis of two high-density canine SNP arrays and whole-genome sequencing. Invited talk, Cat and Dog Workshop, Plant and Animal Genome XIX Conference, San Diego, CA.



## Editing and reviewing

**2016** *Nature Communications*, Netherlands Organization for Scientific Research (NWO), *PLOS Genetics*, *Science*

**2015** *Genome Research*, Israel Science Foundation, *Journal of Heredity*, *Journal of Veterinary Cardiology*, *Molecular Biology and Evolution*, *Nature Communications*, *PLOS Genetics*

**2014** *Genome Biology and Evolution*, *Genome Research*, *Heredity*, *Institute for Laboratory Animal Research Journal*, *Journal of Heredity*, *Journal of Human Evolution*, *Journal of Veterinary Cardiology*, National Science Foundation (*ad hoc*), *PLOS One*, Science for Life Laboratory's National Project Call: The Swedish Genomes Program and the Biodiversity Program, University of Chicago Press

**2013** *BioEssays*, *Genome Biology*, *Molecular Biology and Evolution*, *Nature Communications*, *PLOS Genetics*, *PLOS ONE*

**2012** *Clinical Pharmacology & Therapeutics*, *Genetics*, *PLOS Genetics*, *PLOS ONE*

**pre-2012** *Genome Research*, *Genetics*, *Evolution*, *Molecular Biology and Evolution*, *Molecular Ecology*, *PLOS Genetics*, *Biology Letters*, *Journal of Molecular Evolution*, *Bioinformatics*, *BMC Genomics*, *Journal of Heredity*, *Genetics Research International*, *Journal of Animal Breeding and Genetics*, *PLOS ONE*, *Mitochondrial DNA*, *Evolutionary Genomics: Statistical and Computational Methods* and *Journal of Sports Sciences*

## Service

Session organizer, Cat and Dog workshop, Plant and Animal Genomics XXIII (2015 – 2016)

Cornell Canine Health Center, Executive Committee (2015 – present)

Bioinformatics Facility, Faculty Advisory Board (2014 – present)

Faculty search committee, Epidemiology (Renata Ivanek hired summer 2015)

Graduate admissions, GG&D field (2014 – 2016)

CVG Scholars reviewer (2013)

Graduate admissions, MIP field (2013)

Honor thesis reviewer, GG&D field (2013)

Faculty search committee, Molecular Physiology (Bethany Cummings hired summer 2013).

DNA Bank oversight committee (2012 – present)

3CpG Seed Grant reviewer (2012, 2013, 2014)

Graduate admissions, Computational Biology field (2012)

Session organizer, "Genomics of Domestication", Society for Molecular Biology and Evolution, Lyon, France (2010).

## Teaching

### 2015–16

VTMED 5200, Medical Genetics section leader  
Guest lecture, BioMG 7810 “Problems in Genetics and Development”  
VIP lunch seminar, “Functional Genomics”

### 2014–15

VTMED 5200, Medical Genetics section leader  
Module leader, BIOMS 7070 “Current Research in Genomics”  
Guest lecture, BIOMG 7810 “Problems in Genetics and Development”  
VIP lunch seminar, “Functional Genomics”

### 2013–14

VTMED 5200, Medical Genetics section leader  
Guest lecture, ANSC 2210 “Principles of Animal Genetics”  
VIP lunch seminar, “Functional Genomics”

### 2012–13

Guest lecture, VTMED 5200 “Cell Biology and Genetics”  
Guest lecture, BIOGD 4000 “Genomics”  
VIP lunch seminar, “Functional Genomics”

## Mentoring

### *Post-doctoral fellows trained*

Dr. Laura. M. Shannon (Jan 2013 – current)  
Dr. Jessica J. Hayward (Nov 2011 – current)  
Dr. Sunday O. Peters (Jun 2012 – Aug 2012, joint with I. Imumorin)

### *Graduate fellows trained*

Jennifer Yordy (Ph.D. Joint Graduate Training Program in Biological and Biomedical Sciences) (Jun 2015 – current)  
Michelle White (DVM/Ph.D. program) (Jan 2013 – current)  
Tara L. Baxter (M.S. program in Genetics & Development) (Aug 2012 – Jul 2014)

### *Graduate committees*

Dania Villarnovo (DVM/Ph.D. dual degree program; Kristy Richards)  
Mohammed Al Abri (Ph.D. program in Animal Science; Samantha Brooks)  
Mahya Mehrmohamadi (A-exam; Ph.D. program in Nutrition; Jason Locasale)

### *Post-doctoral mentorship*

Eva M. Oxford (DVM, Ph.D., Resident in Cardiology; N. Sydney Moïse), ACVIM Resident Research Grant recipient (Fall 2013), "Identification of genetic mutations associated with the development of degenerative mitral valve disease in the small breed dog."

### *Visiting scholars*

Meiying Fang (Ph.D., China Agricultural University), Jan 2014 – Dec 2014.

### *Undergraduates*

Joy Li, BIOG 4990, Spring 2014 – present

Kelly Murphy, VIP program, Summer 2015

Margaret Lee, BIOG 4990, Fall 2014 – Spring 2015

Eva Cardé, VIP program, Summer 2014

Alexandra Scott, BIOG 2990, Fall 2013

Kathryn Mercer, VIP program, Summer 2013

Maize Wang, BIOG 4990, Fall 2012

## Graduate field membership

1. Computational Biology
2. Comparative Biomedical Sciences
3. Molecular and Integrative Physiology
4. Genetics and Development
5. Zoology and Wildlife Conservation