

**IN THE UNITED STATES DISTRICT COURT
FOR THE NORTHERN DISTRICT OF IOWA
WESTERN DIVISION**

JENNIFER FROST, an individual; and
JANE DOE, an individual,

Plaintiffs,

v.

THE CITY OF SIOUX CITY, IOWA;
ROBERT PADMORE, in his official capacity; and
CINDY RARRAT, in her official capacity,

Case No. 5:16-cv-4107

**DECLARATION OF
KRISTOPHER J. IRIZARRY, Ph.D.**

I, Kristopher J. Irizarry, Ph.D., swear, state, and testify that the following facts are true and correct:

1. I am over the age of majority and am otherwise competent to make this Declaration. I have personal knowledge of the facts set forth in this Declaration. If called as a witness, I could and would competently testify to the same.

2. I am an associate professor of Genetics and Genomics at Western University of health Science's College of Veterinary Medicine. I received my B.S. in Biochemistry and Biophysics from Rensselaer Polytechnic Institute in 1996 and received my PhD from the department of Biochemistry and Molecular Biology at the University of California, Los Angeles in 2003. Attached as Exhibit 1A is my curriculum vitae.

3. I have been asked to give an expert opinion concerning (1) the reliability of visual identification of dogs; (2) the degree which a mixed breed dog's physical traits provide a scientific or genetic basis to predict the animal's breed; (3) whether the breed of a dog is a predictor of its dangerousness or aggression; (4) the role genetic and heritability in heritability of behavioral traits; and (5) where there is a rational or scientific basis to ban certain breeds of dogs

as more dangerous or more aggressive than other breeds of dogs. Attached as Exhibit 1 is a true and correct copy of my report in which I offer my opinions regarding the above mentioned topics.

4. The basis for the opinions offered in my report is my specialized education, training, knowledge and skill in the area of canine genetics and breed identification. All of the opinions expressed in the report are opinions I hold to a reasonable degree of scientific certainty.

5. My opinions are also wide accepted by virtually all experts in the fields of genetics and neurobiology. I am not aware of any dispute, much less a significant one, by qualified experts in these germane scientific communities concerning the theories and methodologies employed by me in drawing these conclusions.

6. I declare under perjury that the foregoing is true and correct.

Dated: October 27, 2016.

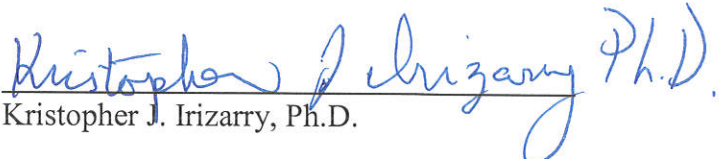

Kristopher J. Irizarry, Ph.D.

Exhibit 1A

AUGUST, 2016

CURRICULUM VITAE

NAME: Kristopher Jason Lawson Irizarry

PRESENT POSITION: Associate Professor, College of Veterinary Medicine Western University of Health Sciences
309 East Second Street, Pomona, CA 91766-1854 USA
Ph: 909-469-5430 FAX: 909-469-5635
Email: kirizarry@westernu.edu

EDUCATION:

University of California, Los Angeles, California; 2003-2005. Postdoctoral Fellowship UCLA Center for Pharmacogenomics: Pharmacogenomics of Antidepressant Treatment Response

University of California, Los Angeles, California; 1996-2003. PhD, Biochemistry & Molecular Biology
Dissertation Title: Identification and Analysis of Single Nucleotide Polymorphisms in the Coding Regions of the Human Genome

Rensselaer Polytechnic Institute, Troy, New York; 1996. Bachelor of Science, Biochemistry & Biophysics

HONORS:

National Canine Research Council Service Awards, 2014, 2015

Society of Phi Zeta, 2009

NIH T32 Psychobiology Postdoctoral Fellowship, 2003-2004

NSF Integrative Graduate Education and Research Traineeship, 2000-2003

NIH Biotechnology Training Grant, 1996-1999

Rensselaer Scholarship, 1994-1996

PROFESSIONAL POSITIONS:

Scientific Judge, NSF IGERT Video and Poster Competition, 2013

Poster Judge, National Science Foundation IGERT Online Poster Competition, March 2011, May 2012

Lecturer/ Researcher, Neuropsychiatric Institute, University of California, Los Angeles, California, 2004-2005

Postdoctoral Fellow, Neuropsychiatric Institute, University of California, Los Angeles, California, 2003-2004

Teaching Assistant, Biochemistry & Molecular Biology, University of California, Los Angeles, California, 2000

Teaching Assistant, Molecular, Cellular & Developmental Biology, University of California, Los Angeles, California, 1998-1999

Bioinformatics Research Internship, Incyte Pharmaceuticals, Palo Alto, California, 1997

Research Assistant, Center for Biophysics, Rensselaer Polytechnic Institute, Troy, New York, 1995-1996

Summer Research Position, NINDS/ NIH, Bethesda, Maryland, 1995

Graduate Student, Laboratory of Bioinformatics & Structural Genomics, University of California, Los Angeles, California, 1998-2003

Exhibit 1A

Research Assistant, Addictions Laboratory, Rensselaer Polytechnic Institute, Troy, New York, 1994-1995

MEMBERSHIP IN PROFESSIONAL ORGANIZATIONS:

California Veterinary Medicine Association- Faculty Membership

California Science Fair- Judges Advisory Committee

Evidence Based Veterinary Medicine Association

International Behavioural and Neural Genetics Society (IBANGS)

International Mammalian Genome Society

California Bullmastiff Fanciers

National Canine Research Council- Genetics Advisor

Birchwood Conservancy, World Heritage Animal Genetics Repository – Genetics Advisor

PROFESSIONAL, GRADUATE & UNDERGRADUATE TEACHING:

Course Leader, Bioinformatics II (GCBS 5087), Graduate College of Biomedical Sciences, 2016

Course Leader, Molecular and Cellular Biology II, CVM6031, College of Veterinary Medicine, 2016

Facilitator, Inter-Professional Education, Western University of Health Sciences, 2016

Facilitator, Veterinary Basic Sciences, College of Veterinary Medicine, 2015

Course Leader, Molecular and Cellular Biology I, CVM6030, College of Veterinary Medicine, 2015

Course Leader, Bioinformatics I (GCBS 5086), Graduate College of Biomedical Sciences, 2015

Course Leader, Bioinformatics for Postdoctoral Researchers and Faculty, GCBS8000 Graduate College of Biomedical Statistics, 2014

Facilitator, Veterinary Basic Sciences, College of Veterinary Medicine, 2014

Course Leader, Biomedical Statistics and Research Design, Graduate College of Biomedical Sciences, 2013

Facilitator, Veterinary Basic Sciences, College of Veterinary Medicine, 2013

Course Leader, Biomedical Statistics and Research Design, Graduate College of Biomedical Sciences, 2012

Facilitator, Veterinary Basic Sciences, College of Veterinary Medicine, 2012

Comparative Mammalian Phenomics. Guest Lecturer at Oregon State University Graduate Course in Genomics, March 4 and March 7, 2011

Molecular Cell Biology, Quarterhorse Genetic Disorders and allele frequencies, Hot-N-Spicy case, 2011

Molecular Cell Biology, Equine Genetics, muscle gene expression, PSSM, Hot-N-Spicy case, 2011

VBS, Grand Rounds, Genetics of mixed breed dogs, IGF1 dog size, OCD, 2011

Exhibit 1A

Veterinary Basic Sciences, PBL Facilitation, 1 block, College of Veterinary Medicine 2011

Biomedical Statistics, GCBS, Course Director, taught course, 2010

VBS, Basic Science Lab, Comparative functional genomics, conservation of genetics across species 2010

VBS, Basic Science Lab, Understanding how genetics provides integration of other disciplines 2010

VBS, Basic Science Lab, Overview of genetic variation and genetic diagnostics in VetMed 2010

VBS, Basic Science Lab, Impact of SNPs on protein function, from DNA to protein, codons, 2010

VBS, Basic Science Lab, Repeat polymorphisms, genetic linkage and genetic studies, 2010

Molecular Cell Biology, Review of transcription with applications to expression of Ca² channels in the gut 2010

Molecular Cell Biology, Genetic regulation of gut calcium absorption gene expression by VitD 2010

Molecular Cell Biology, Genetic tests for equine diseases, 2010

Molecular Cell Biology, Genetic Basis of Disease Phenotypes: sodium channel SNPs, 2010

Molecular Cell Biology, Genetics – relating clinically relevant phenotypes to genetics, 2010

Molecular Cell Biology, Genetics of osteoclast and osteoblast function and regulation, 2010

Veterinary Basic Sciences, PBL Facilitation, 1 block, College of Veterinary Medicine 2010

Biomedical Statistics, GCBS, Course Director, Developed the curriculum and Syllabus 2009

Veterinary Basic Sciences, Co-Course Director, 2009

Veterinary Basic Sciences, PBL Facilitation, 2 blocks, College of Veterinary Medicine 2009

Molecular Cellular Basis of Life Course, GCBS, Developed course and created syllabus, 2008

Basic Science Lab, introduction to canine genome (NIH genome browser), Rascal Rabbit case 2008

Basic Science Lab, Growth Factor mutations and inheritance patterns in dogs, Rascal Rabbit case 2008

Basic Science Lab, The P-locus alleles and polled versus horned phenotypes, 2008

Molecular Cell Biology, Neuromuscular junctions, 2008

Molecular Cell Biology, Regulation of bone development, 2008

Veterinary Basic Sciences, Grand Rounds, as Module Leader, College of Veterinary Medicine 2008

Veterinary Basic Sciences, PBL Facilitation, 1 block, College of Veterinary Medicine 2008

Module Leader, Musculo-Skeletal Module, VBS College of Veterinary Medicine 2008

Molecular Cell Biology, Genetic susceptibility contributes to cancer, Goran Case, 2008

Molecular Cell Biology, Genetic susceptibility cryptorchidism, Duke Case, 2008

Exhibit 1A

Molecular Cell Biology, Genetics of ectopic ureter formation, Nappy Case, 2008

Molecular Cell Biology, Genetics of cartilage formation, Griffin Case, 2008

Molecular Cell Biology, Genetic susceptibility to osteomyelitis, Bunny Case, 2008

Molecular Cell Biology, Allelic variation of sodium channels, NVI case, 2008

Molecular Cell Biology, Genetic regulation of calcium homeostasis, IGGY Case, 2008

Veterinary Basic Sciences, Grand Rounds, as Module Leader, College of Veterinary Medicine 2007

Module Leader, Musculo-Skeletal Module, VBS College of Veterinary Medicine 2007

Veterinary Basic Sciences, PBL Facilitation, 4 blocks, College of Veterinary Medicine 2007

Veterinary Basic Sciences, PBL Facilitation, 2 blocks College of Veterinary Medicine 2006

Veterinary Basic Sciences, Grand Rounds, College of Veterinary Medicine 2006

COMMITTEE MEMBERSHIPS:

Western University Students Research and Technology Symposium (STARS)
Organizational Committee, 2008-2011

Western University IT Committee 2008 – 2010

Western University Financial Aid Committee 2008 – 2010

College of Veterinary Medicine, Ad-Hoc Admissions Committee 2007-2009

Graduate College of Biomedical Sciences (MSBS), Admissions Committee 2009-2011

Graduate College of Biomedical Sciences (MSBS) Curriculum Committee 2009-2011

Graduate College of Biomedical Sciences Advisory Committee 2009-2011

Chair, College of Veterinary Medicine Scholastic Standing Committee 2011

College of Veterinary Medicine, Ad-Hoc Faculty Search Committee, 2011

Graduate College of Biomedical Sciences (MSBS) Curriculum Committee, 2012

Chair, College of Veterinary Medicine, Student Performance Committee, 2012

Chair, College of Veterinary Medicine, Student Performance Committee, 2013

Graduate College of Biomedical Sciences (MSBS) Curriculum Committee, 2013

Chair, College of Veterinary Medicine, Student Performance Committee, 2014

Graduate College of Biomedical Sciences (MSBS) Curriculum Committee, 2014

Chair, College of Veterinary Medicine, Student Performance Committee, 2015

Exhibit 1A

Graduate College of Biomedical Sciences (MSBS) Curriculum Committee, 2015

College of Veterinary Medicine, Student Performance Committee 2016

Graduate College of Biomedical Sciences (MSBS) Curriculum Committee, 2016

FUNDED RESEARCH:

1. **Irizarry, K.J.L.** and Rutllant, J. Genomic Analysis of Anatomical and Reproductive Phenotypes Associated with the Invasive Argentinian Tegu. \$2000 United States Geological Survey 2016-2017 (*Co-principle Investigator*)
2. **Irizarry, K.J.L.** Developing Reptile Genomics Research Program. \$5000 Western University of Health Sciences, Intramural Funding Support 2013 – 2014 (*Principle Investigator*)
3. Barr, M.C., Irizarry, K., Joslin, J., Mockler, T. and Tetzloff, J.: Correlation of Snow Leopard Genetics with Immune Function: A Model for the Integration of Functional Genomics into Endangered Species Captive Breeding Plans. (2009-2011) Institute of Museum and Library services \$100,000 (*Co-principle Investigator*)
4. Collison, E. and Drechsler, Y., Irizarry, K. and Saggese, M.; Impact of immune responses of chickens with defined B haplotypes on resistance to respiratory infection. (2009-2011) USDA \$375,000 (*Co-investigator*)
5. Irizarry, K.: Nutrigenomics: comparative genomics analysis of novel gene sequences. (2008-2011), Hills Pet Nutrition, Research Contract \$22,000 (*Principle Investigator*)
6. Irizarry, K.: Analysis of genes associated with behavioral and neuroeconomic phenotypes in humans. (2007-2008), Center for Neuroeconomic Studies, Claremont Graduate University, Research Subcontract \$20,000 (*Principle Investigator*)
7. Irizarry, K.: Computational Infrastructure for cluster computing genomics applications. (2007), Anonymous gift hardware donation value \$15,000 (*Principle Investigator*)
8. Irizarry, K.: Identification and analysis of genes underlying behavioral phenotypes: combining bioinformatics, comparative genomics and sequencing to accelerate discovery in the canine genome. (2007-2008), Western University of Health Sciences Intramural Research Grant \$15,000 (*Principle Investigator*)
9. Bilder, R.M., Principle Investigator: Cognitive Phenotyping for Neuropsychiatric Therapeutics. (2004-2007), NCRR/ NIH \$42,000. (*Irizarry, K., Co-investigator*)
10. Licinio, J., Principle Investigator: Depression and Metabolic Syndrome in Mexican-American Women. (2002-2007), NIDDK/ NIH \$80,000. (*Irizarry, K., Co-investigator, awarded a minority supplement for this project*)
11. Leuchter, A.F., Principle Investigator: Research Training: Psychological Sciences. (1983-2008), NIMH/ NIH \$33,000 (*Irizarry, K., Postdoctoral Fellow*)

INVITED SCIENTIFIC PROGRAM SPEAKER:

1. **Irizarry, K.J.L.** “Characterization of Bullmastiff Head Morphology and Identification of RUNX2 Allelic Variation within the Breed” The Cat & Dog Workshop, International Plant and Animal Genome Conference XX, San Diego, California Sunday, January 15, 2012
2. **Irizarry, K.J.L.** “Leveraging comparative genomics to decode dog and cat genomes” Pomona College, Claremont California March 1, 2012

Exhibit 1A

3. **Irizarry, K.J.L.** “How to facilitate student use of published and online resources during creation of science projects.” *Presentation for Mentors of California Science Fair Students*, California Science Fair, May 18, 2010
4. **Irizarry, K.J.L.** “Canine bioinformatics and genetics.” *Biology Colloquium*, Harvey Mudd College, April 15, 2009
5. **Irizarry, K.J.L.** “The great debate - Does behavioral genetics imply behavior is deterministic? Reflections on free will, determinism and the contributions of nature and nurture to animal behavior.” *Western University College of Veterinary Medicine Behavior Club*, November 10, 2008
6. **Irizarry, K.J.L.** “Developing novel comparative genomics based phenotype annotation for use in the publicly available gene expression analysis software package dChip.” *Department of Biostatistics and Computational Biology*, Dana Farber Cancer Institute, Harvard University, Boston, Massachusetts, October 29, 2008
7. **Irizarry, K.J.L.** “An introduction to the genetics of behavior.” *Charles Drew University*, Los Angeles, California, August 12, 2008
8. **Irizarry, K.J.L.** “Understanding canine genetics as it relates to dog breeds and behavior.” *The Animal Farm Foundation*, New York, October 2007
9. **Irizarry, K.J.L.**, Day, A., Mitsouras K., Lee C., and Licinio, J. “Identifying candidate SNPs for high-throughput pharmacogenomics studies of CNS disorders.” *International Pharmacogenomics Joint Cold Spring Harbor Laboratory/Wellcome Trust Conference*, Hinxton, United Kingdom, September 25, 2003

SUBMITTED AND ACCEPTED SCIENTIFIC PROGRAM SPEAKER:

1. **Irizarry, K.J.L.** “Bioinformatics and Comparative Genomics Approaches for Annotating the Chicken Genome.” *USDA Multistate Immunogenetics Research Poultry Meeting*, Washington DC, October 16, 2008
2. **Irizarry, K.J.L.** “Leveraging Comparative Genomics to Infer-Functional Consequences of Gene Expression Changes: Accelerating Microarray Discovery via Phenomics Annotation.” *Cambridge Healthtech's 8th Annual Integrative Data Analysis Conference*, Providence, Rhode Island, September 24, 2008
3. Voith, V., and **Irizarry, K.J.L.** “Dog Breed Identification Quiz and DNA results.” *Orange Belt Veterinary Medical Association*, Riverside, California, September 16, 2008
4. **Irizarry, K.J.L.** “Decoding Dog DNA: finding physiology and pathology in the canine genome.” *Western University of Health Sciences Research Seminar*, Pomona, California, August 27, 2008
5. **Irizarry, K.J.L.** “Comparative Genomics: From Mice to Men and Dogs.” *Western/ Drew Research Retreat at the California Endowment Center for Healthy Communities in Los Angeles*, July 15, 2008
6. **Irizarry, K.J.L.** “Managing a collaborative Problem-Based Learning Curriculum.” *Lilly-West International Alliance of Teacher Scholars Conference*, Pomona, California, March 22, 2008

SCIENTIFIC ABSTRACT PRESENTATION

1. **Irizarry, K.J.L.**, Bryden, R, Rutllant, J. “Comparative Genomics Analysis Identifies Genes Associated with Reproductive Phenotypes in Burmese Python (*Python bivittatus*)” *International Plant and Animal*

Exhibit 1A

Genome Conference XXIV, San Diego, California January 8-13th, 2016

2. Voith, V. Trevejo R., Dowling-Guyer S., Marder A., Johnson, V., **Irizarry, K.J.L.** “Comparison of Visual and DNA Breed Identification of Dogs and Inter-Observer Reliability” 2nd International Scientific Meeting of Anatomy and Physiology: Fundamentals of Medicine. Department of Physiology and Radiobiology, Heinzelova 55, 10000 Zagreb, Croatia. June 16 and 17, 2014
3. **Irizarry, K.J.L.**, Scudder J., Mitsouras K, Josep Rutllant “Characterization of Bullmastiff Head Morphology and Identification of RUNX2 Allelic Variation within the Breed” International Plant and Animal Genome Conference XX, San Diego, California 2012
4. Mitsouras, K., Faulhaber, E.A., Hui, G., and **Irizarry, K.J.L.** “Development of a PCR-assay to detect papillomavirus in the snow leopard.” *Plant and Animal Genome XIX International Conference*. San Diego, California, January 15-19, 2011
5. Priest, H.D., Fox, S., Hui, G., Mitsouras, K., Joslin, J., Barr, M.C., Tetzloff, J., **Irizarry, K.J.L.**, and Mockler, T. “Sequencing the *Uncia uncia* Genome: Endangered Species Conservation Genomics.” *Oregon State University*, Corvallis, Oregon, September 21, 2010
6. Hui, G., Faulhaber, E.A., Camacho, A., Mitsouras, K., and **Irizarry, K.J.L.** “Construction of a Comparative Genomics Map to Facilitate the Annotation of the Draft Snow Leopard Genome.” *Merial Veterinary Scholar's Symposium*, Athens, Georgia, August 5-7, 2010
7. Voith, V., Chadik, C., Ingram, E., **Irizarry, K.J.L.**, Mitsouras, K., and Marilo, J. “Dog Breed Identification.” *American College of Veterinary Behaviorists and The American Veterinary Society of Animal Behaviorists Symposium*, Atlanta, Georgia, July 30, 2010
8. Barr, M.C., Wournell, A.L., Mitsouras, K., **Irizarry, K.J.L.**, and Bridges, K.A. “Molecular Epidemiology of Canine Parvovirus 2c in Southern California Dogs.” *Epidemics² 2nd International Conference on Infectious Disease Dynamics*, Athens, Greece, December 2-4, 2009
9. Mitsouras, K., Galgoul, G., Hoholm, A., Li, C., and **Irizarry, K.J.L.** “Using bioinformatics and comparative genomics to map cancer associated phenotypes to the canine genome.” *Genes, Dogs & Cancer: 5th International Canine Cancer Conference*, Orlando Florida, February 13–15, 2009
10. **Irizarry, K.J.L.**, Day, A., Mitsouras, K., Lee, C.J., Wong, M.L., and Licinio, J. “Novel Strategies for Psychiatric Pharmacogenomics.” *Pharmacogenetics Research and Knowledge Base Fourth Scientific Meeting*, Los Angeles, California, March 8, 2004
11. **Irizarry, K.J.L.**, Day, A., Mitsouras, K., Lee, C., Wong, M.L., and Licinio, J. “Identification and Integration of Diverse Genomic Signals: Building Neuroinformatics Tools for Pharmacogenomics Applications.” *International Society of Pharmacogenomics Meeting* Los Angeles, California, November 2003
12. **Irizarry, K.J.L.**, Galbraith, S., Miller, D., and Lee, C. “Genomic SNP Mapping.” *Lake Tahoe Symposia on Molecular Diversity*, January 29 - February 2, 2001
13. Lin, X.J., **Irizarry, K. J.L.**, and Lengyel, J.A. “Drosophila Arc, a novel membrane associated PDZ domain protein is involved in epithelial morphogenesis.” *39th Annual Drosophila Research Conference*, Washington D.C., March 1998
14. Chambers, M. D., **Irizarry, K.J. L.**, Boswell, K. J., Hubbell, C. L., and Reid, L. D., “A Selective Opioid Antagonist Block's Cocaine's Rewarding Effects.” *American Psychological Association Annual Conference*, New York, New York, August 1995

OTHER PROFESSIONAL CONTRIBUTIONS:

Exhibit 1A

1. **Irizarry, K.J.L.** interviewed live on internet radio program focused on legal issues associated with dogs. Topic of interview: “Difference between DNA-based breed testing of dogs versus DNA-based forensic identification of a specific dog.” July 3, 2012.
2. **Irizarry, K.J.L.** “Why the science of genetics does not support breed specific legislation” the Riverside County California Board of Commissioners Meeting. October 8th, 2013.
3. **Irizarry, K.J.L.** Expert Canine Genetics Witness in Federal Trial. Nelson et al. versus Town of New Llano, United States District Court, Western District of Louisiana, Lake Charles Division, Judge in Case: Honorable Patricia Minaldi. Docket Number: 2:14-CV-00803. July 1, 2014. Case successfully won.
4. **Irizarry, K.J.L.** Interviewed and quoted regarding genetics and dog breeds in published Esquire article: Junod, Tom “The State of the American Dog” *Esquire* Jul 14, 2014.
<http://www.esquire.com/news-politics/a23731/american-dog-0814/>
5. **Irizarry, K.J.L.** Interviewed and quoted regarding genetics and dog breeds in published book: Dickey, Bronwen. *Pit Bull: The Battle over an American Icon* Knopf, Published May 10, 2016.
ISBN-10:0307961761, ISBN-13: 978-0307961761

PUBLICATIONS

Lead author: Refereed Journals

1. **Irizarry, K.J.L.**, Kustanovich, V., Cheng, L., Brown, N., Nelson, S., Wong, W., and Lee, C.J. “Genome Wide Analysis of Single Nucleotide Polymorphisms in Human Expressed Sequences.” *Nature Genetics* 2000, 26: 233-236
2. **Irizarry, K.J.L.**, Hu, G., Wong, M.L., Licinio, J., and Lee., C.J. “Single Nucleotide Polymorphism Identification in Candidate Gene Systems of Obesity.” *The Pharmacogenomics Journal* 2001, 1(3):193-203
3. **Irizarry, K.J.L.**, and Galbraith, S.J. “Significance of SNP combination patterns.” *Molecular Psychiatry* 2004 9(5): 430
4. **Irizarry, K.J.L.**, and Galbraith, S.J. “Complex disorders reloaded: causality, action, reaction, cause and effect.” *Molecular Psychiatry* 2004, 9(5): 431-2
5. **Irizarry, K.J.L.**, Merriman, B., Bahamonde, M., Wong, M.L., and Licinio, J. “The evolution of signaling complexity suggests a mechanism for reducing the genomic search space in human association studies.” *Molecular Psychiatry* 2005, 10(1): 14-26
6. **Irizarry, K.J.L.**, and Licinio, J. “An explanation for the placebo effect?” *Science* 2005, 307(5714): 1411-2
7. David, J., and **Irizarry, K.J.L.** “Using the PubMatrix literature mining resource to accelerate student-centered learning in a veterinary PBL curriculum.” *Journal of Veterinary Medical Education*, 2009, 36(2): 202-8
8. Voith, V.L., Ingram, E., Mitsouras, K., and **Irizarry, K.J.L.** “Comparison of adoption agency breed identification and DNA breed identification of dogs.” *J Appl Anim Welf Sci* 2009, 12(3): 253-6
9. Mitsouras, K., Faulhaber, E.A., Hui ,G., Joslin, J., Eng, C., Barr, M.C., and **Irizarry, K.J.L.** “Development of a PCR Assay to Detect Papillomavirus Infection in the Snow Leopard.” *BMC Veterinary Research* 2011, 7: 38

Exhibit 1A

10. **Irizarry, K.J.L.**, Malladi, S., Gao, X., Mitsouras, K., Melendez, L., Burris, P., Brockman, J., and Al-Murrani, S. "Sequencing and Comparative Genomic Analysis of 1227 *Felis catus* cDNA Sequences Enriched for Developmental, Clinical and Nutritional Phenotypes." *BMC Genomics*, **13**:31 18 January 2012.
11. **Irizarry, K.J.L.** and Rutllant, J. "Leveraging Comparative Genomics to Identify and Functionally Characterize Genes Associated with Sperm Phenotypes in Python bivittatus (Burmese Python)" *Genet Res Int.* 2016; 2016:7505268. doi:10.1155/2016/7505268. Epub 2016 Apr 20.
12. **Irizarry K.J.L.** , Bryant D, Kalish J, Eng C, Schmidt PL, Barrett G, Barr MC. "Integrating Genomic Data Sets for Knowledge Discovery: An Informed Approach to Management of Captive Endangered Species" *International Journal of Genomics* Accepted for Publication Accepted 21 March 2016. In Press.
13. **Irizarry, K.J.L.** "Leveraging Naked Mole Rat (*Heterocephalus Glaber*) Comparative Genomics to Identify Canine Genes Modulating Susceptibility to Tumorigenesis and Cancer Phenotypes" *Journal of Veterinary Science and Technology.* Accepted April 26, 2016. In Press
14. **Irizarry, K.J.L.** and Bryden, R. "In-Silico Analysis of Gene Expression Network Components Underlying Pigmentation Phenotypes in the Python Identified Evolutionarily Conserved Clusters of Transcription Factor Binding Sites" *Advances in Bioinformatics.* Accepted 2 June 2016. In Press

Chapters in Books

1. **Irizarry, K.J.L.** "Bioinformatics approaches for identifying allelic variants in candidate pathways underlying major depression and antidepressant treatment response." In *Biology of Depression* Wiley-VCH Verlag GmbH & Co. KGaA, Weinheim Germany 901-942 copyright 2005.

Other authorships: Refereed Journals

1. Reid, L.D., Hubbell, C. L., Glick, S.D., Boswell, K.J., Chen, A.M., Moran, C.M., Cramer, C.M., Mullen, U.D., Chambers, M.D., Gonzales, P.M., **Irizarry, K.J.L.**, and Amendola, C.A. "Initial Analysis of Naltriben, a Delta Opioid Antagonist, As a Putative Medicine for Treating Cocaine Abuse." *Experimental and Clinical Psychopharmacology* 1996, 4: 271-284
2. Salerno, J.C., Harris, D.E., **Irizarry, K.J.L.**, Patel, B., Morales, A.J., Smith, S.M.E., Jones, C., Weissman, B.A., Liu, Q., and Gross, S.S. "The autoinhibitory control element defines calcium regulated isoforms of nitric oxide synthase." *Journal of Biological Chemistry* 1997, 272(47): 29769 -29777
3. Lee, C. and **Irizarry, K.J.L.** "The GeneMine System for Genome Proteome Annotation and Collaborative Data Mining." *IBM Systems Journal* 2001, 40(2): 592-603
4. Lee, C.J., and **Irizarry, K.J.L.** "Alternative Splicing in the Nervous System: An Emerging Source of Diversity and Regulation." *Biological Psychiatry* 2003, 54(8): 771-6
5. Licinio, J., O'Kirwan, F., **Irizarry, K.J.L.**, Merriman, B., Thakur, S., Jepson, R., Lake, S., Tantisira, K.G., Weiss S.T., and Wong, M.L. "Association of a corticotropin-releasing hormone receptor 1 haplotype and antidepressant treatment response in Mexican Americans." *Molecular Psychiatry* 2004, 9(12): 1075-82
6. Wong, M.L., O'Kirwan, F., Hannestad, J.P., **Irizarry, K.J.L.**, Elashoff, D., and Licinio, J. "St. John's wort and imipramine-induced gene expression profiles identify cellular functions relevant to antidepressant action and novel pharmacogenetic candidates for the phenotype of antidepressant treatment response." *Molecular Psychiatry* 2004, 9: 237-251

Exhibit 1A

7. Liao, G., Wen, Z., **Irizarry, K.J.L.**, Huang, Y., Mitsouras, K., Darmani, M., Leon, T., Shi, L., and Bi, X. "Abnormal gene expression in cerebellum of Npc1^{-/-} mice during postnatal development." *Brain Research* 2010, 1325: 128-40
8. Jennifer L. Buur, Peggy Schmidt, Dean Smylie, **Kristopher Irizarry**, Carlos Crocker, John Tyler, and Margaret Barr (in press). "Validation of a scenario based assessment of critical thinking using an externally validated tool." *J Vet Med Ed.* 2012 Fall;39(3):276-82.
9. Pearce DD, Mitsouras K, **Irizarry KJ**. Discriminating the effects of Cannabis sativa and Cannabis indica: a web survey of medical cannabis users. *J Altern Complement Med.* 2014 Oct;20(10):787-91.

PATENTS

1. Licinio, J., Wong, M.L., Irizarry, K.J.L., **Irizarry, K.M.** "Compositions and Methods for Determining and Predicting Treatment Response for Depression and Anxiety." International Patent PCT/US2005/028790, Publication Date:16.02.2006, International Filing Date:12.08.2005
2. Irizarry, K.J.L. & Oakley B. "High Throughput Bioinformatics Hypothesis Driven Molecular Phenotyping Platform" Provisional Patent Application submitted on May 19, 2016.

Exhibit 1

Kristopher J. Irizarry, Ph.D
Associate Professor, College of Veterinary Medicine
Western University of Health Sciences
Pomona CA 91766

My name is Dr. Kristopher Irizarry and I am an associate professor of Genetics and Genomics at Western University of Health Science's College of Veterinary Medicine. I received my B.S. in Biochemistry and Biophysics from Rensselaer Polytechnic Institute in 1996 and received my PhD from the department of Biochemistry and Molecular Biology at the University of California, Los Angeles in 2003. My curriculum vitae is attached. (Ex. A).

For more than a decade my research has focused on how DNA encodes traits of interest. Aspects of my research have investigated how genetic variation gives rise to differences and similarities between members of the same species (such as two dogs or two humans) as well as how genetic differences between species contribute to observable differences in traits such as health, longevity, behavior, and disease susceptibility.

Some of my research projects include investigations into (1) the genetic basis of dog breed identification and how DNA based tests for dog breed composition compare to visual identification of dog breeds; (2) the role of specific genetic variations within human genes underlying behavioral traits and how these genetic differences affect human behavior; and (3) canine genetics associated with disease, breed and anatomical traits.

I am familiar with and have participated in Dr. Victoria Voith's research and work relating to the accuracy of visual identification of breeds of mixed breed dogs and was a co-author of *Comparison of Adoption Agency Breed Identification and DNA Breed identification of Dogs*, Journal of Applied animal Welfare Science, 12:253-262, 2009 and *Comparison of Visual and DNA Breed Identification of Dogs and Inter-Observer Reliability*, American Journal of Sociological Research 2013, 3(2): 17-29. The results of this research establish that using visual identification to predict the breed of mixed breed dogs is fundamentally unreliable. As these studies show, mixed breed dogs often express physical traits associated with breeds that are not a part of the animal's actual genetic breed composition and fail to express physical traits that are associated with breeds that are a part of the animal's actual genetic breed composition. Therefore, reliance upon physical appearance to predict the predominant breeds of mixed breed dogs of unknown origin is inherently unreliable. This result is not surprising because less than 1 percent of the canine genome is associated with the expression of physical traits commonly used to categorize animals by breed. Moreover, dominant phenotypes may be visible in heterozygous animals while recessive phenotypes cannot be observed within heterozygous individuals.

Breeds

The biology and genetics of dogs and dog breeds have been heavily studied during the last ten to fifteen years as a direct result of genetics and genomics discoveries made possible by the genome sequencing era and, specifically, the canine genome sequence (released to the public in July 2004). Some of these discoveries include: (1) identifying the single region within the dog genome responsible for encoding small dog size, (2) the extent of genetic similarity within and between breeds, (3) the specific regions of the genome responsible for breed-associated anatomical and morphological traits, (4) methods to determine relative contributions of ancestral breed compositions in mixed breed dogs, (5) the identification of thousands of dog genes as well as the commercial development of clinical genetic diagnostics for use in canine veterinary medicine.

Domestic dogs (*Canis lupus familiaris*) exhibit tremendous morphological (physical) variation within the species. They vary in anatomical features such as coat color and type, height, weight, frame size, head shape, ear shape, snout size and length, musculature and leg length. Although today there are many breeds of dogs, breeds were developed as a result of human interaction to deliberately select breedings between animals with similar traits to produce offspring expressing those traits. Over time with repeated selected breeding, the population within a given breed lost the genetic variation present in the general species population to express those physical traits not associated with the breed, i.e., German Shepherds lack the genetic variants associated with the short snout found in the French Bulldog and Standard Poodles lost the genetic variants associated with smooth coats. A breed then is a population of animals who have been intentionally selected and bred to express similar morphological traits. Breeds within a given species are a human creation and not the result of natural selection or normal genetic variation.

Historically, the creation of breed standards and development of breed registries resulted in founder events involving only a few dogs and, thereafter, reproductive dominance by popular sires that conformed most closely to the breed standard. These restrictive breeding practices reduced effective population size and increased genetic drift¹ which resulted in the loss of genetic diversity within

¹ Genetic drift is commonly illustrated by using 20 marbles in a jar to represent 20 organisms in a population. In the starting population, half of the marbles in the jar are red and half blue, and both colors correspond to two different alleles of one gene in the population. In each new generation the organisms reproduce at random. To represent this reproduction, randomly select a marble from the original jar and deposit a new marble with the same color as its “offspring” into a new jar. (The selected marble remains in the original jar.) Repeat this process until there are 20 new marbles in the second jar. The second jar then contains a second generation of “offspring,” consisting of 20 marbles of various colors. Unless the second jar contains exactly 10 red marbles and 10 blue marbles, a random shift occurred in the allele frequencies.

Repeat this process a number of times, randomly reproducing each generation of marbles to form the next. The numbers of red and blue marbles picked each generation fluctuates; sometimes more red and sometimes more blue. This fluctuation is analogous to genetic drift – a change in

Exhibit 1

breeds and allele frequency divergence among them. Registered or purebred dogs within a breed were the result of a breeding between two animals both of whose ancestry traces to the group of animals recognized as a “breed” by the entity undertaking the registration. For example, in most cases for a dog to be registered with the American Kennel Club (“AKC”), the animal to be registered must result from a breeding between two animals of the same breed that are both registered with the AKC as members of that breed. The registration of purebred dogs of a specific breed results in creating a closed gene pool in which all dogs recognized as part of a breed come from ancestors also recognized as being part of that same breed. By continually mating dogs within a closed gene pool, the genetic variants associated with physical traits not usually expressed within that gene pool are eventually eliminated.

Genetics of Physical Appearance and Behavior

The genome of domestic dogs contains approximately 20,000 protein encoding genes. Approximately 50 of these genes relate to the expression of breed defining anatomical traits. That is 0.25% of the domestic dog’s genes relate to the expression of physical traits that are commonly associated with physical breed identification while the remaining 19,950 genes encode traits that are not typically associated with breed-defining appearance.

It is incorrect to assume that because the population of animals within a breed share similar physical traits, the animals share other traits such as behavior, health, and disease susceptibility. Unlike identical twins in humans, who have identical DNA, members of dog breeds may look the same but have very different DNA. The 0.25% of the domestic dogs’ genes relating to physical traits that are similar within a breed population are unrelated to other genetic traits including those genes which encode the brain, connections of brain cells, and involved in encoding the behavior of an animal at a genetic level. Similarly, the notion that the presence of an anatomical feature, i.e., smooth coat, round head, or muscular body, correlates with behavior is not based in science. Even within the closed gene pool of purebred animals of a given breed, the selection pressure applied to physical characteristics does not result in the limitation of genetic variability for other traits, including behavior.

Because animal and human behavior arises from complex properties of the brain, including particular patterns of brain cell connectivity and chemical composition, within specific regions of the brain, it is relatively well accepted among the

the population's allele frequency resulting from a random variation in the distribution of alleles from one generation to the next.

Breed standards result in selection pressure making it possible that in any one generation no marbles of a particular color are chosen, meaning they have no offspring. In this example, if no red marbles are selected, the jar representing the new generation contains only blue offspring. If this happens, the red allele has been lost permanently in the population, while the remaining blue allele has become fixed: all future generations are entirely blue. In small populations, fixation can occur in just a few generations.

Exhibit 1

scientific community that attempts to infer behavior based upon externally visible morphological features of the skull is unscientific and has even been disproven. Such methods were attempted during the 1700s and 1800s in under the field of “Phrenology” which has since been disproven.

Anatomical traits associated with particular dog breeds have no predictive value in characterizing the behavior of dogs exhibiting similar morphological characteristics.

Heritability

The genetic heritability of a trait is the fraction of the total variation in the trait among the animals in a population that can be accounted for by genetics. Heritability is measured on a scale between 0 and 1. Some traits have a high genetic heritability, while other traits are influenced by multiple factors which include genetics and environment. For example, coat color and almost all other physical traits are controlled solely by genetics. As a result, we know that offspring inherit coat color solely from the genes of its parents and that environment or other facts will not alter the manner in which coat color is expressed.

Behavior is a complex trait that results from a lifetime of experiences. Domestic dogs were selected to live among humans and conform to the social and familial structure of humans. The domestication of dogs resulted in companion animals that were more attuned to human communication and more easily adapted and trained by their human counter parts. All domesticated dog breeds inherited these and share these traits and no specific breed of dog is genetically lacking in these artificially selected traits that were carefully acquired over a 30,000 year domestication period.

Opinions

In addition to the opinions expressed above, it is also my opinion to a reasonable degree of scientific certainty that:

1. Visual breed identification of dogs, even when made by animal care professionals, is unreliable to predict the actual breed composition of an animal.
2. A mixed breed dog's physical traits do not provide an adequate scientific or genetic basis to predict the animal's breed.
3. Breeds are not a predictor of dangerousness or aggression
4. Domestic dogs were selected to live among humans and conform to the social and familial structure of humans.
5. All domesticated dog breeds inherited these and share these traits and no specific breed of dog is genetically lacking in these artificially selected traits that were carefully acquired over a 30,000 year domestication period.
6. No rational, genetic or scientific basis to ban certain breeds of dogs as more dangerous or more aggressive than other breeds of dogs