

## Mark Zlojutro Kos, Ph.D.

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### Education & Training

#### **Ph.D., Anthropology, University of Kansas, Lawrence, KS, 2008**

- Concentration in Anthropological Genetics
- Dissertation: "Mitochondrial DNA and Y-Chromosome Variation in Aleut Populations: Genetic Implications of Founder Effect, Asymmetrical Gene Flow and the Original Peopling of the Aleutian Archipelago"
- Ph.D. advisor and committee chair: Dr. Michael H. Crawford

#### **M.A., Anthropology, University of Kansas, Lawrence, KS, 2006**

- Thesis: "Mitochondrial DNA Variation in Yakutia: The Genetic Structure of an Expanding Population"

#### **B.S., Biology, McMaster University, Hamilton, ON, Canada, 1997**

- Minor in History
- Senior thesis: "A Population Genetic Study of Three Microsatellite Loci in the Indian Subcontinent"

### Research Interests

Areas of interest include statistical genetics and genetic epidemiology, bioinformatics, methods and software development, and genetics of complex traits. My research has mostly focused on identifying the genetic and epigenetic determinants of psychiatric and neurological disorders (e.g., schizophrenia, epilepsy) and brain-related correlates (e.g., electrophysiology, neurocognition), as well as diabetes and obesity. I have conducted case-control and family-based genetic studies, including genome-wide association studies (GWAS), linkage analysis, pathway enrichment tests, hierarchical clustering and network construction, and polygenic risk scoring routines. Currently, my research has been investigating the genetics of generalized epilepsy in the baboon colony at the Southwest National Primate Research Center (SNPRC; San Antonio, TX), with the objective

of identifying key pathophysiological mechanisms and to develop a multi-omic, preclinical platform for developing and testing novel therapies in the baboon that can translate to human applications and be a unique resource for the wider epilepsy research community.

My graduate research at the University of Kansas was in the field of molecular anthropology and human evolution, which I still have an abiding interest in. This work resulted in publications on the population genetics of Native American and Siberian populations and its implications for the peopling of the Americas, with a focus on the native communities of the Aleutian archipelago and the consequences of male-biased gene flow from European populations.

My research skills include R statistical programming; Perl and Unix shell scripting; BerkeleyDB embedded databases; SOLAR software package for genetic variance components analysis; PLINK program for genome-wide association testing and polygenic risk scoring; pathway enrichment analysis; weighted gene co-expression network analysis (WGCNA); and bioinformatics pipelines for processing, aligning, and annotating variant calls from whole-genome sequence (WGS), RNA-seq, and Meth-seq data.

## Publications

### Scientific Articles

1. **Kos MZ**, Puppala S, Cruz D, Neary JL, Ashish K, Dalan E, Li C, Nathanielsz P, and Carless MA (2022) Blood-Based miRNA Biomarkers as Correlates of Brain-Based miRNA Expression. *Frontiers in Molecular Neuroscience* 15 In press.
2. **Kos MZ**, Carless MA, Blondell L, Leland MM, Knape KD, Göring HHH, and Szabó CA (2021) Whole genome sequence data from captive baboons implicate *RBFOX1* in epileptic seizure risk. *Frontiers in Genetics* 12: 714282.
3. Blondell L, **Kos MZ**, Blangero J, and Göring HHH (2021) Genz and Mendell-Elston estimation of the high-dimensional multivariate normal distribution. *Algorithms* 14: 296.
4. Blackburn AN, Blondell L, **Kos MZ**, Blackburn N, Peralta JM, Stevens PT, Lehman DM, Blangero J, and Göring HHH (2020) Genotype phasing in pedigrees using whole genome sequence data. *European Journal of Human Genetics* 28(6): 790-803.
5. **Kos MZ**, Duan J, Sanders AR, Blondell L, Drigalenko EI, Carless MA, MGS, Gejman PV, and Göring HHH (2018) Dopamine perturbation of gene co-expression networks reveals differential response in schizophrenia for translational machinery. *Translational Psychiatry* 8(1): 278.
6. Arya R, Escalante A, Farook V, Restrepo JF, Battafarano DF, Almeida M, **Kos MZ**, Fourcaudot MJ, Mummidi S, Kumar S, Curran JE, Jenkinson CP, Blangero J, Duggirala R, and del Rincon I (2018) Data on Genetic Associations of Carotid Atherosclerosis Markers in Mexican American and European American Rheumatoid Arthritis Subjects. *Data in Brief* 17: 820-829.

7. Arya R, Escalante A, Farook V, Restrepo JF, Battafarano DF, Fourcaudot MJ, Almeida M, **Kos MZ**, Kumar S, Curran JE, Jenkinson CP, Blangero J, Duggirala R, and del Rincon I (2018) A genetic association study of carotid intima-media thickness (CIMT) and plaque in Mexican Americans and European Americans with rheumatoid arthritis. *Atherosclerosis* 271: 92-101.
8. Blondell L, Blackburn A, **Kos MZ**, Blangero J, and Göring HHH (2018) Contribution of inbred singletons to variance component estimation of heritability and linkage. *Human Heredity* 83(2): 92-99.
9. Duan J, Göring HHH, Sanders AR, Moy W, Freda J, Drigalenko EI, **Kos M**, He D, and Gejman PV (2018) Transcriptomic signatures of schizophrenia revealed by dopamine perturbation in an ex vivo model. *Translational Psychiatry* 8(1): 158.
10. **Kos MZ**, Carless MA, Peralta J, Curran JE, Quillen EE, Almeida M, Blackburn, A, Blondell L, Roalf DR, Pogue-Geile MF, Prasad K, Gur RC, Göring HHH, Nimgaonkar V, Gur RE, and Almasy L (2017) Exome sequences of multiplex, multigenerational families reveal schizophrenia risk loci with potential implications for neurocognitive performance. *American Journal of Medical Genetics Part B* 174(8): 817-827.
11. Mathies LD, Aliev F, Porjesz B, Hesselbrock V, Edenberg H, Bierut L, Nurnberger J Jr, Foroud T, Kuperman S, Kramer J, Porjesz B, Bierut L, Rice J, Bucholz K, Agrawal A, Schuckit M, Tischfield J, Brooks A, Almasy L, Goate A, Taylor R, Bauer L, McClintick J, Wetherill L, Xuei X, Liu Y, Lai D, O'Connor S, Plawecki M, Lourens S, Chan G, Meyers J, Chorlian D, Kamarajan C, Pandey A, Zhang J, Wang JC, Kapoor M, Bertelsen S, Anokhin A, McCutcheon V, Saccone S, Salvatore J, Cho B, **Kos M**, Parsian A, Reilly M, Davies AG, Dick DM, and Bettinger JC (2017) Variation in SWI/SNF chromatin remodeling complex proteins is associated with alcohol dependence and antisocial behavior in human populations. *Alcoholism: Clinical and Experimental Research* 41(12): 2033-2040.
12. **Kos MZ**, Carless MA, Peralta J, Blackburn A, Almeida M, Roalf D, Pogue-Geile MF, Prasad K, Gur RC, Nimgaonkar V, Curran JE, Duggirala R, Glahn DC, Blangero J, Gur RE, and Almasy L (2016) Exome sequence data from multigenerational families implicate AMPA receptor trafficking in neurocognitive impairment and schizophrenia risk. *Schizophrenia Bulletin* 42(2): 288-300.
13. Kulkarni H, **Kos MZ**, Neary J, Dyer TD, Kent JW Jr, Göring HH, Cole SA, Comuzzie AG, Almasy L, Mahaney MC, Curran JE, Blangero J, and Carless MA (2015) Novel epigenetic determinants of type 2 diabetes in Mexican-American families. *Human Molecular Genetics* 24(18): 5330-5344.
14. **Kos MZ**, Glahn DC, Carless MA, Olvera R, McKay DR, Quillen EE, Gelernter J, Chen X-D, Deng H-W, Kent JW, Dyer TD, Göring HHH, Curran JE, Duggirala R, Blangero J, and Almasy L (2014) Novel QTL at chromosome 6p22 for alcohol consumption: Implications for the genetic liability of alcohol use disorders. *American Journal of Medical Genetics B* 165B: 294-302.

15. Yan J, Aliev F, Webb BT, Kendler KS, Williamson VS, Edenberg HJ, Agrawal A, **Kos MZ**, Almasy L, Nurnberger JI Jr, Schuckit MA, Kramer JR, Rice JP, Kuperman S, Goate AM, Tischfield JA, Porjesz B, and Dick DM (2014) Using genetic information from candidate gene and genome-wide association studies in risk prediction for alcohol dependence. *Addiction Biology* 19:708-721.
16. **Kos MZ**, Yan J, Dick DM, Agrawal A, Bucholz KK, Rice JP, Johnson EO, Schuckit M, Kuperman S, Kramer J, Goate AM, Tischfield JA, Foroud T, Nurnberger J Jr, Hesselbrock V, Porjesz B, Bierut LJ, Edenberg HJ, and Almasy L (2013) Common biological networks underlie genetic risk for alcoholism in African- and European-American populations. *Genes, Brain and Behavior* 12: 532-542.
17. Anderson-Schmidt H, Beltcheva O, Brandon MD, Byrne EM, Diehl EJ, Duncan L, Gonzalez SD, Hannon E, Kantojärvi K, Karagiannidis I, **Kos MZ**, Kotyuk E, Laufer BI, Mantha K, McGregor NW, Meier S, Nieratschker V, Spiers H, Squassina A, Thakur GA, Tiwari Y, Viswanath B, Way MJ, Wong CC, O'Shea A, and DeLisi LE (2013) Selected rapporteur summaries from the XX World Congress of Psychiatric Genetics, Hamburg, Germany, October 14-18, 2012. *American Journal of Medical Genetics B* 162B: 96-121.
18. Carless MA, Kulkarni H, **Kos MZ**, Charlesworth J, Peralta JM, Göring HHH, Curran JE, Almasy L, Dyer TD, Comuzzie AG, Mahaney MC, and Blangero J (2013) Genetic effects on DNA methylation and its potential relevance for obesity in Mexican Americans. *PLoS One* 8: e73950.
19. **Zlojutro M**, Manz N, Rangaswamy M, Xuei X, Flury-Wetherill L, Koller D, Beirut L, Cloninger R, Goate A, Hesselbrock V, Kuperman S, Nurnberger J, Rice J, Schuckit M, Foroud T, Edenberg HJ, Porjesz B, and Almasy L (2011) Genome-wide association study of theta band event-related oscillations identifies serotonin receptor gene *HTR7* influencing risk of alcohol dependence. *American Journal of Medical Genetics: Part B* 156B: 44-58.
20. Kumar S, Bellis C, **Zlojutro M**, Melton PE, Blangero J, and Curran J (2011) Large scale mitochondrial sequencing in Mexican Americans suggests a reappraisal of Native American origins. *BMC Evolutionary Biology* Oct. 7: 293.
21. Crawford MH, Rubicz RC, and **Zlojutro M** (2010) Origins of Aleuts and the genetic structure of populations of the archipelago: molecular and archaeological perspectives. *Human Biology* 82: 695-717.
22. Graf OM, **Zlojutro M**, Rubicz R, and Crawford MH (2010) Surname distributions and their association with Y-chromosome markers in the Aleutian Islands. *Human Biology* 82: 745-757.
23. Melton PE, Mosher MJ, Rubicz R, **Zlojutro M**, and Crawford MH (2010) Mitochondrial DNA diversity in Mennonite communities from the Midwestern United States. *Human Biology* 82: 267-289.

24. Rubicz R, **Zlojutro M**, Sun G, Spitsyn V, Deka R, Young K, and Crawford MH (2010) Genetic architecture of a small, recently aggregated Aleut population: Bering Island, Russia. *Human Biology* 82: 719-736.
25. **Zlojutro M**, Rubicz R, and Crawford MH (2009) Mitochondrial DNA and Y-chromosome variation in five eastern Aleut communities: evidence for genetic substructure in the Aleut population. *Annals of Human Biology* 36 (5): 511-526.
26. **Zlojutro M**, Tarskaia LA, Sorensen M, Snodgrass JJ, Leonard WR, and Crawford MH (2009) Coalescent Simulations of Yakut mtDNA Diversity suggest Small Founding Population. *American Journal of Physical Anthropology* 139 (4): 474-482.
27. Devor EJ, Abdurakhmonov I, **Zlojutro M**, Millis MP, Galbraith JJ, Crawford MH, Shermatov S, Buriev Z, and Abdukarimov A (2009) Gene flow at the crossroads of humanity: mtDNA sequence diversity and *Alu* insertion polymorphism frequencies in Uzbekistan. *The Open Genomics Journal* 2: 1-11.
28. **Zlojutro M**, Tarskaia LA, Sorensen M, Snodgrass JJ, Leonard WR, and Crawford MH (2008) The Origins of the Yakut People: Evidence from Mitochondrial DNA Diversity. *International Journal of Human Genetics* 8 (1-2): 119-130.
29. Moscoso J, Crawford MH, Vicario JL, **Zlojutro M**, Serrano-Vela JI, Reguera R, and Arnaiz-Villena A (2008) HLA genes of Aleutian Islanders living between Alaska (USA) and Kamchatka (Russia) suggest a possible southern Siberia origin. *Molecular Immunology* 45 (4): 1018-1026.
30. **Zlojutro M**, Roy R, Palikij J, and Crawford MH (2006) Autosomal STR Variation in a Basque Population. *Human Biology* 78 (5): 599-618.
31. **Zlojutro M**, Rubicz R, Devor E, Spitsyn V, Wilson K, and Crawford MH (2006) Genetic Structure of the Aleuts and Circumpolar Populations Based on Mitochondrial DNA Sequence: A Synthesis. *American Journal of Physical Anthropology* 129 (3): 446-464.
32. Melton PE, **Zlojutro M**, Kimminau K, and Crawford MH (2006) Biological Aging and Cox hazard analysis of mortality trends in a Mennonite community from south-central Kansas. *American Journal of Human Biology* 18 (3): 387-401.
33. Phillips-Krawczak C, Devor E, **Zlojutro M**, and Crawford MH (2006) mtDNA variation in the Altai-Kizhi population of Southern Siberia: A synthesis of genetic variation. *Human Biology* 78 (4): 477-494.
34. Crawford MH, Banerjee P, Demarchi DA, **Zlojutro M**, McComb J, Livshits G, Henneberg M, Mosher MJ, Schanfield MS, and Knowles JA (2005) Applications of pooled DNA samples to the assessment of population affinities: short tandem repeats. *Human Biology* 77 (6): 723-733.

## Book Chapters

35. Almasy L, **Kos MZ**, and Blangero J (2015) Linkage mapping: Localizing the genes that shape human variation. In *Genome Mapping and Genomics in Human and non-Human Primates*, R Duggirala, L Almasy, S Williams-Blangero, SFD Paul, and C Kole eds. Heidelberg, Germany: Springer-Verlag.

#### **In Preparation**

36. **Kos MZ**, Blackburn AN, Stevens P, Blondell L, and Göring HHH. Software for peak alignment and quantification of comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry metabolomics data.

37. Kumar A, **Kos MZ**, and Carless MA. Differential hydroxymethylation levels in patient-derived neural stem cells implicate altered cortical development in bipolar disorder.