

## **Curriculum Vitae**

Ripan S. Malhi

Department of Anthropology, University of Illinois Urbana-Champaign, 209E Davenport Hall, 607 Matthews Ave., Urbana, IL 61801. 217-265-0721.malhi@illinois.edu.

### **Education**

Ph.D. Anthropology, University of California, Davis, 2001.

Dissertation: Investigating prehistoric population movements in North America using ancient and modern mtDNA.

M.A. Anthropology, University of California, Davis, 1998.

B.S. Anthropology, Minor in Biological Science, University of California, Davis, 1994.

### **Current Appointments (Academic and Service)**

August 2017 to present - Full Professor in Anthropology, University of Illinois Urbana-Champaign.

August 2018 to present – Chair, Carl R. Woese Institute for Genomic Biology Committee on Diversity.

August 2015 to present – Co-Director of the Increasing Diversity in Evolutionary Anthropological Sciences (IDEAS) program. American Association of Physical Anthropologists (AAPA).

January 2015 to present – Associate Editor of *American Journal of Physical Anthropology*.

September 2013 to present – Executive Editor of *Human Biology*.

August 2011 to present – Director of Summer internship for INdigenous peoples in Genomics (SING) U.S.A. Program. Summer program to train indigenous students in genomic research.

### **Past Appointments and Research**

January 2015-2017 – Co-Chair Committee on Diversity (COD). American Association of Physical Anthropologists (AAPA).

August 2011-2017 Associate Professor in Anthropology, University of Illinois Urbana-Champaign.

August 2006 – 2011 Assistant Professor in Anthropology, University of Illinois Urbana-Champaign.

June 2005-June 2006 - Research Director, Trace Genetics, Inc (A DNAPrint Genomics Company). Job duties included develop new products and services, manage scientific

and customer service staff, create and manage budgets, perform scientific research and publish in peer-review journals.

November 2002-June 2005 – Chief Executive Officer and Co-Founder, Trace Genetics, Inc. Founder and Manager of a biotechnology company (10 employees) with a focus on genetic ancestry, forensic DNA, and biomedical DNA testing (acquired 6/2005 by DNAPrint Genomics, Inc).

November 2001-November 2002 – Postdoctoral Fellow, Department of Human Genetics, University of Michigan. Dr. Jeffery C. Long, advisor. Conducted research on genetic variation in aldehyde dehydrogenase genes. Skills: population genetic analyses, heterozygote detection, long range PCR.

September 2001-October 2001 – Visiting Researcher, Department of Biological Sciences, Stanford University. Analysis of ancient mtDNA from Catalhoyuk. Collaboration with Dr. Joanna Mountain and Dr. Elizabeth Hadly. Pilot project to set up ancient human DNA extraction facilities for the department of Anthropological Sciences and determine if tooth samples from the Catalhoyuk site contain amplifiable DNA.

Expert Witness 2006-2018 – Will County, IL Public Defender’s Office (2006); King County, WA Public Defender’s Office (2015); Manchester, New Hampshire (2016)

## Publications

In Press. Bader AC, Malhi RS. How Subjectivity Strengthens Research: Developing an Integrative Approach to Investigating Human Diet in the Pacific Northwest Coast. **American Anthropologist**.

In Press. **Malhi RS**, Anton SC, Fuentes A. Increasing Diversity in Evolutionary Anthropological Sciences – the IDEAS Program. **American Anthropologist**.

In Press. Fogleman AJ, Zahnd WE, Lipka AE, **Malhi RS**, Ganai S, Delfino KR, Jenkins WD. Knowledge, attitudes, and perceived barriers towards genetic testing across three rural Illinois communities. **Journal of Community Genetics**.

2019 Schablitsky JM, Witt KE, Madrigal JR, Ellegaard MR, **Malhi RS**, Schroeder H. Ancient DNA analysis of a nineteenth century tobacco pipe from a Maryland slave quarter. **Journal of Archaeological Science** 105:11-18.

2018 Moreno-Mayar J, Vinner L, Damgaard PdB, de la Fuente C, Chan J, Spence JP, Allentoft ME, Vimala T, Racimo F, Pinotti T, Rasmussen S, Margaryan A, Orbegozo MI, Milopotamitaki D, Wooller M, Bataille C, Becerra-Valdivia L, Chivall D, Comeskey D, Deviese T, Grayson DK, George L, Harry H, Andersen V, Pramaeu C, Erlandson J, Rodrigues-Carvalho C, Reis S, Baston MQR, Cybulski J, Vullo C, Morello F, Vilar M, Wells S, Gregersen K, Hansen KL, Lynnerup N, Lahr MM, Kjaer K, Strauss A, Alfonso-Durruty M, Salas A, Schroeder H, Higham T, **Malhi RS**, Rasic JT, Souza L, Santos FR,

Malaspinas A-S, Sikora M, Nielsen R, Song YS, Meltzer DJ, Willerslev E. Early Human Dispersals Within the Americas. **Science** 362 (6419).

2018 Brandt JR, Groot PJvC, Witt KE, Engelbrektsson PK, Helgen KM, **Malhi RS**, Ryder OA, Roca AL. Genetic structure and diversity among historic and modern populations of the Sumatran Rhinoceros (*Dicerorhinus sumatrensis*). **Journal of Heredity** 109: 553-565.

2018 Potter BA, Baichtal JF, Beaudoin AB, Fehren-Schmitz L, Haynes CV, Holliday CT, Holmes CE, Ives JW, Kelly RL, Llamas B, **Malhi RS**, Miller DS, Reich D, Reuther JD, Schiffels S, Surovell TA. Current evidence allows multiple models for the peopling of the Americas. **Sci Adv** 8: eaat5473.

2018 Claw KG, Anderson MZ, Begay RL, Tsosie KS, Fox K, Garrison NA, **Summer internship for INdigenous peoples in Genomics (SING) Consortium**. A framework for enhancing ethical genomic research with Indigenous communities. **Nat Commun** 9: 2957.

2018 Mallott EK, Garber PA, **Malhi RS**. *trnL* outperforms *rbcL* as a DNA metabarcoding marker when compared with the observed plant component of the diet of wild white-faced capuchins (*Cebus capucinus*, Primates). **PLoS One** 26:e0199556.

2018 Leathlobhair MN, Perri AR, Irving-Pease EK, Witt KE, Boyko A, Brace S, Cortes YN, Crockford SJ, Dimopoulos EA, Eldridge M, Gopalakrishnan S, Grimes V, Guiry E, Hansen AJ, Hulme-Beaman A, Johnson J, Kitchen A, Kwon Y-M, Lope CP, Manin A, Martin T, Meyer M, Myers KN, Omura M, Sciulli P, Sinding M-H S, Strakova A, Widga C, Willerslev E, Barnes I, Gilbert MTP, Dobney KM, **Malhi RS**, Murchinson EP, Larson G, Frantz LA. The Evolutionary History of Dogs in the Americas. **Science** 361: 81-85.

2018 Scheib CL, Li H, Link V, Kendell C, Dewar G, Griffith PW, Moerseburg A, Johnson JR, Potter A, Kerr SL, Endicott P, Lindo J, Haber M, Xue Y, Smith CT, Sandhu M, Durbin R, Lorenz JG, Randall TD, Faltyskova Z, Pagain L, Danecek P, O'Connell TC, Martz P, Boraas AS, Lindgren AS, Byrd BF, Leventhal A, Cambra R, Williamson R, Lesage L, Tosas JT, Ygnacio-De Soto E, Metspalu M, Stock JT, Manica A, Wegmann D, **Malhi RS**, Kivisild T. Terminal Pleistocene parallel lineages within North America both contributed to a Pacific coastal expansion. **Science** 360:1024-1027.

2018 Brandt JR, Van Coeverden de Groot PJ, Witt KE, Engelbrektsson PK Helgen KM, **Malhi RS**, Ryder OA, Roca AL. Genetic structure and diversity among historic and modern populations of the Sumatran rhinoceros (*Dicerorhinus sumatrensis*). **Journal of Heredity** 109: 553-565.

2018. Lindo J, Rogers M, Petzelt B, Mitchell J, Archer D, Cybulski J, **Malhi RS**, DeGiorgio M. Patterns of Genetic Coding Variation in a Native American Population Before and After European Contact. **American Journal of Human Genetics** 102: 806-815.

2018. Bardill J, Bader AC, Garrison NA, Bolnick DA, Raff JA, Walker A, **Malhi RS**, SING Consortium. Advancing the Ethics of Paleogenomics. **Science** 360: 384-385.
2018. Potter BA, Beaudoin AB, Haynes CV, Holliday VT, Holmes CE, Ives JW, Kelly R, Llamas B, **Malhi R**, Miller S, Reich D, Reuther JD, Schiffels S, Surovell T. Arrival routes of first Americans uncertain. **Science** 359: 1224-1225.
2018. Anton SC, Fuentes A, **Malhi RS**. Race and Diversity in U.S. Biological Anthropology: A decade of AAPA initiatives. **Yearbook of Physical Anthropology** 165 Suppl 65: 158-180.
2018. Mallott EK, Amato KR, Garber PA, **Malhi RS**. Influence of fruit and invertebrate consumption on the gut microbiota of wild white-faced capuchins (*Cebus capucinus*). **American Journal of Physical Anthropology** 165: 576-588.
- 2018 Moreno-Mayar JV, Potter BA, Vinner L, Steinrücken M, Rasmussen S, Terhorst J, Kamm JA, Albrechtsen A, Malaspina A-S, Sikora M, Reuther JD, Irish JD, **Malhi RS**, Orlando L, Song YS, Nielsen R, Meltzer DJ, Willerslev E. Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. **Nature** 553(7687): 203-207.
- 2017 Claw KG, Lippert D, Bardill J, Cordova A, Fox K, Yracheta JM, Bader AC, Bolnick DA, **Malhi RS**, TallBear K, Garrison NA. Chaco Canyon Dig Unearths Ethical Concerns. **Hum Biol**: 89: 177-180.
- 2017 Molto JE, Loreille O, Mallott EK, **Malhi RS**, Fast S, Daniels-Higginbotham J, Marshall C, Parr R. Complete Mitochondrial Genome Sequencing of a Burial from a Romano-Christian Cemetery in the Dakhleh Oasis, Egypt: Preliminary Indications. **Genes** 8(10) (October Cover).
- 2017 Yao L, Li H, Martin RD, Moreau CS, **Malhi RS**. Tracing the phylogeographic history of Southeast Asian long-tailed macaques through mitogenomes of museum specimens. **Molecular Phylogenetics and Evolution** 116:227-238.
- 2017 Dean C, Fogelman AJ, Zahnd WE, Lipka AE, **Malhi RS**, Delfino K, Jenkins WD. Engaging rural communities in genetic research: challenges and opportunities. **Journal of Community Genetics** 8(3): 209-219.
- 2017 Lindo J, Achilli A, Perego U, Archer D, Valdiosera C, Petzelt B, Mitchell J, Worl R, Dixon EJ, Fifield T, Rasmussen M, Willerslev E, Cybulski J, Kemp BM, DeGiorgio M, **Malhi RS**. Ancient individuals from the North American Northwest Coast reveal 10,000 years of regional genetic continuity. **Proc Natl Acad Sci U S A**. 114(16):4093-4098.

2017 Mallott EK, Garber PA, **Malhi RS**. Integrating feeding behavior, ecological data, and DNA barcoding to identify developmental differences in invertebrate foraging strategies in wild white-faced capuchins (*Cebus capucinus*). **American Journal of Physical Anthropology** 162: 241-254.

2017 Figueiro G, Perez LC, Lindo J, Mallot EK, Owings A, **Malhi RS**, Sans M. Analisis del genoma mitochondrial de dos individuos inhumados en el sitio arqueologico CG14e01 “Isla Larga” (Rocha, Uruguay). **Revista Argentina de Antropologia Biologica** 19: 1-17.

2016 Hughes CE, Rogers MP, Owings AC, Petzelt B, Mitchell J, Harry H, Williams T, Goldbeg D, Labuda D, Smith DG, Cybulski JS, **Malhi RS**. Genetic structure of First Nation communities in the Pacific Northwest. **Hum Biology** 88(4): 251-263.

2016 Lindo J, Huerta-Sanchez E, Rasmussen M, Petzelt B, Mitchell J, Cybulski J, Willerslev E, DeGiorgio M, **Malhi RS**. A time transect of exomes from a Native American population before and after European contact. **Nature Communications** 7: 13175.

2016 Jenkins W, Lipka A, Fogleman A, Delfino K, **Malhi RS**, Hendricks B. Variance in disease risk: rural populations and genetic diversity. **Genome** 59: 519-525.

2016 Hughes CE, Hunter CD, Vargas PT, Schlosser MD, **Malhi RS**. Police endorse color-blind racial beliefs more than lay. **Race and Social Problems** 8: 160-170.

2015 Bader AC, **Malhi RS**. Case Study on Ancestry Estimation in an Alaskan Native Family: Identity and Safeguards Against Reductionism. **Human Biology** 87: 338-351.

2015 Mott J, Hagelberg E, **Malhi RS**, Lindo J, Bravi CM, Guichon RA. Primer genoma mitocondrial en restos humanos de la costa de Santa Cruz, Argentina. **Magallania** 43 Online.

2015 **Malhi RS**, Bader A. Vital Topics: Engaging Native Americans in genomics research and diversifying science. **American Anthropologist** 117: 736-749.

2015 Eerkens JW, Carlson T, **Malhi RS**, Blake J, Bartelink EJ, Barfod GH, Estes A, Garibay R, Glessner J, Greenwald AM, Lentz K, Li H, Marshall CK. Isotopic and genetic analyses of a mass grave in central California: Implications for precontact hunter-gatherer warfare. **American Journal of Physical Anthropology** 159: 116-125.

2015 Sans M, Figueiro G, Hughes CE, Lindo J, Hidalgo PC, **Malhi RS**. A South American prehistoric mitogenome: context, continuity, and the place of C1d haplogroup. **PLoS One** 10(10): e0141808.

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2015 Dong Y, Li C, Luan F, Li Z, Li H, Cui Y, Zhou H, **Malhi RS**. Low mitochondrial DNA diversity in an ancient population from China: Insight into social organization at the Fujia site. **Human Biology** 87: 71-84.

2015 Raghavan M, Steinrücken M, Harris K, Schiffels S, Rasmussen S, DeGiorgio M, Albrechtsen A, Valdiosera C, Ávila-Arcos MC, Malaspina AS, Eriksson A, Moltke I, Metspalu M, Homburger JR, Wall J, Cornejo OE, Moreno-Mayar JV, Korneliussen TS, Pierre T, Rasmussen M, Campos PF, Damgaard PB, Allentoft ME, Lindo J, Metspalu E, Rodríguez-Varela R, Mansilla J, Henrickson C, Seguin-Orlando A, Malmström H, Stafford T Jr, Shringarpure SS, Moreno-Estrada A, Karmin M, Tambets K, Bergström A, Xue Y, Warmuth V, Friend AD, Singarayer J, Valdes P, Balloux F, Leboreiro I, Vera JL, Rangel-Villalobos H, Pettener D, Luiselli D, Davis LG, Heyer E, Zollikofer CP, Ponce de León MS, Smith CI, Grimes V, Pike KA, Deal M, Fuller BT, Arriaza B, Standen V, Luz MF, Ricaut F, Guidon N, Osipova L, Voevoda MI, Posukh OL, Balanovsky O, Lavryashina M, Bogunov Y, Khusnutdinova E, Gubina M, Balanovska E, Fedorova S, Litvinov S, Malyarchuk B, Derenko M, Mosher MJ, Archer D, Cybulski J, Petzelt B, Mitchell J, Worl R, Norman PJ, Parham P, Kemp BM, Kivisild T, Tyler-Smith C, Sandhu MS, Crawford M, Villemans R, Smith DG, Waters MR, Goebel T, Johnson JR, **Malhi RS**, Jakobsson M, Meltzer DJ, Manica A, Durbin R, Bustamante CD, Song YS, Nielsen R, Willerslev E. Genomic evidence for the Pleistocene and recent population history of Native Americans. **Science** 349(6250): aab3884.

2015 Rasmussen M, Sikora M, Albrechtsen A, Komeliussen TS, Moreno-Mayar JV, Poznik GD, Zollikofer CP, Ponce de Leon MS, Allentoft ME, Moltke I, Jonsson H, Valdiosera C, **Malhi RS**, Orlando L, Bustamante CD, Stafford TW Jr, Meltzer DJ, Nielsen R, Willerslev E. The ancestry and affiliations of Kennewick Man. **Nature** 523(7561): 455-8.

2015 Witt KE, Judd K, Kitchen A, Grier C, Kohler TA, Ortman SG, Kemp BM, **Malhi RS**. DNA analysis of ancient dogs of the Americas: Identifying possible founding haplotypes and reconstructing population histories. **Journal of Human Evolution** 79: 105-18.

2015 Kistler L, Ratan A, Godfrey LR, Crowley BE, Hughes CE, Lei R, Cui Y, Wood ML, Muldoon KM, Andriamialison H, McGraw JJ, Tomsho LP, Schuster SC, Miller W, Louis EE, Yoder AD, **Malhi RS**, Perry GH. Comparative and population mitogenomic analyses of Madagascar's extinct, giant 'subfossil' lemurs. **Journal of Human Evolution** 79: 45-54.

2014 **Malhi RS**, Kemp BM. Providing a venue for influential research in anthropological genomics. Introduction. **Human Biology** 86(1): 5-6.

2014 Shattuck MR, Satkoski-Trask J, Deinard A, Tito RY, Smith DG, Melnick DJ, **Malhi RS**. Patterns of genetic variation and the role of selection in HTR1A and HTR1B in macaques (*Macaca*). **BMC Genetics** 15(1): 116.

2014 Mallot EK, **Malhi RS**, Garber PA. High-throughput sequencing of fecal DNA to identify insects consumed by wild Weddell's saddleback tamarins (*Saguinus weddelli*, Cebidae, Primates) in Bolivia. **American Journal of Physical Anthropology** 156: 474-81.

2014 Verdu P, Pemberton TJ, Laurent R, Kemp BM, Gonzalez-Oliver A, Gorodezky C, Hughes CE, Shattuck MR, Petzelt B, Mitchell J, Harry H, William T, Worl R, Cybulski JS, Rosenberg NA, **Malhi RS**. Patterns of admixture and population structure in native populations of northwest North America. **PLoS Genetics** 10(8): e1004530.

2014 Kennet DJ, Asmerom Y, Kemp BM, Polyak V, Bolnick DA, **Malhi RS**, Culleton BJ. Early Americans: misstated results. **Science** 345(6195): 390.

2014 Chatters JC, Kennett DJ, Asmerom Y, Kemp BM, Polyak V, Blank AN, Beddows PA, Reinhardt E, Arroyo-Cabrales J, Bolnick DA, **Malhi RS**, Culleton B, Erreguerena PL, Rissolo D, Morell-Hart S, Stafford TW. Late Pleistocene human skeleton and mtDNA from Mexico links Paleoamericans and modern Native Americans. **Science** 344(6185): 750-754.

2014 Shattuck MR, Satkoski-Trask J, Deinard A, Tito RY, Smith DG, **Malhi RS**. The evolutionary history of SLC6A4 and the role of plasticity in macaca. **American Journal of Physical Anthropology** 153: 605-616.

2014 Rasmussen M, Anzick SL, Waters MR, Skoglund P, DeGiorgio M, Stafford TW, Rasmussen S, Moltke I, Albrechtsen A, Doyle SM, Poznik GD, Gudmundsdottir V, Yadav, Malaspinas S, White SS, Allentoft ME, Cornejo OE, Tamberts K, Eriksson A, Heintzman PD, Karmin M, Korneliussen TS, Meltzer DJ, Pierre TL, Stenderup J, Saag L, Warmuth VM, Lopes MC, **Malhi RS**, Brunak S, Sicheritz-Ponten T, Barnes I, Collins M, Orlando L, Balloux F, Manica A, Gupta R, Metspaul M, Bustamante CD, Jakobsson M, Nielsen R, Willerslev E. The genome of a Late Pleistocene human from a Clovis burial site in western Montana. **Nature** 506: 225-229.

2013 Achilli A, Perego UA, Lancioni H, Olivieri A, Gandini F, Hooshiar Kashani B, Battaglia V, Grugni V, Angerhofer N, Rogers MP, Herrera RJ, Woodward SR, Labuda D, Smith DG, Cybulski JS, Semino O, **Malhi RS**, Torroni A. Reconciling migration models to the Americas with the variation of North American native mitogenomes. **Proc Natl Acad Sci U S A**. 2013 Aug 27;110(35):14308-13.

2013 Cui Y, Lindo J, Hughes CE, Johnson JW, Hernandez AG, Kemp BM, Ma J, Cunningham R, Petzelt B, Mitchell J, Archer D, Cybulski JS, **Malhi RS**. Ancient DNA analysis of Mid-Holocene individuals from the Northwest Coast of North America reveals different evolutionary paths for mitogenomes. **PLoS ONE** 8(7): e66948

2012 **Malhi RS**. Genetics of Southern Athapaskans. From the Land of Ever Winter to the American Southwest. **University of Utah Press**.

- 2012 Yan C, Shattuck MR, Thimmapuram J, Vullaganti D, **Malhi RS**. Developing SNPs and STR DNA markers for snub-nosed monkeys (*Rhinopithecus roxellana*) using next-generation sequencing technology. **Conservation Genetics Resources** 4: 451-453.
- 2011 Schroeder KB, Villa Jr G, **Malhi RS**, Rode AR, Smith DG. Biological Continuity in the Central Valley: Evidence from Ancient and Modern Mitochondrial DNA. **Journal of California and Great Basin Anthropology** 31(1): 37-56.
- 2011 Trask JS, Garnica WT, Kanthaswamy S, **Malhi RS**, Smith DG. 4040 SNPs for genomic analysis in the rhesus macaque (*Macaca mulatta*). **Genomics** 98(5): 352-8.
- 2011 Wilson BJ, Crockford SJ, Johnson JW, **Malhi RS**, Kemp BM. Genetic and archaeological evidence for a former breeding population of Aleutian Cackling Goose (*Branta hutchinsii leucopareia*) on Adak Island, central Aleutians, Alaska. **Canadian Journal of Zoology** 89(8): 732-743.
- 2011 Satkoski Trask J, Garnica WT, **Malhi RS**, Kanthaswamy S, Smith DG. High-throughput single-nucleotide polymorphism discovery and the search for candidate genes for long-term SIVmac nonprogression in Chinese rhesus macaques (*Macaca mulatta*). **Journal of Medical Primatology** 40(4): 224-32.
- 2011 **Malhi RS**, Trask JS, Shattuck M, Johnson J, Chakraborty D, Kanthaswamy S, Ramakrishnan U, Smith DG. Genotyping single nucleotide polymorphisms (SNPs) across species in Old World Monkeys. **American Journal of Primatology** 73(10):1031-40
- 2011 Trask JA, **Malhi RS**, Kanthaswamy S, Johnson J, Garnica WT, Malladi VS, Smith DG. The effect of SNP discovery method and sample size on estimation of population genetic data for Chinese and Indian rhesus macaques (*Macaca mulatta*). **Primates** 52(2): 129-38.
- 2010 Kemp BM, Gonzalez-Oliver A, **Malhi RS**, Monroe C, Schroeder KB, McDonough J, Rhett G, Resendez A, Pealoza-Espinosa RI, Buentello-Malo L, Gorodesky C, Smith DG. Evaluating the Farming/Language Dispersal Hypothesis with genetic variation exhibited by populations in the Southwest and Mesoamerica. **Proc Natl Acad Sci U.S.A.** 107:6759-64.
- 2010 **Malhi RS**, Cybulski JS, Tito RY, Johnson J, Harry H, Dan C. Brief communication: mitochondrial haplotype C4c confirmed as a founding genome in the Americas. **American Journal of Physical Anthropology** 141: 494-7.
- 2010 Luetkemeier ES, Sodhi M, Schook LB, **Malhi RS**. Multiple Asian pig origins revealed through genomic analyses. **Molecular Phylogenetics and Evolution** 54: 680-6.
- 2009 **Malhi RS**, Schroeder KB, Kemp BM. Uses and limitations of genetic data relating to Athapaskan migrations: a reply to Seymour. **American Journal of Physical Anthropology** 140: 203-4.

- 2009 Schroeder KB, Jakobsson M, Crawford MH, Schurr TG, Boca SM, Conrad DF, Tito RY, Osipova LP, Taraskaia LA, Zhadanov SI, Wall JD, Pritchard JK, **Malhi RS**, Smith DG, Rosenberg NA. Haplotypic background of a private allele at high frequency in the Americas. **Molecular Biology and Evolution** 26: 995-1016.
- 2009 **Malhi RS**. Implications of the Genographic Project for Molecular Anthropologists. **International Journal of Cultural Property** 16: 193-194.
- 2009 Luetkemeier ES, **Malhi RS**, Beever JE, Schook LB. Diversification of porcine MHC class II genes: evidence for selective advantage. **Immunogenetics** 61: 119-29.
- 2008 **Malhi RS**, Gonzalez-Oliver A, Schroeder KB, Kemp BM, Greenberg JA, Dobrowski SZ, Smith DG, Resendez A, Karafet T, Hammer M, Zegura S, Brovko T. Distribution of Y chromosomes among native North Americans: a study of Athapaskan population history. **American Journal of Physical Anthropology** 137: 412-24.
- 2008 Satkoski JA, **Malhi RS**, Kanthaswamy S, Tito R, Malladi V, Smith DG. Pyrosequencing as a method for SNP identification in the rhesus macaque (*Macaca mulatta*). **BMC Genomics** 9: 256.
- 2007 **Malhi RS**. Book Review: The First Americans Race, Evolution, and the Origins of Native Americans. **American Journal of Physical Anthropology** 135: 492-493.
- 2007 Cybulski JS, McMillan AD, **Malhi RS**, Kemp BM, Harry H, Cousins S. The Big Bar Lake Burial: Middle Period Human Remains from the Canadian Plateau. **Canadian Journal of Archaeology** 31: 55-78.
- 2007 Tamm E, Kivisild T, Reidla M, Metspalu M, Smith DG, Mulligan CJ, Bravi CM, Rickards O, Martinez-Labarga C, Khusnutdinova EK, Fedorova SA, Golubenko MV, Stepanov VA, Gubina MA, Zhanadov SL, Ossipova LP, Damba L, Voevoda MI, Dipierra JE, Villemans R, **Malhi RS**. Beringian Standstill and spread of Native American founders. **PLoS ONE** 2: e829.
- 2007 **Malhi RS**, Sickler B, Lin D, Satkoski J, Tito RY, George D, Kanthaswamy S, Smith DG. MamuSNP: a resource for Rhesus Macaque (*Macaca mulatta*) genomics. **PLoS ONE** 2: e438.
- 2007 Kemp BM, **Malhi RS**, McDonough J, Bolnick DA, Eshleman JA, Rickards O, Martinez-Labarga C, Johnson JR, Lorenz JG, Dixon J, Fifield TE, Heaton T, Worl R, and Smith DG. Timing of the peopling of the Americas: genetic analysis of an early Holocene skeleton. **American Journal of Physical Anthropology** 132: 605-621.
- 2007 **Malhi RS**, Kemp BM, Eshleman JA, Cybulski J, Smith DG, Cousins S, Harry H. Haplogroup M Discovered in Prehistoric North America. **Journal of Archaeological Science** 34: 642-648.

2006 **Malhi RS**, Rhett G, Bell AM. Mitochondrial DNA evidence of an early Holocene population expansion of threespine sticklebacks from Scotland. **Molecular Phylogenetics and Evolution** 40: 148-154.

2006 Schroeder KB, **Malhi RS**, Smith DG. Opinion: Native American Participation in Genetic Research. **Evolutionary Anthropology** 13(3) 88-92.

2005 **Malhi RS** and Schilling AJ. Discovering your Native American heritage using genetic ancestry testing. **New Mexico Genealogist**. December 2005.

2005 Smith DG, **Malhi RS**, Eshleman JA, Kaestle FA, Kemp BM. Mitochondrial DNA Haplogroups of Paleoamericans in North America. *Paleoamerican Origins: Beyond Clovis*. **Texas A&M University Press**.

2005 Kemp BM, Resendez A, Berrelleza JAR, **Malhi RS**, and Smith DG. An analysis of ancient Aztec mtDNA from Tlatelolco: Pre-Columbian relations and the spread of Uto-Aztecan. *Biomolecular Archaeology: Genetic Approaches to the Past*. **Carbondale University Press**.

2005 **Malhi RS**, Van Tuinen M, Mountain J, Hadley L. Pilot project: Catalhoyuk ancient DNA project. *Catalhoyuk Research Project 4*, McDonald Institute for Archaeological Research 2005. **British Institute at Ankara Monograph** 38.

2004 Eshleman JA, **Malhi RS**, Johnson JR, Kaestle FA, Lorenz JG, and Smith DG. Mitochondrial DNA and prehistoric settlements: Native migrations on the Western edge of North America. **Human Biology** 76: 55-75.

2004 **Malhi RS**, Breece KE, Shook BAS, Kaestle FA, Chatters JC, Hackenberger S, and Smith DG. Patterns of mtDNA diversity in Northwestern North America. **Human Biology** 76: 33-54.

2003 Eshleman JA, **Malhi RS**, and Smith DG. Mitochondrial DNA studies of Native Americans: Conceptions and misconceptions of the population prehistory of the Americas. **Evolutionary Anthropology** 12: 7-18.

2003 **Malhi RS**, Mortensen HM, Eshleman JA, Lorenz JG, Kaestle FA, Johnson JR, Gorodesky C, and Smith DG. Native American mtDNA prehistory in the American Southwest. **American Journal of Physical Anthropology** 120: 108-124.

2002 **Malhi RS**, Smith DG. Brief Communication: Haplogroup X confirmed in Prehistoric North America. **American Journal of Physical Anthropology** 119: 84-88.

2002 **Malhi RS**, Eshleman JA, Greenberg JA, Weiss DA, Schultz BA, Kemp BM, Kaestle FA, Lorenz JG, Johnson JR, and Smith DG. The structure and diversity within

New World mtDNA haplogroups: Implications for the prehistory of North America. **American Journal of Human Genetics** 70: 905-919.

2002 Smith DG, **Malhi RS**, Eshleman JA, and Kaestle FA. Mitochondrial DNA haplogroups of Paleoamericans in North America. In Bonnichsen R, Gruhn R, Steele DG, Stanford D, Lepper B, and Warren CN, (eds.) *Beyond Clovis: Where We Have Been, Where We Are, and Where We Are Going*. College Station, TX: **Texas A&M University Press**.

2002 Smith DG, Rolfs BK, Kaestle FA, **Malhi RS**, and Doran GH. Serum albumin phenotypes and a preliminary study of the mtDNA haplogroups of the prehistoric population of Windover. In: G.H. Doran (ed.) *Multidisciplinary Investigations at Windover*. **University of Florida Press**.

2001 **Malhi RS**, Schultz BA, and Smith DG. Distribution of mitochondrial DNA lineages among Native American tribes of Northeastern North America. **Human Biology** 73 23-51.

2000 Smith DG, Lorenz JG, Rolfs BK, Bettinger RL, Green B, Eshleman JA, Schultz BA, and **Malhi RS**. Implications of the distribution of Albumin Naskapi and Albumin Mexico for New World Prehistory. **American Journal of Physical Anthropology** 111: 557-572.

1999 Smith DG, **Malhi RS**, Eshleman JA, Lorenz JG, and Kaestle FA. Disribution of mtDNA Haplogroup X among Native North Americans. **American Journal of Physical Anthropology** 110: 271-284.

1997 Bettinger RL, **Malhi RS**, and McCarthy H. Central place models of acorn and mussel processing. **Journal of Archaeological Science** 24: 887-899.

## Grants

2018-2023 **Large-Scale Applied Research Project Genome Canada**. Silent Genomes: Reducing health care disparities and improving diagnostic success for children with genetic diseases from Indigenous populations. **Co-applicant**. \$5,000,000.

2017-2018 **National Science Foundation**. Doctoral Dissertation Research: DNA Methylation in Relationships to Pubertal Timing and Adult Reproductive Hormonal Concentrations in Polish and Polish American Women. **Co-Principal Investigator** to Mary Rogers. \$31,712.

2017-2019 **National Science Foundation**. Doctoral Dissertation Research: An integrative approach to investigating human diet and the oral microbiome in ancient and

living Pacific Northwest Coast indigenous communities. **Principal Investigator** to Co-Principal Investigator Alyssa Bader. \$31,701.

2016-2019 **National Institutes of Health-National Human Genome Research Institute**. Expanding the impact of the Summer Internship for Native Americans in Genomics (SING) short course. **Principal Investigator**. \$125,518.

2016-2021 **IBSS National Science Foundation**. Epigenomic Effects of European Colonization on Alaskan Natives. **Principal Investigator**. \$860,000.

2016-2017 **Wenner-Gren Foundation**. Using Ancient Dog DNA to test Models of Human Migration. **Principal Investigator** to Co-Principal Investigator Kelsey Witt. \$19,352.

2015-2017 **National Science Foundation**. Doctoral Dissertation Research: Human population inferences via canine genetics. **Principal Investigator** to Co-Principal Investigator Kelsey Witt. \$31,491.

2015-2019 **National Science Foundation**. Collaborative Research: Using paleogenomic data to decipher genomic effects of European Colonization on indigenous North Americans. **Principal Investigator**. \$165,000.

2015-2018 **National Science Foundation**. AAPA IDEAS Program: Increasing Diversity in Evolutionary Anthropological Sciences. **Co-Principal Investigator**. \$159,000.

2014-2016 **University of Illinois Research Board**. Identifying DNA methylation patterns in ancient individuals as potential indicators of stress. **Principal Investigator**. \$20,000.

2014-2016 **National Science Foundation**. Doctoral Dissertation Research: Identifying Adaptations to Pathogens and the Environments of the Americas via Native American Paleogenomic Diversity. **Principal Investigator** to Co-Principal Investigator John Lindo. \$31,215.

2013-2016 **National Institutes of Health - National Human Genome Research Institute**. Guiding indigenous students in next-generation genomic studies with the Summer Internship for Native Americans in Genomics (SING) Short Course. **Principal Investigator**. \$107,025.

2012-2015 **Interdisciplinary Innovation Initiative Program – Office of the Vice Chancellor for Research at University of Illinois**. Uses and Limitations of Genomic Research in Forensic Science. **Principal Investigator**. \$181,740.

2010-2013 **National Science Foundation**. Collaborative Research: Anthropological-Genomic Effects of European Colonization on Native North Americans. **Principal Investigator**. \$165,681.

2010-2011 **University of Illinois Research Board**. Analysis of Mitochondrial Genomes of Early Holocene Skeletal Remains of North America. **Principal Investigator**. \$25,000.

2009-2011 **National Science Foundation**. Doctoral Dissertation Improvement Grant: The Molecular Evolution of the Serotonin System in Rhesus Macaques. Principal Investigator. **Principal Investigator** to Co-Principal Investigator Milena Shattuck. \$13,977.

2009-2010 **University of Illinois Research Board**. Genetic Identity of Prehistoric Remains from British Columbia. **Principal Investigator**. \$19,000.

2008-2010 **National Science Foundation**. Mitochondrial Genome Diversity in the North American Subarctic. **Principal Investigator**. \$83,735.

2007-2010 **United States Department of Agriculture**. High Density SNP discovery validation and characterization in swine. **Co-Principal Investigator**. \$999,978.

2004-2007 **National Science Foundation**. Genetic Diversity in the American Southwest and Mesoamerica. **Principal Investigator**. \$139,000.

2000-2001 **Wenner-Gren Dissertation Fieldwork Grant**. Investigating prehistoric population movements in North America using ancient and modern mtDNA. **Co-Principal Investigator**. \$13,000.

2000-2001 **National Science Foundation**. Dissertation Improvement Grant: Investigating prehistoric population movements in North America using ancient and modern mtDNA. **Co-Principal Investigator**. \$11,220.

### Courses Taught

*Human Origins and Culture* (ANTH 102 – developed and taught)

*Human Variation and Race* (ANTH 241 – developed and taught)

*Forensic Science* (ANTH 246 – created, developed and taught, including online)

*Forensic Science DNA Laboratory* (ANTH 247 – co-created and co-taught)

*Human Evolutionary Genetics* (ANTH 441 - developed and taught)

*Paleogenomics* (ANTH 499 – created, developed and taught)

*Genes, Language & Culture Seminar* (ANTH 499 – created, developed and taught)

*Biological Ethics in the Genomics Age* (ANTH 399 –co-created and co-taught)

### Honors and Awards

2006 National Academy of Sciences Frontiers of Science Fellow

2010 Arnold Beckman Award

2010 Center for Advanced Studies Fellow

2018 Richard and Margaret Romano Professorial Scholar

### Science Communication

My work has received coverage or I've been invited to comment of other's research in (incomplete list): *The Signal*, *The San Diego Union-Tribune*, *New Scientist*, *The Scientist*, *The News-Gazette*, *American Archaeology Magazine*, *Science Daily*, *NPR – All Things Considered*, *Mammoth Trumpet*, *Science Now*, *German Public Radio*, *The Associated Press*, *The Los Angeles Times*, *Toronto Star*, *WAMC Academic Minute*, *The New York Times*, *Le Monde*, and *The Vancouver Sun*, *Science*.

### **Invited Talks (Past 8 years)**

- 2018 Sealaska Heritage Institute, Juneau
- 2018 Dartmouth College
- 2018 Western-Stemmed Workshop, Victoria, Canada (invited for April 2018)
- 2017 Field Museum, Chicago
- 2017 Santa Barbara Museum of National History
- 2017 Migration Conference, Mexico City
- 2016 Wanapum Heritage Center, Washington
- 2016 Beringian “Standstill” Workshop, University of Colorado, Boulder.
- 2015 DNA and Indigeneity Workshop, Simon Fraser University, British Columbia.
- 2015 Advanced Judicial Academy: Science in the Courtroom, University of Illinois, Urbana.
- 2015 American Association of Anthropological Genetics Education Workshop, St. Louis.
- 2015 Thinking anthropologically about genetics, American Association of Physical Anthropology. St. Louis.
- 2014 DNA Bootcamp, Cook County Public Defender Office, Chicago.
- 2014 Genomics for Prosecutors, University of Illinois, Urbana.
- 2014 Santa Barbara Symposium on Human Origins II, Santa Barbara Museum of Natural History.
- 2014 NSF and AAPA Committee on Diversity, Developing Effective Broader Impact Plans.
- 2013 Royal Society Meeting. Three Decades of Ancient DNA, London.
- 2013 Genomics for Judges, University of Illinois, Urbana.
- 2013 Department of Anthropology, University of British Columbia, Okanagan.
- 2012 Department of Anthropology, Pennsylvania State University, State College.
- 2011 Department of Archaeology, Simon Fraser University, Vancouver.
- 2010 Department of Anthropology, Emory University, Atlanta.
- 2010 American Quaternary Association, Laramie.
- 2010 Centre for GeoGenetics, University of Copenhagen, Denmark.
- 2010 Anthropological Genetics in the Genomic Era: Challenges, Opportunities & Directions, American Association of Physical Anthropology Meetings, Albuquerque.
- 2010 Department of Anthropology, University of California, Davis.
- 2010 Center for Society and Genetics, University of California, Los Angeles.
- 2010 Migration International Conference, University of Kansas, Lawrence.
- 2010 American Historical Association, San Diego, CA.

### **External Service**

Granting agencies. National Science Foundation (Panel, Archaeology, Biological Anthropology), National Institutes of Health (Panel, BD2K special emphasis, Native American Health Prevention special emphasis, Native American Research Center for Health), M.J. Murdoch Charitable Trust, Mardsen Fund, Canadian Social Science and Humanities Research Council, Israeli Science Foundation, European Science Council.  
Article reviewer. Nature, Nature Communications, Science, Science Advances, Journal of Human Evolution, PLoS ONE, Mitochondrion, American Journal of Primatology, Animal Biotechnology, Animal Genetics, Frontiers in Ecology and Evolution, Proceedings of the National Academy of Science USA, Annals of Human Biology, Current Anthropology, American Anthropologist, South African Journal of Science, Annals of Human Genetics, Molecular Biology and Evolution, Human Biology, Journal of Archaeological Science, American Journal of Physical Anthropology, PLOS Genetics. Current Biology, Journal of Archaeological Research.

### **Professional Affiliations**

American Association of Physical Anthropology  
American Society of Human Genetics  
Society of American Archaeology  
American Association of Anthropological Genetics