学位論文（要約）

Genetic structure of indigenous Mesoamerican populations revealed by mitochondrial genome and analysis of ancient genome by next-generation sequencing

（ミトコンドリアゲノムから明らかになった メソアメリカ現生人類集団の遺伝構造ならびに 次世代シーケンサによる古人骨ゲノム分析法構築と解析)

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Abstract

Mesoamerica has played an important role in the expansion of Paleoamericans by providing a route to South America. The aims of this study were to examine the peopling of Mesoamerica, to facilitate reconstruction of the ancient dispersal of indigenous people through Mesoamerica from North to South America, and to develop a new approach essential for the explore ancient populations genetic data by next-generation sequencing (NGS).

In Chapter 1, I present the complete mitochondrial genome (mitogenome) sequences of 113 unrelated individuals from two indigenous populations of Mesoamerica, Mazahua and Zapotec. All newly sequenced mitogenomes were classified into haplogroups A2, B2, C1, and D1, but one sequence in Mazahua was classified as D4h3a, a subclade of haplogroup D4. This haplogroup has been mostly found along the Pacific coast of South America. Haplogroup X2a was not found in either of the populations. Genetic similarity determined by phylogenetic tree construction and principal component analysis showed that these two populations are distantly related to each other. Actually, the Mazahua and Zapotec shared no sequences (haplotypes) in common, while each also showed a number of unique subclades. Surprisingly, the Zapotec formed a cluster with indigenous populations living in an area from central Mesoamerica to Central America. By contrast, the Mazahua formed a cluster with indigenous populations living in external areas, including northern Mesoamerica, southwestern North America, and South America. This intriguing genetic relationship suggests the presence of two paleo-Mesoamerican groups, invoking a scenario in which one group had expanded into South America and the other resided in Mesoamerica. The availability of population-based complete mitogenome sequences from other indigenous people should greatly refine the evolutionary scenario concerning the population history of Mesoamerica hypothesized here.

Population-based ancient genome information enables us to reveal the details of the dual structure of Mesoamerican populations. Ancient mitogenomic analysis provides direct evidence of what happened in our past, such as dispersal, migration, and demography, and the relationships among populations, including admixture.

In Chapter 2, I describe a method that makes it feasible to obtain reliable high-throughput sequencing data for the target of interest from ancient material in an efficient and cost-effective manner, thus broadly relishing the benefits of NGS in the field of ancient DNA research. Because of the difficulties of deep sequencing, high-throughput sequencing of ancient DNA has been limited to exceptionally well-preserved ancient materials. The primary factor is the microbial attack often observed in buried material, which causes a marked increase in the relative ratio of microbial DNA in the extracted DNA. I present a unified strategy in which emulsion PCR is coupled with target enrichment followed by NGS. This method made it possible to efficiently obtain non-duplicated reads mapped to target sequences of interest, and this can provide deep, reliable sequencing of ancient DNA from typical materials, even if they are poorly preserved.

In Chapter 3, I describe a composite approach to the deduction of complete mitogenome sequences of ancient humans from low-depth data. I analyzed a mitochondrial genome of a sacrifice at the Moon Pyramid at Teotihuacan by applying this technique. The state of DNA preservation was extremely poor, as expected from a previous study using a conventional PCR method. I covered 89.3% of the entire mitochondrial genome by unique mapped reads; however, it was difficult to get sufficient depth by NGS. I estimated that the sacrifice belongs to haplogroup A2, one of the major haplogroups in indigenous Americans. Furthermore, I attempted a method to supplement the genome sequence by imputation based on a k-nearest neighbor (KNN) algorithm if reads were chipped off. I found that it was valid that imputation using the same haplogroup sequences because the combination of SNPs was similar in each haplogroup of mtDNA. Although this method

has the shortcoming that singletons and high-frequency polymorphic sites cannot be rescued, it can be useful in obtaining entire sequences of ancient mitogenomes for population-based analysis. I obtained a whole mitogenome sequence by rescuing 3930 bases except for one site (np 153) that was polymorphic in haplogroup A2. The availability of population-based ancient genome information enables us to reveal the details of the haplotype diversity of sacrifices. Thus, I might expect the sphere of Teotihuacan influence through the genetic origins of individuals offered as sacrifices.

In addition to modern genomic information, spatiotemporal genetic information obtained from archaeological remains makes it possible to pursue human population history chronologically. I conclude that the composite approach may be useful in obtaining entire sequences of ancient mitogenomes efficiently and reliably, even if obtaining sufficient sequence data by NGS is difficult. This approach may be useful in the analysis of population-based ancient genomes when the state of DNA preservation is extremely poor.

Contents

Chapter 2:

Emulsion PCR-coupled target enrichment: An effective fishing method for high-throughput sequencing of poorly preserved ancient DNA

Chapter 3:

A composite approach to deduce complete mitogenome sequence from low depth data: Application to a sacrifice of the Moon pyramid at Teotihuacan

インターネット公表に関する共著者全員の同意が得られていないため、本文については非公開。

References

Achilli, A., Perego, U.A., Bravi, C.M., Coble, M.D., Kong, Q.P., Woodward, S.R. Salas, A, Torroni, A, Bandelt, H.J. 2008. The phylogeny of the four pan-American MtDNA haplogroups: implications for evolutionary and disease studies. PLoS One. 3, e1764.

Adler, C.J., Haak, W., Donlon, D., Cooper, A., The Genegraphic Consortium. 2011. Survival and recovery of DNA from ancient teeth and bones. J. Archaeol. Sci. 38, 956-964

Allentoft, M.E., Collins, M., Harker, D., Haile, J., Oskam, C.L., Hale, M.L., Campos, P.F., Samaniego, J.A., Gilbert, M.T., Willerslev, E., Zhang, G., Scofield, R.P., Holdaway, R.N., Bunce, M. 2013. The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. Proc. Biol. Sci. 279, 4724-4733.

Anderson, S., Bankier, A.T., Barrell, B.G., de Bruijn, M.H., Coulson, A.R., Drouin, J., Eperon, I.C., Nierlich, D.P., Roe, B.A., Sanger, F., Schreier, P.H., Smith, A.J., Staden, R., Young, I.G. 1981. Sequence and organization of the human mitochondrial genome. Nature. 290, 457-65.

Anderung, C., Persson, P., Bouwman, A., Elburg, R., Götherström, A. 2008. Fishing for ancient DNA. Forensic Sci. Int. Genetics. 2, 104-107.

Andrews, R.M., Kubacka, I., Chinnery, P.F., Lightowlers, R.N., Turnbull, D.M., Howell, N. 1999. Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA. Nat. Genet. 23, 147.

Ávila-Arcos, M.C., Cappellini, E., Romero-Navarro, J.A., Wales, N., Moreno-Mayar, J.V., Rasmussen, M., Fordyce, S.L., Montiel, R., Vielle-Calzada, J-P., Willerslev, E., Gilberta, M.T.P. 2011. Application and comparison of large-scale solution-based DNA capture enrichment methods on ancient DNA. Sci. Rep. 1, 74.

Baeta, M., Núñez, C., Sosa, C., Bolea, M., Casalod, Y., González-Andrade, F. Roewer, L, Martínez-Jarreta, B. 2012. Mitochondrial diversity in Amerindian Kichwa and Mestizo populations from Ecuador. Int. J. Legal. Med. 126, 299-302.

Bandelt, H.J., Herrnstadt, C., Yao, Y.G., Kong, Q.P., Kivisild, T., Rengo, C., Scozzari, R., Richards, M., Villems, R., Macaulay, V., Howell, N., Torroni, A., Zhang, Y.P. 2003. Identification of Native American founder mtDNAs through the analysis of complete mtDNA sequences: some caveats, Ann. Hum. Genet. 67, 512-524.

Bandelt, H.J., Forster, P., and Röhl, A. 1999. Median-joining networks for inferring intraspecific phylogenies. M. B. E. 16, 37-48.

Batista, O., Kolman, C.J., Bermingham, E. 1995. Mitochondrial DNA diversity in the Kuna Amerinds of Panamá. Hum. Mol. Genet. 4, 921-929.

Beals, R.L. 1974. Cultural relations between Northern Mexico and the Southwest United States: Ethnologically and archaeologically, The Mesoamerican Southwest: Readings in Archaeology Ethnohistory and Ethnology (eds Hedrick BC Kelley JC Riley CL.) 52-57 (Southern Illinois University Press Carbondale IL).

Behar, D.M., van Oven, M., Rosset, S., Metspalu, M., Loogväli, E.L., Silva, N.M. Kivisild, T., Torroni, A., Villems, R. 2012. A "Copernican" reassessment of the human mitochondrial DNA tree from its root. Am. J. Hum. Genet. 90, 675-684.

Bodner, M., Perego, U.A., Huber, G., Fendt, L., Röck, A.W., Zimmermann, B., Olivieri, A., Gómez-Carballa, A., Lancioni, H., Angerhofer, N., Bobillo, M.C., Corach, D., Woodward, S.R., Salas, A., Achilli, A., Torroni, A., Bandelt, H.J., Parson, W. 2012. Rapid coastal spread of First Americans: novel insights from South America's Southern Cone mitochondrial genomes. Genome Res. 22, 811-820.

Brandt, G., Haak, W., Adler, C.J., Roth, C., Szécsényi-Nagy, A., Karimnia, S., Möller-Rieker, S., Meller, H., Ganslmeier, R., Friederich, S., Dresely, V., Nicklisch, N., Pickrell, J.K., Sirocko, F., Reich, D., Cooper, A., Alt, K.W., Der Sarkissian, C., Adhikarla, S., Prasad, A.K., Pitchappan, R., Santhakumari, A.V., Balanovska, E., Balanovsky, O., Bertranpetit, J., Comas, D., Martínez-Cruz, B., Melé, M., Clarke, A.C., Matisoo-Smith, E.A., Dulik, M.C., Gaieski, J.B., Owings, A.C., Schurr, T.G., Vilar, M.G., Hobbs, A., Soodyall, H., Javed, A., Parida, L., Platt, D.E., Royyuru, A.K., Jin, L., Li, S., Kaplan, M.E., Merchant, N.C., Mitchell, R.J., Quintana-Murci, L., Renfrew, C., Lacerda, D.R., Santos, F.R., Hernanz, D.F., Wells, S., Swamikrishnan, P., Tyler-Smith, C., Vieira,

P.P., Ziegle, J.S. 2013. Ancient DNA reveals key stages in the formation of central European mitochondrial genetic diversity. Science. 342, 257-61.

Briggs, A.W., Good, J.M., Green, R.E., Krause, J., Maricic, T., Stenzel, U., Lalueza-Fox, C., Rudan, P., Brajkovic, D., Kucan, Z., Gusic, I., Schmitz, R., Doronichev, V.B., Golovanova, L.V., de la Rasilla, M., Fortea, J., Rosas, A., Pääbo, S. 2009. Targeted retrieval and analysis of five Neandertal mtDNA genomes. Science. 325, 318-321.

Briggs, A.W., Stenzel, U., Johnson, P.L., Green, R.E., Kelso, J., Prufer, K., Meyer, M., Krause, J., Ronan, M.T., Lachmann, M., Pääbo, S. 2007. Patterns of damage in genomic DNA sequences from a Neandertal. Proc. Natl. Acad. Sci. USA. 104, 14616-14621.

Brotherton, P., Haak, W., Templeton, J., Brandt, G., Soubrier, J., Jane Adler, C. Richards, S.M., Sarkissian, C.D., Ganslmeier, R., Friederich, S., Dresely, V., van Oven, M., Kenyon, R., Van der Hoek, M.B., Korlach, J., Luong, K., Ho, S.Y., Quintana-Murci, L., Behar, D.M., Meller, H., Alt, K.W., Cooper, A., Adhikarla, S., Ganesh Prasad, A.K., Pitchappan, R., Varatharajan Santhakumari, A., Balanovska, E., Balanovsky, O., Bertranpetit, J., Comas, D., Martínez-Cruz, B., Melé, M., Clarke, A.C., Matisoo-Smith, E.A., Dulik, M.C., Gaieski, J.B., Owings, A.C., Schurr, T.G., Vilar, M.G., Hobbs, A., Soodyall, H., Javed, A., Parida, L., Platt, D.E., Royyuru, A.K., Jin, L., Li, S., Kaplan, M.E., Merchant, N.C., John Mitchell, R., Renfrew, C., Lacerda, D.R., Santos, F.R., Soria Hernanz, D.F., Spencer Wells, R., Swamikrishnan, P. 2013. Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans. Nat. Commun. 4, 1764.

Brown, M.D., Hosseini, S.H., Torroni, A., Bandelt, H.J., Allen, J.C., Schurr, T.G., Scozzari, R., Cruciani, F., Wallace, D.C. 1998. mtDNA haplogroup X: An ancient link between Europe/Western Asia and North America? Am. J. Hum. Genet. 63, 1852-1861.

Brown, W.M., George, M., Wilson, A.C. 1979. Rapid evolution of animal mitochondrial DNA. Pro.c Nat.l Acad. Sci. U S A. 76, 1967-1971.

Bryant, D. and Moulton, V. 2004. Neighbor-net: an agglomerative method for the

construction of phylogenetic networks. Mol. Biol. Evol. 21, 255–265.

Burbano, H.A., Hodges, E., Green, R.E., Briggs, A.W., Krause, J., Meyer, M., Good, J.M., Maricic, T., Johnson, P.L., Xuan, Z., Rooks, M., Bhattacharjee, A., Brizuela, L., Albert, F.W., de la Rasilla, M., Fortea, J., Rosas, A., Lachmann, M., Hannon, G.J., Pääbo, S. 2010. Targeted investigation of the Neandertal genome by array-based sequence capture. Science. 328, 723-725.

Carmack, R.M., Gasco, J.L., Gossen, G.H. 1996. Legacy of Mesoamerica, The History and Culture of a Native American Civilization. New Jersey: Prentice Hall. ISBN 0-13-337445-9.

Cox, M.P. 2009. Accuracy of molecular dating with the rho statistic: deviations from coalescent expectations under a range of demographic models. Hum. Biol. 80, 335-357.

Dabney, J., Knapp, M., Glocke, I., Gansauge, M.T., Weihmann, A., Nickel, B., Valdiosera, C., García, N., Pääbo, S., Arsuaga, J.L., Meyer, M. 2013. Complete mitochondrial genome sequence of a Middle Pleistocene cave bear reconstructed from ultrashort DNA fragments. Proc. Natl. Acad. Sci. U S A. 110, 15758-15763.

Derenko, M., Malyarchuk, B., Grzybowski, T., Denisova, G., Dambueva, I., Perkova, M., Dorzhu, C., Luzina, F., Lee, H.K., Vanecek, T., Villems, R., Zakharov, I. 2007. Phylogeographic analysis of mitochondrial DNA in northern Asian populations. Am. J. Hum. Genet. 81, 1025-1041.

de Saint Pierre, M., Bravi, C.M., Motti, J.M., Fuku, N., Tanaka, M., Llop, E. Bonatto, S.L., Moraga, M. 2012. An alternative model for the early peopling of southern South America revealed by analyses of three mitochondrial DNA haplogroups. PLoS One. 7, e43486.

Doebley, J. 2004. The genetics of maize evolution. Annu. Rev. Genet. 38, 37-59.

Excoffier, L., Laval, G., Schneider, S. 2005. Arlequin (version 3.0): an integrated software package for population genetics data analysis. Evol. Bioinform. Online. 1, 47-50.

Fagundes, N.J., Kanitz, R., Bonatto, S.L. 2008b. A reevaluation of the Native American mtDNA genome diversity and its bearing on the models of early colonization of Beringia. PLoS One. 3, e3157.

Fagundes, N.J., Kanitz, R., Eckert, R., Valls, A.C., Bogo, M.R., Salzano, F.M., Smith, D.G., Silva, W.A., Zago, M.A., Ribeiro-dos-Santos, A.K., Santos, S.E., Petzl-Erler, M.L., Bonatto, S.L. 2008a. Mitochondrial population genomics supports a single pre-Clovis origin with a coastal route for the peopling of the Americas. Am. J. Hum. Genet. 82, 583-592.

Forster, P., Harding, R., Torroni, A., Bandelt, H.J. 1996. Origin and evolution of Native American mtDNA variation: a reappraisal. Am. J. Hum. Genet. 59, 935-945.

García-Garcerà, M., Gigli, E., Sanchez-Quinto, F., Ramirez, O., Calafell, F., Civit, S., Lalueza-Fox, C. 2011. Fragmentation of contaminant and endogenous DNA in ancient samples determined by shotgun sequencing; prospects for human palaeogenomics. PLoS One. 6, e24161.

Gilbert, M.T., Kivisild, T., Grønnow, B., Andersen, P.K., Metspalu, E., Reidla, M., Tamm, E., Axelsson, E., Götherström, A., Campos, P.F., Rasmussen, M., Metspalu, M., Higham, T.F., Schwenninger, J.L., Nathan, R., De Hoog, C.J., Koch, A., Møller, L.N., Andreasen, C., Meldgaard, M., Villems, R., Bendixen, C., Willerslev, E. 2008. Paleo-Eskimo mtDNA genome reveals matrilineal discontinuity in Greenland. Science. 320, 1787-1789.

Gilbert, M.T.P., Binladen, J., Miller, W., Wiuf, C., Willerslev, E., Poinar, H., Carlson, J.E., Leebens-Mack, J.H., Schuster, S.C. 2007. Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. Nucleic Acids Res. 35, 1-10.

Gilbert, M.T., Kivisild, T., Grønnow, B., Andersen, P.K., Metspalu, E., Reidla, M. Tamm, E., Axelsson, E., Götherström, A., Campos, P.F., Rasmussen, M., Metspalu, M., Higham, T.F., Schwenninger, J.L., Nathan, R., De Hoog, C.J., Koch, A., Møller, L.N., Andreasen, C., Meldgaard, M., Villems, R., Bendixen, C., Willerslev, E. 2008. Paleo-Eskimo mtDNA genome reveals matrilineal discontinuity in Greenland. Science. 320, 1787-1789.

Giles, R.E., Blanc, H., Cann, H.M., Wallace, D.C. Maternal inheritance of human mitochondrial DNA. 1980. Proc. Natl. Acad. Sci. U S A, 77, 6715-6719.

Ginolhac, A., Rasmussen, M., Gilbert, M.T.P., Willerslev, E., Orlando, L. 2011. mapDamage: testing for damage patterns in ancient DNA sequences. Bioinfomatics. 27, 2153-2155.

Gnirke, A., Melnikov, A., Maguire, J., Rogov, P., LeProust, E.M., Brockman, W., Fennell, T., Giannoukos, G., Fisher, S., Russ, C., Gabriel, S., Jaffe, D.B., Lander, E.S., Nusbaum, C. 2009. Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing. Nat. Biotechnol. 27, 182-189.

Gorostiza, A., Acunha-Alonzo, V., Regalado-Liu, L., Tirado, S., Granados, J., Sámano, D., Rangel-Villalobos, H., González-Martín, A. 2013. Reconstructing the history of Mesoamerican populations through the study of the mitochondrial DNA control region. PLoS One. 7, e44666.

Green, R.E., Krause, J., Briggs, A.W., Maricic, T., Stenzel, U., Kircher, M, Patterson, N., Li, H., Zhai, W., Fritz, M.H., Hansen, N.F., Durand, E.Y., Malaspinas, A.S., Jensen, J.D., Marques-Bonet, T., Alkan, C., Prüfer, K., Meyer, M., Burbano, H.A., Good, J.M., Schultz, R., Aximu-Petri, A., Butthof, A., Höber, B., Höffner, B., Siegemund, M., Weihmann, A., Nusbaum, C., Lander, E.S., Russ, C., Novod, N., Affourtit, J., Egholm, M., Verna, C., Rudan, P., Brajkovic, D., Kucan, Z., Gusic, I., Doronichev, V.B., Golovanova, L.V., Lalueza-Fox, C., de la Rasilla, M., Fortea, J., Rosas, A., Schmitz, R.W., Johnson, P.L., Eichler, E.E., Falush, D., Birney, E., Mullikin, J.C., Slatkin, M., Nielsen, R., Kelso, J., Lachmann, M., Reich, D., Pääbo, S. 2010. A draft sequence of the Neandertal genome. Science. 328, 710-722.

Green, R.E., Briggs, A.W., Krause, J., Prüfer, K., Burbano, H.A., Siebauer, M., Lachmann, M., Pääbo, S. 2009. The Neandertal genome and ancient DNA authenticity. EMBO J. 28, 2494-2502.

Green, R.E., Malaspinas, A.S., Krause, J., Briggs, A.W., Johnson, P.L., Uhler, C., Meyer, M., Good, J.M., Maricic, T., Stenzel, U., Prüfer, K., Siebauer, M., Burbano, H.A., Ronan, M., Rothberg, J.M., Egholm, M., Rudan, P., Brajković, D.,

Kućan, Z., Gusić, I., Wikström, M., Laakkonen, L., Kelso, J., Slatkin, M., Pääbo, S. 2008. A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. Cell. 134, 416-426.

Gunnarsdóttir, E.D., Li, M., Bauchet, M., Finstermeier, K., Stoneking, M. 2011. High-throughput sequencing of complete human mtDNA genomes from the Philippines. Genome Res. 21, 1-11.

Hartmann, A., Thieme, M., Nanduri, L.K., Stempfl, T., Moehle, C., Kivisild, T. Oefner, P.J. 2008. Validation of microarray-based resequencing of 93 worldwide mitochondrial genomes. Hum. Mutat. 30, 115-122.

Higuchi, R., Bowman, B., Freiberger, M., Ryder, O.A., Wilson, A.C. 1984. DNA sequences from the quagga, an extinct member of the horse family. Nature. 312, 282-284.

Huang, X., Wei, X., Sang, T., Zhao, Q., Feng, Q., Zhao, Y., Li, C., Zhu, C., Lu, T., Zhang, Z., Li, M., Fan, D., Guo, Y., Wang, A., Wang, L., Deng, L., Li, W., Lu, Y., Weng, Q., Liu, K., Huang, T., Zhou, T., Jing, Y., Li, W., Lin, Z., Buckler, E.S., Qian, Q., Zhang, Q.F., Li, J., Han, B. 2010. Genome-wide association studies of 14 agronomic traits in rice landraces. Nat. Genet. 42, 961-967.

Huson, D.H. and Bryant, D. 2005. Application of phylogenetic networks in evolutionary studies. Mol. Biol. Evol. 23, 254-267.

Ingman, M., Kaessmann, H., Pääbo, S., Gyllensten, U. 2000. Mitochondrial genome variation and the origin of modern humans. Nature. 408, 708-713.

Jans M.M.E., Nielsen-Marsh C.M., Smith C.I., Collins M.J., Kars H., 2004. Characterisation of microbial attack on archaeological bone. J. Archaeol. Sci. **31**, 87-95.

Keller, A., Graefen, A., Ball, M., Matzas, M., Boisguerin, V., Maixner, F., Leidinger, P., Backes, C., Khairat, R., Forster, M., Stade, B., Franke, A., Mayer, J., Spangler, J., McLaughlin, S., Shah, M., Lee, C., Harkins, T.T., Sartori, A., Moreno-Estrada, A., Henn, B., Sikora, M., Semino, O., Chiaroni, J., Rootsi, S., Myres, N.M., Cabrera, V.M., Underhill, P.A., Bustamante, C.D., Vigl, E.E., Samadelli, M., Cipollini, G., Haas, J., Katus, H., O'Connor, B.D., Carlson, M.R., Meder, B., Blin, N., Meese, E., Pusch, C.M., Zink, A. 2012. New insights into

the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. Nat. Commun. 3, 698.

Kemp, B.M., Malhi, R.S., McDonough, J., Bolnick, D.A., Eshleman, J.A., Rickards, O., Martinez-Labarga, C., Johnson, J.R., Lorenz, J.G., Dixon, E.J., Fifield, T.E., Heaton, T.H., Worl, R., Smith, D.G. 2007. Genetic analysis of early holocene skeletal remains from Alaska and its implications for the settlement of the Americas. Am. J. Phys. Anthropol. 132, 605-621.

Kemp, B.M., González-Oliver, A., Malhi, R.S., Monroe, C., Schroeder, K.B., McDonough, J., Rhett, G., Resendéz, A., Peñaloza-Espinosa, R.I., Buentello-Malo, L., Gorodesky, C., Smith, D.G. 2010. 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, 6759-6764.

Kemp, B.M. and Schurr, T.G. 2010. Ancient and modern genetic variation in the Americas. Center for Archaeological Investigations, Occasional Paper No. 38, 12-50.

Kimura, M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. J. Mol. Evol. 16, 111–120.

Kirchhoff, P. 1943. Mesoamérica: sus límites geográficos composición étnica y caracteres culturales, Acta Americana 92-107 (Inter-American Society of Anthropology and Geography, 1,).

Kirchhoff, P. 1952. Mesoamerica: Its geographic limits ethnic composition and cultural characteristics. (Heritage of Conquest ed Tax S.) 17-31 (The Free Press Publishers Glencoe IL).

Kitchen, A., Miyamoto, M.M., Mulligan, C.J. 2008. A three-stage colonization model for the peopling of the Americas. PLoS One. 3, e1596.

Kivisild, T., Shen, P., Wall, D.P., Do, B., Sung, R., Davis, K., Passarino, G., Underhill, P.A., Scharfe, C., Torroni, A., Scozzari, R., Modiano, D., Coppa, A., de Knijff, P., Feldman, M., Cavalli-Sforza, L.L., Oefner, P.J. 2006. The role of selection in the evolution of human mitochondrial genomes. Genetics, 172, 373-387.

Kolman, C.J., Bermingham, E. 1997. Mitochondrial and nuclear DNA diversity in the Chocó and Chibcha Amerinds of Panamá. Genetics. 147, 1289-1302.

Kolman, C.J., Bermingham, E., Cooke, R., Ward, R.H., Arias, T.D. 1995. Reduced mtDNA diversity in the Ngöbé Amerinds of Panamá. Genetics. 140, 275-283.

Krause, J., Briggs, A.W., Kircher, M., Maricic, T., Zwyns, N., Derevianko, A., Pääbo, S. 2010b. A Complete mtDNA Genome of an Early Modern Human from Kostenki, Russia. Curr. Biol. 20, 231-236.

Krause, J., Fu, Q., Good, J.M., Viola, B., Shunkov, M.V., Derevianko, A.P., Pääbo, S. 2010a. The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. Nature. 464, 894-897.

Kryukov, K. and Saitou, N. 2010. MISHIMA--a new method for high speed multiple alignment of nucleotide sequences of bacterial genome scale data. BMC Bioinformatics. 11, 142.

Kumar, S., Bellis, C., Zlojutro, M., Melton, P.E., Blangero, J., Curran, J.E. 2012. Large scale mitochondrial sequencing in Mexican Americans suggests a reappraisal of Native American origins. BMC Evol. Biol. 11, 293.

Kurosaki, K., Matsushita, T., Ueda, S. 1993. Individual DNA identification from ancient human remains, Am. J. Hum. Genet. 53, 638-643.

Li, H. and Durbin, R. 2009. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics. 25, 1754-1760.

Li, H., Handsaker, B., Wysoker, A., Fennell, T., Ruan, J., Homer, N., Marth, G., Abecasis, G., Durbin, R., and 1000 Genome Project Data Processing Subgroup. 2010. The Sequence Alignment/Map format and SAMtools. Bioinformatics. 25, 2078-2079.

Lindahl, T. 1993. Instability and decay of the primary structure of DNA. Nature. 362, 709-715.

Malhi, R.S., Cybulski, J.S., Tito, R.Y., Johnson, J., Harry, H., Dan, C. 2010. Brief communication: mitochondrial haplotype C4c confirmed as a founding genome in the Americas. Am. J. Phys. Anthropol. 141, 494-497.

Malhi, R.S., Eshleman, J.A., Greenberg, J.A., Weiss, D.A., Schultz Shook, B.A., Kaestle, F.A., Lorenz, J.G., Kemp, B.M., Johnson, J.R., Smith, D.G. 2002. The structure

of diversity within New World mitochondrial DNA haplogroups: implications for the prehistory of North America. Am. J. Hum. Genet. 70, 905-919.

Mamanova, L., Coffey, A.J., Scott, C.E., Kozarewa, I., Turner, E.H., Kumar, A., Howard, E., Shendure, J., Turner, D.J. 2010. Target-enrichment strategies for next generation sequencing. Nat. Methods. 7, 111-118.

Maniatis, T., Fritsch, E.F., Sambrook, J. 1982. Molecular Cloning A Laboratory Manual. Cold Spring Harbor Laboratory.

Merriwether, D.A., Clark, A.G., Ballinger, S.W., Schurr, T.G., Soodyall, H., Jenkins, T., Sherry, S.T., Wallace, D.C. 1991. The structure of human mitochondrial DNA variation. J. Mol. Evol. 33, 543-555.

Meyer, M., Fu, Q., Aximu-Petri, A., Glocke, I., Nickel, B., Arsuaga, J.L., Martínez, I., Gracia, A., de Castro, J.M., Carbonell, E., Pääbo, S. 2013. A mitochondrial genome sequence of a hominin from Sima de los Huesos. Nature. 505, 403-406.

Meyer, M., Kircher, M., Gansauge, M.T., Li, H., Racimo, F., Mallick, S., Schraiber, J.G., Jay, F., Prüfer, K., de Filippo, C., Sudmant, P.H., Alkan, C., Fu, Q., Do, R., Rohland, N., Tandon, A., Siebauer, M., Green, R.E., Bryc, K., Briggs, A.W., Stenzel, U., Dabney, J., Shendure, J., Kitzman, J., Hammer, M.F., Shunkov, M.V., Derevianko, A.P., Patterson, N., Andrés, A.M., Eichler, E.E., Slatkin, M., Reich, D., Kelso, J., Pääbo, S. 2012. A high-coverage genome sequence from an archaic Denisovan individual. Science. 338, 222-226.

Miller, W., Drautz, D.I., Ratan, A., Pusey, B., Qi, J., Lesk, A.M., Tomsho, L.P., Packard, M.D., Zhao, F., Sher, A., Tikhonov, A., Raney, B., Patterson, N., Lindblad-Toh, K., Lander, E.S., Knight, J.R., Irzyk, G.P., Fredrikson, K.M., Harkins, T.T., Sheridan, S., Pringle, T., Schuster, S.C. 2008. Sequencing the nuclear genome of the extinct woolly mammoth. Nature. 456, 387-390.

Mishmar, D., Ruiz-Pesini, E., Golik, P., Macaulay, V., Clark, A.G., Hosseini, S., Brandon, M., Easley, K., Chen, E., Brown, M.D., Sukernik, R.I., Olckers, A., Wallace, D.C. 2003. Natural selection shaped regional mtDNA variation in humans. Proc. Natl. Acad. Sci. U S A. 100, 171-176.

Mulligan, C.J., Kitchen, A., Miyamoto, M.M. 2008. Updated three-stage model for the peopling of the Americas. PLoS One. 3, e3199.

Nichols, J., 1992. Linguistic diversity in space and time. the University of Chicago

Nielsen, R., Beaumont, M.A. 2009. Statistical inferences in phylogeography. Mol. Ecol. 18, 1034-1047.

Nielsen-Marsh, C.M., Smith, C.I., Jans, M.M.E., Nord, A., Kars, H., Collins, M.J. 2007. Bone diagenesis in the European Holocene II: taphonomic and environmental considerations. J. Archaeol. Sci. 34, 1523-1531.

Oota, H., Saitou, N., Matsushita, T., Ueda, S. 1999. Molecular genetic analysis of remains of a 2,000-year-old human population in China - and its relevance for the origin of the modern Japanese population, Am. J. Hum. Genet. 64, 250-258.

Oota, H., Saitou, N., Matsushita, T., Ueda, S. 1995. A genetic-study of 2,000-year-old human remains from japan using mitochondrial-DNA sequences, Am. J. Phys. Anthropol. 98, 133-145.

Orlando, L., Ginolhac, A., Raghavan, M., Vilstrup, J., Rasmussen, M., Magnussen, K., Steinmann, K.E., Kapranov, P., Thompson, J.F., Zazula, G., Froese, D., Moltke, I., Shapiro, B., Hofreiter, M., Al-Rasheid, K.A., Gilbert, M.T., Willerslev, E. 2011. True singlemolecule DNA sequencing of a pleistocene horse bone. Genome Res. 21, 1705-1719.

Orlando, L., Ginolhac, A., Zhang, G., Froese, D., Albrechtsen, A., Stiller, M., Schubert, M., Cappellini, E., Petersen, B., Moltke, I., Johnson, P.L., Fumagalli, M., Vilstrup, J.T., Raghavan, M., Korneliussen, T., Malaspinas, A.S., Vogt, J., Szklarczyk, D., Kelstrup, C.D., Vinther, J., Dolocan, A., Stenderup, J., Velazquez, A.M., Cahill, J., Rasmussen, M., Wang, X., Min, J., Zazula, G.D., Seguin-Orlando, A., Mortensen, C., Magnussen, K., Thompson, J.F., Weinstock, J., Gregersen, K., Røed, K.H., Eisenmann, V., Rubin, C.J., Miller, D.C., Antczak, D.F., Bertelsen, M.F., Brunak, S., Al-Rasheid, K.A., Ryder, O., Andersson, L., Mundy, J., Krogh, A., Gilbert, M.T., Kjær, K., Sicheritz-Ponten, T., Jensen, L.J., Olsen, J.V., Hofreiter, M., Nielsen, R., Shapiro, B., Wang, J., Willerslev, E. 2013. Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature. 499, 74-78.

Pääbo, S. 1985. Molecular cloning of Ancient Egyptian mummy DNA. Nature. 314, 644-645.

Peñaloza-Espinosa, R.I., Arenas-Aranda, D., Cerda-Flores, R.M., Buentello-Malo, L., González-Valencia, G., Torres, J. Alvarez, B., Mendoza, I., Flores, M., Sandoval, L., Loeza, F., Ramos, I., Muñoz, L., Salamanca, F. 2007. Characterization of mtDNA haplogroups in 14 Mexican indigenous populations. Hum. Biol. 79, 313-320.

Perego, U.A., Achilli, A., Angerhofer, N., Accetturo, M., Pala, M., Olivieri, A., Hooshiar Kashani, B., Ritchie, K.H., Scozzari, R., Kong, Q.P., Myres, N.M., Salas, A., Semino, O., Bandelt, H.J., Woodward, S.R., Torroni, A. 2009. Distinctive Paleo-Indian migration routes from Beringia marked by two rare mtDNA haplogroups. Curr. Biol. 19, 1-8.

Perego, U.A., Angerhofer, N., Pala, M., Olivieri, A., Lancioni, H., Hooshiar Kashani, B., Carossa, V., Ekins, J.E., Gómez-Carballa, A., Huber, G., Zimmermann, B., Corach, D., Babudri, N., Panara, F., Myres, N.M., Parson, W., Semino, O., Salas, A., Woodward, S.R., Achilli, A., Torroni, A. 2010. The initial peopling of the Americas: a growing number of founding mitochondrial genomes from Beringia. Genome Res. 20, 1174-1179.

Piperno, D.R., Ranere, A.J., Holst, I., Iriarte, J., Dickau, R. 2009. Starch grain and phytolith evidence for early ninth millennium B.P. maize from the Central Balsas River Valley, Mexico. Proc. Natl. Acad. Sci. U S A. 106, 5019-5024.

Pohl, M.E., Piperno, D.R., Pope, K.O., Jones, J.G. 2007. Microfossil evidence for pre-Columbian maize dispersals in the neotropics from San Andres Tabasco Mexico. Proc. Natl. Acad. Sci. U S A. 104, 6870-6875.

Poinar H.N., Schwarz C., Qi J., Shapiro B., Macphee R.D., Buigues B., Tikhonov A., Huson D.H., Tomsho L.P., Auch A., Rampp M., Miller W., Schuster S.C. 2006. Metagenomics to paleogenomics: large-scale sequencing of mammoth DNA. Science. 311, 392-394.

Prüfer, K., Racimo, F., Patterson, N., Jay, F., Sankararaman, S., Sawyer, S., Heinze, A., Renaud, G., Sudmant, PH., de Filippo, C., Li, H., Mallick, S., Dannemann, M., Fu, Q., Kircher, M., Kuhlwilm, M., Lachmann, M., Meyer, M., Ongyerth, M., Siebauer, M., Theunert, C., Tandon, A., Moorjani, P., Pickrell, J., Mullikin, J.C., Vohr, S.H., Green, R.E., Hellmann, I., Johnson, P.L., Blanche, H., Cann,

H., Kitzman, J.O., Shendure, J., Eichler, E.E., Lein, E.S., Bakken, T.E., Golovanova, L.V., Doronichev, V.B., Shunkov, M.V., Derevianko, A.P., Viola, B., Slatkin, M., Reich, D., Kelso, J., Pääbo, S. 2013. The complete genome sequence of a Neanderthal from the Altai Mountains. Nature. 505, 43-49.

R Development Core Team. R. 2010. A language and environment for statistical computing: R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org.

Raghavan, M., Skoglund, P., Graf, K.E., Metspalu, M., Albrechtsen, A., Moltke, I., Rasmussen, S., Stafford, T.W., Orlando, L., Metspalu, E., Karmin, M., Tambets, K., Rootsi, S., Mägi, R., Campos, P.F., Balanovska, E., Balanovsky, O., Khusnutdinova, E., Litvinov, S., Osipova, L.P., Fedorova, S.A., Voevoda, M.I., DeGiorgio, M., Sicheritz-Ponten, T., Brunak, S., Demeshchenko, S., Kivisild, T., Villems, R., Nielsen, R., Jakobsson, M., Willerslev, E. 2013. Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. Nature. 505, 87-91.

Ranere, A.J., Piperno, D.R., Holst, I., Dickau, R., Iriarte, J. 2009. The cultural and chronological context of early Holocene maize and squash domestication in the Central Balsas River Valley Mexico. Proc. Natl. Acad. Sci. U S A. 106, 5014-5018.

Rasmussen, M., Li, Y., Lindgreen, S., Pedersen, J.S., Albrechtsen, A., Moltke, I., Metspalu, M., Metspalu, E., Kivisild, T., Gupta, R., Bertalan, M., Nielsen, K., Gilbert, M.T., Wang, Y., Raghavan, M., Campos, P.F., Kamp, H.M., Wilson, A.S., Gledhill, A., Tridico, S., Bunce, M., Lorenzen, E.D., Binladen, J., Guo, X., Zhao, J., Zhang, X., Zhang, H., Li, Z., Chen, M., Orlando, L., Kristiansen, K., Bak, M., Tommerup, N., Bendixen, C., Pierre, T.L., Grønnow, B., Meldgaard, M., Andreasen, C., Fedorova, S.A., Osipova, L.P., Higham, T.F., Ramsey, C.B., Hansen, T.V., Nielsen, F.C., Crawford, M.H., Brunak, S., Sicheritz-Pontén, T.,Villems, R., Nielsen, R., Krogh, A., Wang, J., Willerslev, E. 2010. Ancient human genome sequence of an extinct Palaeo-Eskimo. Nature. 463, 757-762.

Rasmussen, M., Li, Y., Lindgreen, S., Pedersen, J.S., Albrechtsen, A., Moltke, I., Metspalu, M., Metspalu, E., Kivisild, T., Gupta, R., Bertalan, M., Nielsen, K., Gilbert, M.T., Wang, Y., Raghavan, M., Campos, P.F., Kamp, H.M., Wilson, A.S., Gledhill, A., Tridico, S., Bunce, M., Lorenzen, E.D., Binladen, J., Guo, X., Zhao, J., Zhang, X., Zhang, H., Li, Z., Chen, M., Orlando, L., Kristiansen, K., Bak, M., Tommerup, N., Bendixen, C., Pierre, T.L., Grønnow, B., Meldgaard, M., Andreasen, C., Fedorova, S.A., Osipova, L.P., Higham, T.F., Ramsey, C.B., Hansen, T.V., Nielsen, F.C., Crawford, M.H., Brunak, S., Sicheritz-Pontén, T., Villems, R., Nielsen, R., Krogh, A., Wang, J., Willerslev, E. 2010. Ancient human genome sequence of an extinct Palaeo-Eskimo. Nature. 463, 757-762.

Reed, F.A., Kontanis, E.J., Kennedy, K.A.R., Aquadro, C.F. 2008. Ancient DNA prospects from Sri Lankan highland dry caves support an emerging global pattern. Am. J. Phys. Anthropol. 121, 112-116.

Reich, D., Green, R.E., Kircher, M., Krause, J., Patterson, N., Durand, E.Y., Viola, B., Briggs, A.W., Stenzel, U., Johnson, P.L., Maricic, T., Good, J.M., Marques-Bonet, T., Alkan, C., Fu, Q., Mallick, S., Li, H., Meyer, M., Eichler, E.E., Stoneking, M., Richards, M., Talamo, S., Shunkov, M.V., Derevianko, A.P., Hublin, J.J., Kelso, J., Slatkin, M., Pääbo, S. 2010. Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature. 468, 1053-1060.

Reich, D., Patterson, N., Campbell, D., Tandon, A., Mazieres, S., Ray, N., Tamm, E., Axelsson, E., Götherström, A., Campos, P.F., Rasmussen, M., Metspalu, M., Higham, T.F., Schwenninger, J.L., Nathan, R., De Hoog, C.J., Koch, A., Møller, L.N., Andreasen, C., Meldgaard, M., Villems, R., Bendixen, C., Willerslev, E. 2012. A Reconstructing Native American population history. Nature. 488, 370-374.

Saitou, N., Nei, M. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4, 406–425.

Sandoval, K., Buentello-Malo, L., Peñaloza-Espinosa, R., Avelino, H., Salas, A., Calafell, F. Comas, D. 2009. Linguistic and maternal genetic diversity are not correlated in Native Mexicans. Hum. Genet. 126, 521-53.

Sandoval, K., Moreno-Estrada, A., Mendizabal, I., Underhill, PA., Lopez-Valenzuela, M., Peñaloza-Espinosa, R., Lopez-Lopez, M., Buentello-Malo, L., Avelino, H., Calafell, F., Comas, D. 2012. Y-chromosome diversity in Native Mexicans reveals continental transition of genetic structure in the Americas. Am. J. Phys. Anthropol. 148, 395-405.

Schönberg, A., Theunert, C., Li, M., Stoneking, M., Nasidze, I. 2011. High-throughput sequencing of complete human mtDNA genomes from the Caucasus and West Asia: high diversity and demographic inferences. Eur. J. Hum. Genet. 19, 988-994.

Schurr, T.G., Ballinger, S.W., Gan, Y.Y., Hodge, J.A., Merriwether, D.A., Lawrence, D.N., Knowler, W.C., Weiss, K.M., Wallace, D.C. 1990. Amerindian mitochondrial DNAs have rare Asian mutations at high frequencies, suggesting they derived from four primary maternal lineages. Am. J. Hum. Genet. 46, 613-623.

Shao, K., Ding, W., Wang, F., Li, H., Ma, D., Wang, H. 2011. Emulsion PCR: A High Efficient Way of PCR Amplification of Random DNA Libraries in Aptamer Selection. PLoS ONE, 6, e24910.

Smith, C.I., Nielsen-Marsh, C.M., Jans, M.M.E., Collins, M.J. 2007. Bone diagenesis in the European Holocene I: patterns and mechanisms. J. Archaeol. Sci. 34, 1485-1493.

Spence, M.W. and Pereira, G. 2007. The Human Skeletal Remains Of The Moon Pyramid, Teotihuacan. Ancient Mesoamerica. 18, 147-157.

Stoneking, M. and Krause, J. 2011. Learning about human population history from ancient and modern genomes. Nature Reviews Genetics. 12, 603-614.

Suárez, J.A. 1983. The Mesoamerican Indian Languages 11-29 (Cambridge University Press New York).

Sugiyama, S., and Luján, L.L. 2007. Dedicatory Burial Offering Complexs at The Moon Pyramid,Teotihucan. Ancient Mesoamerica 18, 127-146

Tamm, E., Kivisild, T., Reidla, M., Metspalu, M., Smith, D.G., Mulligan, C.J., Bravi, C.M., Rickards, O., Martinez-Labarga, C., Khusnutdinova, E.K., Fedorova, S.A., Golubenko, M.V., Stepanov, V.A., Gubina, M.A., Zhadanov, S.I.,

Ossipova, L.P., Damba, L., Voevoda, M.I., Dipierri, J.E., Villems, R., Malhi, R.S. 2007. Beringian standstill and spread of Native American founders. PLoS One. 2, e829.

Tamura, K., Dudley, J., Nei, M., Kumar, S. 2007. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Mol. Biol. Evol. 24, 1596-1569.

Torres, M.M., Bravi, C.M., Bortolini, M.C., Duque, C., Callegari-Jacques, S., Ortiz, D. Bedoya, G, Groot de Restrepo, H., Ruiz-Linares, A. 2006. A revertant of the major founder Native American haplogroup C common in populations from northern South America. Am. J. Hum. Biol. 18, 59-65.

Torroni, A., Achilli, A., Macaulay, V., Richards, M., Bandelt, H.J. 2006. Harvesting the fruit of the human mtDNA tree. Trends Genet. 22, 339-345.

Torroni, A., Schurr, T.G., Cabell, M.F., Brown, M.D., Neel, J.V., Larsen, M., Smith, D.G., Vullo, C.M., Wallace, D.C. 1993a. Asian affinities and continental radiation of the four founding Native American mtDNAs. Am. J. Hum. Genet. 53, 563-590.

Torroni, A., Sukernik, R.I., Schurr, T.G., Starikorskaya, Y.B., Cabell, M.F., Crawford, M.H., Comuzzie, A.G., Wallace, D.C. 1993b. mtDNA variation of aboriginal Siberians reveals distinct genetic affinities with Native Americans. Am. J. Hum. Genet. 53, 591-608.

Torroni, A., Schurr, T.G., Yang, C.C., Szathmary, E.J., Williams, R.C., Schanfield, M.S. Troup, G.A, Knowler, W.C, Lawrence, D.N, Weiss, K.M. 1992. Native American mitochondrial DNA analysis indicates that the Amerind and the Nadene populations were founded by two independent migrations. Genetics. 130, 153-162.

van Heerwaarden, J., Doebley, J., Briggs, W.H., Glaubitz, J.C., Goodman, M.M., de Jesus Sanchez Gonzalez, J. Ross-Ibarra, J. 2011. Genetic signals of origin spread and introgression in a large sample of maize landraces. Proc. Natl. Acad. Sci. U S A. 108, 1088-1092.

van Oven, M, Kayser, M. 2008. Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation. Hum. Mutat. 30, E386-394.

Volodko, N.V, Starikovskaya, E.B, Mazunin, I.O, Eltsov, N.P, Naidenko, P.V, Wallace, D.C, Sukernik, R.I. 2008. Mitochondrial genome diversity in arctic Siberians, with particular reference to the evolutionary history of Beringia and Pleistocenic peopling of the Americas. Am. J. Hum. Genet. 82, 1084-1100.

Wang, L., Oota, H., Saitou, N., Jin, F., Matsushita, T., Ueda, S. 2000. Genetic structure of a 2500-year-old human population in China and its spatiotemporal changes, Mol. Biol. Evol. 17, 1396-1400.

White, C.D., Price, T.D., and Longstaffe, F.J. 2007. Residential histories of the human sacrifices at the Moon Pyramid, Teotihuacan: evidence from oxygen and strontium isotopes. Ancient Mesoamerica. 18, 159-172

Williams, R., Peisajovich, S.G., Miller, O.J., Magdassi, S., Tawfik, D.S., Griffiths, A.D. 2006. Amplification of complex gene libraries by emulsion PCR. Nat. Methods. 3, 545-550

Wilson, A.C., Cann, R.L., Carr, S.M., George, M., Gyllensten, U.B., Helm-Bychowski, K.M., Higuchi, R.G., Palumbil, S.R., Prager, E.M., Sage, R.D., and Stoneking, M. 1985. Mitochondria1 DNA and two perspectives on evolutionary genetics. Biological journal of the Linnean Sociey. 26, 375-400

White, C.D., Price, T.D., and Longstaffe, F.J. 2007. Residental Histories of The Human Sacrificies at The Moon Pyramid, Teotihuacan. Ancient Mesoamerica. 18, 159-172.