<http://www.sciencedirect.com/science/article/pii/S0002929712006441> barbieri

<http://www.nature.com/ejhg/journal/v21/n4/full/ejhg2012192a.html> barbiericlicks

<http://mbe.oxfordjournals.org/content/29/4/1213.long> barbierimandenka

<http://www.sciencedirect.com/science/article/pii/S0002929707638774> derenko

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4067553/> duggan

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC378623/> endicott

<http://evolutsioon.ut.ee/publications/Fedorova2003.pdf> federova

<http://www.academia.edu/3846779/Expanding_Southwest_Pacific_Mitochondrial_Haplogroups_P_and_Q> friedlaender

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1274484/> helgason

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1914908/> horai

<http://evolutsioon.ut.ee/MAIT/pdf/Kivisild_1999b.pdf> kivisild

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC379225/#!po=25.8621> kivisildindia

<http://www.biomedcentral.com/1471-2156/9/47> marchani

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC516768/> metspalu

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3126835/> peng

<http://mbe.oxfordjournals.org/content/27/10/2417.long> pengcham

<http://onlinelibrary.wiley.com/store/10.1046/j.1469-1809.2003.00039.x/asset/j.1469-1809.2003.00039.x.pdf?v=1&t=i13dtcng&s=eb8722a63d9fa79b2555056d3e2f552ebbefdb94> plaza

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1181978/> quintana

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC385086/#__ffn_sectitle> salas

<http://www.biomedcentral.com/1471-2148/13/56> schlebusch

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC524407/> tanaka

<http://mbe.oxfordjournals.org/content/22/3/725.full> wen

<http://mbe.oxfordjournals.org/content/early/2011/09/13/molbev.msr221.full.pdf+html> yunusbayev

mtdna sequences database: <http://www.mtdb.igp.uu.se/>

Barbieri C, Butthof A, Bostoen K, Pakendorf B. Genetic perspectives on the origin of clicks in Bantu languages from southwestern Zambia. Eur J Hum Genet 2013;21:430-436.

Barbieri C, Vicente M, Rocha J, Mpoloka SW, Stoneking M, Pakendorf B. Ancient substructure in early mtDNA lineages of Southern Africa. Am J Hum Genet 2013;92(2):285-292.

Derenko M, Malyarchuk B, Grzybowski T, DenisovaG, DambuevaI, PerkovaM, DorzhuC, LuzinaF, Lee HK, Vanecek T, VillemsR, ZakharovI. Phylogeographic analysis of mitochondrial DNA in Northern Asian populations. Am J Hum Genet 2007;81(5):1025-1041.

Endicott P, Gilbert MT, Stringer C, et al. The genetic origins of the Andaman Islanders [J] Am J Hum Genet. 2003;72(1):178–184

Fedorova, S. A., et. al., Analysis of Mitochondrial DNA Lineages in Yakuts, Molecular Biology 37: 544-553, 2003, Translated from Molekulyarnaya Biologiya 37: 643-653, 2003

Friedlaender , Jonathan, et. al., Expanding Southwest Pacific Mitochondrial Haplogroups P and Q, Mol. Biol. Evol. 22: 1506–1517, 2005

Helgason, Agnar, et. al., mtDNA and the Islands of the North Atlantic: Estimating the Proportions of Norse and Gaelic Ancestry, Am. J. Hum. Genet. 68: 723-737, 2001

Kivisild, T, et. al., The Place of the Indian mtDNA Variants in the Global Network of Maternal Lineages and the Peopling of the Old World, In 'Genomic Diversity', Edited by Deka, R. Papiha, S.S.Kluwer/Academic/Plenum Publishers, pp. 135-152, 1999

Kivisild T,

Marchani EE, Watkins WS, Bulayeva K, Harpending HC, Jorde LB. Culture creates genetic structure in the Caucasus: autosomal, mitochondrial, and Y-chromosomal variation in Daghestan. BMC Genetics 2008;9:47.

Peng MS, Quang HH, Dand KP, Trieu AV, Wang HW, Yao YG, Kong QP, Zhang YP. Tracing the Austronesian Footprint in Mainland Southeast Asia: A Perspective from Mitochondrial DNA. Mol Biol Evol. 2010;27(10):2417-2430.

Peng MS, Zhang YP. Inferring the population expansions in peopling of Japan. PLoS One. 2011;6(6):e21509.

Plaza S, et. al., Joining the Pillars of Hercules, mtDNA Sequences Show Multidirectional Gene Flow in the Western Mediterranean, Ann. Hum. Genetics 67: 312-328, 2003

Quintana-Murci L, Chaix R, Wells RS, Behar DM, Sayar H, et al. Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Am J Hum Genet 2004:74: 827–845

Salas A, Richards M, De La Fe T, Laureu MV, Sbrino B, Sánchez-Diz P, Macauley V, Carracedo A. The making of the African mtDNA landscape. Am J Hum genet. 2002;71(5):1082-1111.

Schlebusch CM,Lombard M, Soodyall H. MtDNA control region variation affirms diversity and deep sub-structure in populations from southern Africa. BMC Evolutionary Biology 2013;13:56.

Tanaka M, Cabrera VM, Gonzalez AM, Larruga JM, Takeyasu T, et al. Mitochondrial genome variation in eastern Asia and the peopling of Japan. Genome Res 2004;14: 1832–1850

* Wen B, Li H, Gao S, Mao X, Gao Y, Li F, Zhang F, He Y, Dong Y, Zhang Y, Huang W, Jin J, Xiao C, Lu D, Chakraborty R, Su B, Deka R, Jin L.

Genetic Structure of Hmong-Mien Speaking Populations in East Asia as Revealed by mtDNA Lineages. Mol Biol Evol 2005;22 (3): 725-734.

Yunusbayev B, Metspalu M, Järve M, Kutuev I, Rootsi S, Metspalu E, Behar DM, Varendi K, Sahakyan H, Khusainova R, Yepiskoposyan L, Khusnutdinova EK, Underhill PA, Kivisild T, Villems R. The Caucasus as an asymmetric semipermeable barrier to ancient human migrations. Mol Biol Evol 2012;29(1):359-365.