

Chromosome 10 – Native American Segment

Background: Based on genealogy, the author has a 6th great grandmother on the maternal side who was Mohawk, from the Six Nations of the Grand River. In an exploration of a maternal segment on chromosome 18 as seen [here](#), the present author showed how more in depth “academic testing” was able to determine that this segment (and one on chromosome 8) was somewhat different from “standard” Native American segments and the scientist who performed the analysis called it “Beringian”. This latter term fits with recent ancient DNA studies from Canada and East Asia resulting in a categorization as “Beringian – Ancestral B” (see below).

The study of the author’s genome also flagged a segment on chromosome 10 which was labelled Native American, but considered to be of a more common Amerindian rather than Beringian variety. At a later date the author learned that this segment came from his paternal side of the family, with his father having about 2% Native American ancestry as seen [here](#). It is not likely that the analysis of the chromosome segment on chromosome 10 can provide as much information as those on the maternal side, however the author considered it potentially informative to include all of the available data to see what can be learned from this one small chunk of DNA.

Commercial Testing: It is unfortunate that the “big five” DNA ancestry testing companies downplay small segments and only report them (if at all) as “Unassigned”. In terms of the author’s DNA, 23andMe has also reported segments of Cypriot and North African DNA, the origin of which is a mystery to the author.

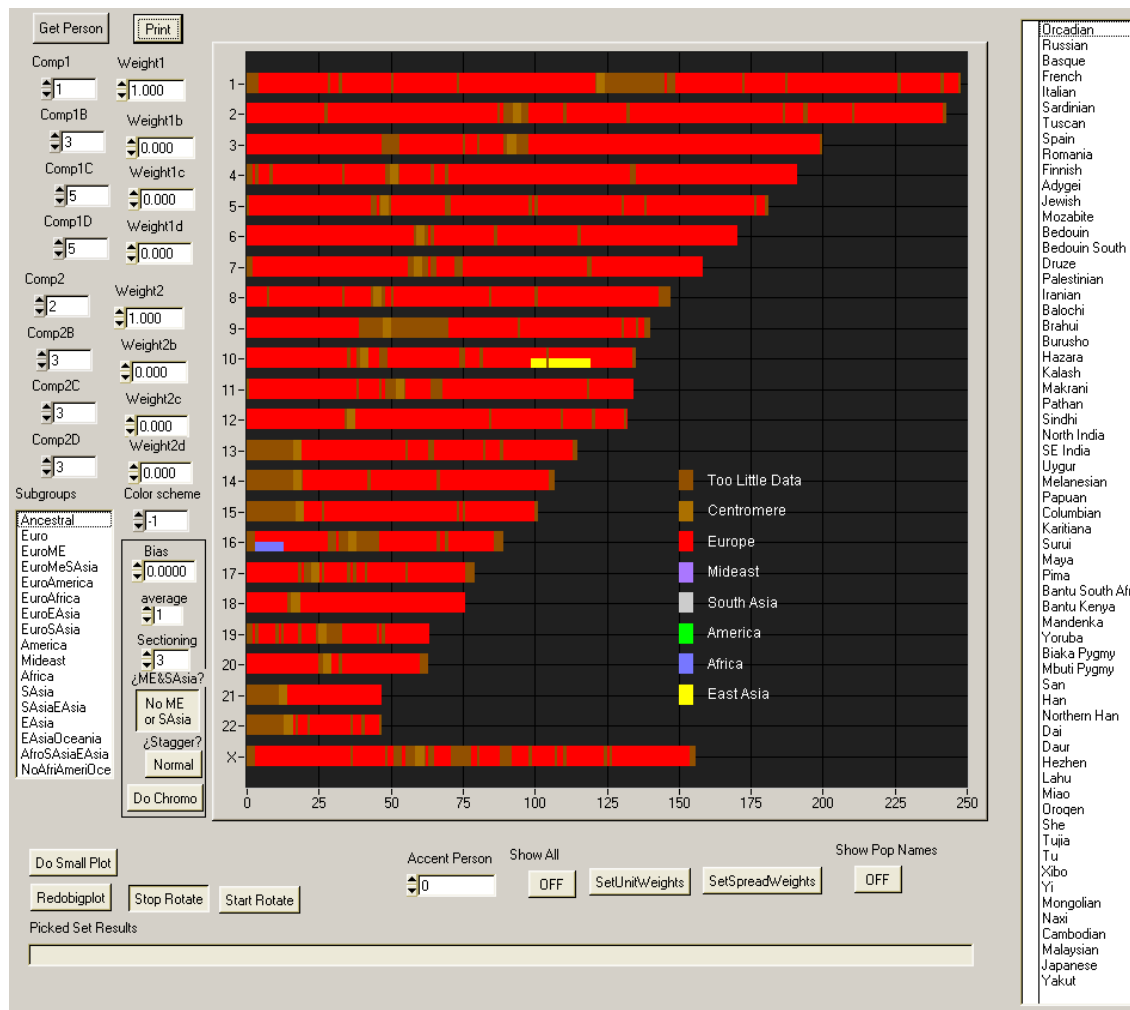
23andMe Unassigned 2019: Below is a diagram showing some of the unassigned segments in the author’s genome – there were more above and below but at the time the author was interested in chromosomes 8 and 18. It does show an unassigned segment on chromosome 10 of undetermined size.



Ancestry.com: Here this company only flags the segment on chromosome 18 (Native American) and chromosome 7 (0.5% North African by 23andMe) to be placed in the “Unassigned” category.

The only way to resolve the “Unassigned” segments would be to have more comprehensive reference samples. For example, there are zero reference samples from Pre-Columbian Eastern North America. If perchance samples such as the skeletal material from the Huron – Wendat ossuaries from Southern Ontario were tested, this would offer the opportunity to see how closely these samples match those from South America presently used to represent Native American ancestry – and perhaps transform some “Unassigned” to an “Eastern North America” category.

Dr. Doug McDonald Testing: Circa 2010 Dr. McDonald, a Chemistry Professor in Illinois established a robust protocol for the analysis of individuals using the reference groups then available. Needless to say, the number of such groups have expanded significantly since those early days. What follows is a chart showing the author’s maternal African segment on chromosome 16, as well as an “East Asian” segment on chromosome 10.



In 2010 Native American segments tended to be lumped together with their closest relatives, East Asian. The segments labelled thus for the genome of the author’s wife (MF) have been “converted” to Native American. Never the less, further testing would be needed to confirm that what we are seeing above would be more correctly labelled as Native American if the procedure were to be repeated using a more diverse array of reference samples.

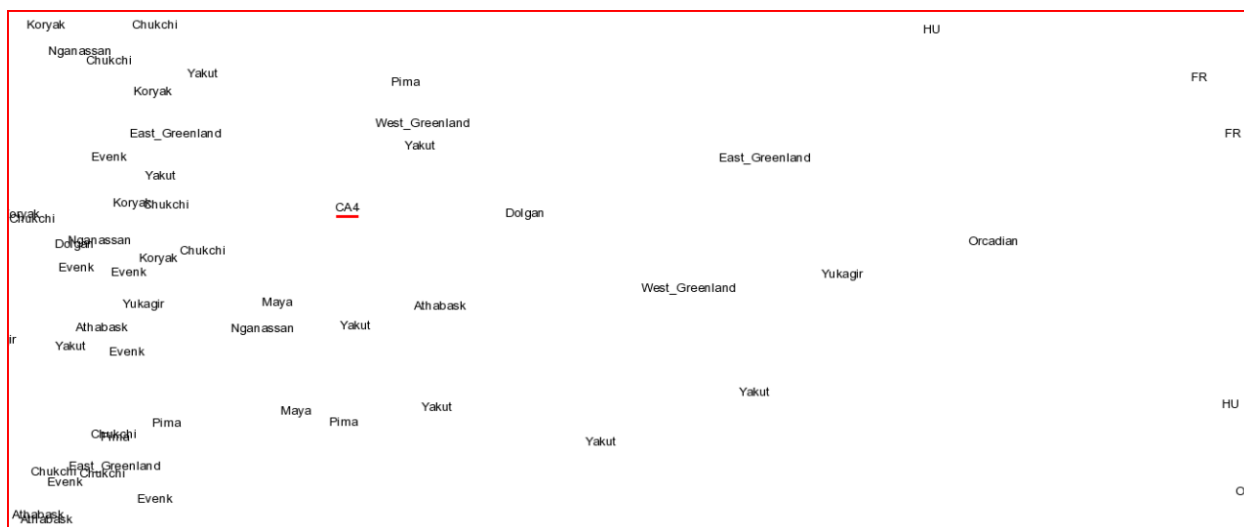
Eurogenes - Haplotype Matching, Dating the Admixture Plus MDS Analysis:

About 2010 DavidW developed a new methodology which used two entirely independent types of approaches, and compared the two. Here he ran a haplotype comparison between participants in his project such as the present author, and individuals in a large set of reference groups. When a segment of interest is detected by the algorithm, DavidW then uses multidimensional scaling to look “microscopically” at the flagged segment. He noted that generally the two methods are in high agreement, but one assesses whether the admixture was ancient or recent (e.g., last 350 years). DavidW also used a number of procedures to check on the validity of his findings. He used a program called GEDI-ADMX which is, in his words, *what I used to find the haplotypes, plus PLINK MDS and Eigenstrat PCA to double check them. I also used LAMP 2.4 (+ WINPOP) on a friend's computer to scan your genome* (DavidW, personal communication, 28 May 2011).

When running some segments with the above highly enhanced and upgraded software and algorithm, DavidW located three relevant segments, all of which reflected “recent” admixture, plus a fourth on chromosome 2 which showed “ancient” admixture. The later was later determined to be Finnish, often highly similar to Native American before the use of Finnish reference samples – even assig. He labeled two of the findings, (chr 8) and (chr 18) “**Bering Strait segments**” and chr 10 as “**Amerindian**”, and testing revealed that each was a recent admixture event that occurred less than 350 years ago.

In the chromosome 10 segment below, the icon for the author being labelled CA4, one can see that there are a number of Eastern Siberian groups mixed among the Native Americans, but that in addition to the Mayans and Athabaskans viewed in relation to the segments on chromosomes 8 and 18, we also see the Pima (of the Arizona – Mexican border) which did not occur in any of the other MDS plots, and also somewhat rare in those whose primary ancestry is Native American from the Eastern Woodlands.

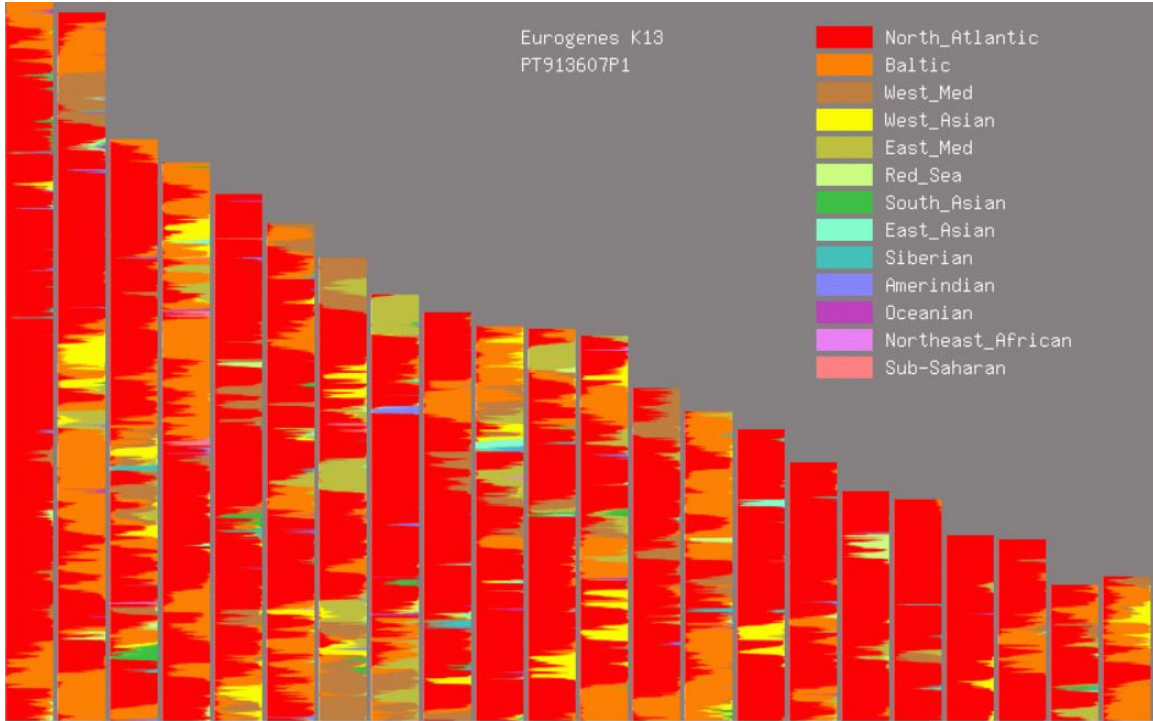
Here is a screenshot of the near neighbours on **chromosome 10 labeled as Amerindian**:



The icon for the author is embedded among various reference samples even though his segment is only one half Native American (the maternal half her being European). The reason for this anomaly is unclear. The above segment on chromosome 10 extends at a minimum from about 94,661,093 to 97,851,432 Mb.

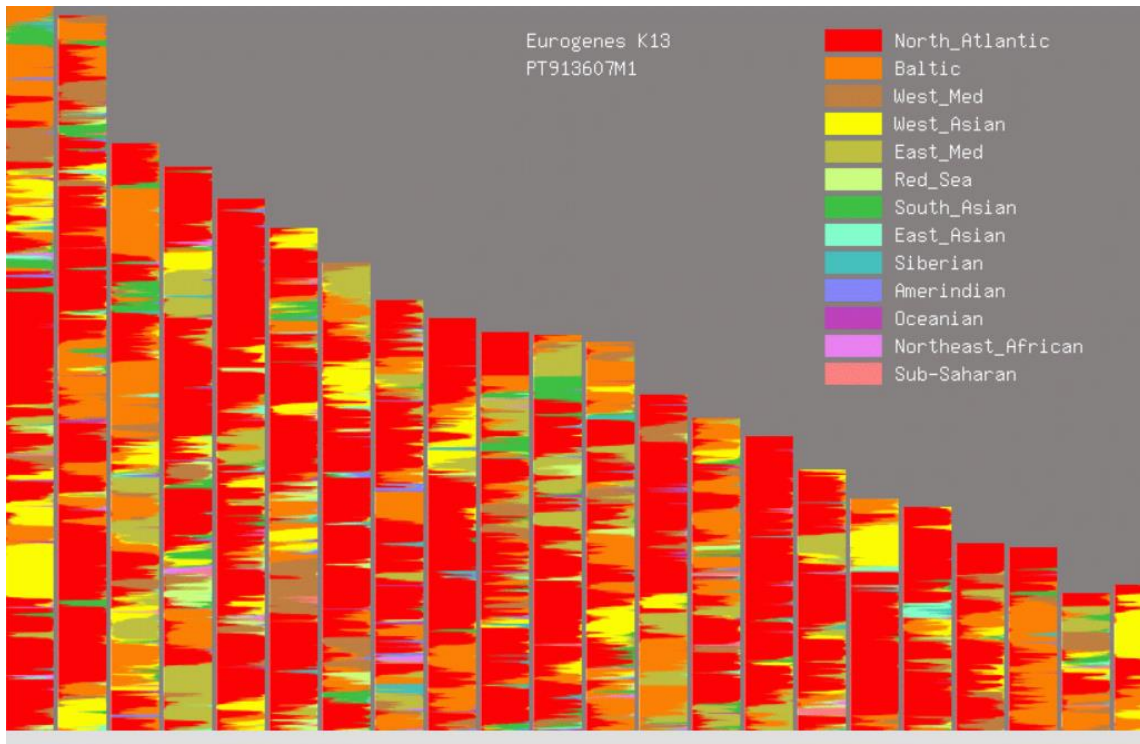
As noted above, since the original version of this manuscript was written, the author has had his father’s DNA (supposedly 100% English ancestry) tested, and employing the various Gedmatch calculators he has typically 1.5% Native American, and an inspection of the chromosome paintings shows that the chromosome 10 segment was indeed inherited from him. The phased data only shows what ancestry comes from each parent, and is shown well in the Gedmatch Eurogenes K13 Chromosome Paintings below.

Paternal Side



The East Asian / Native American segment on chromosome 10 is seen clearly here.

Maternal Side



As seen in the above diagram of the relative position of various ancestral segments, the Native American (“Beringian”) segment on chromosome 8, and (even more clearly) the one on chromosome 18 were inherited by the author from his maternal side.

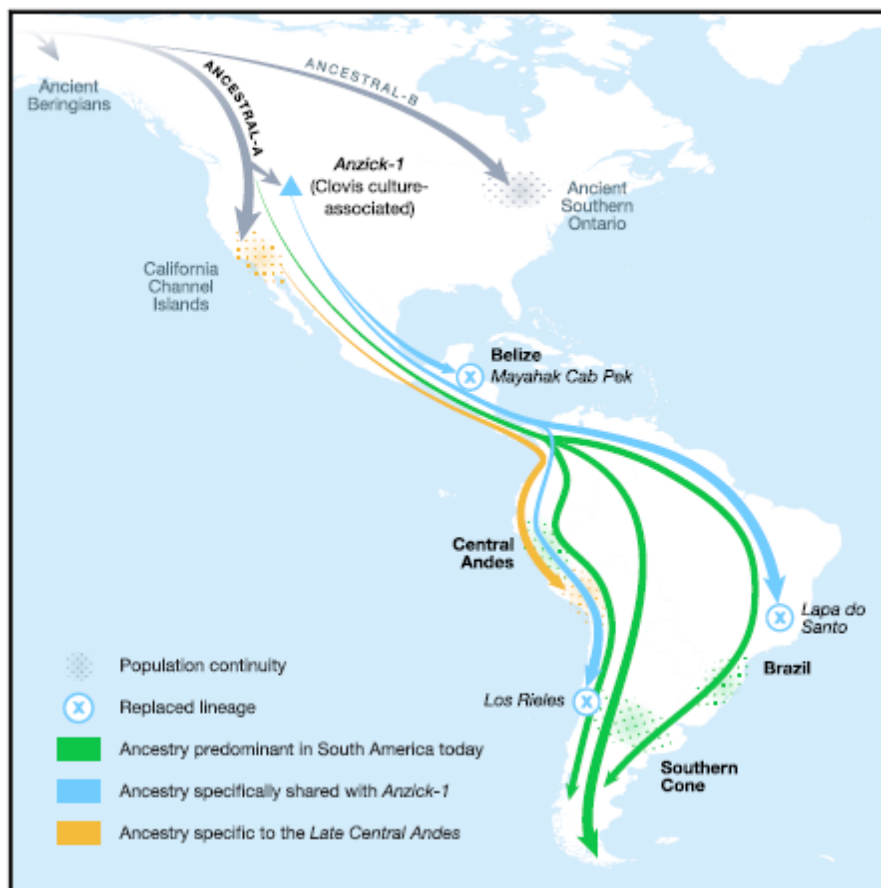
It is important to note that DavidW found that unadmixed English and Irish did not show these “Bering Strait” segments. Any facsimile tended to be “surrounded” by Europeans and a scattered, indecipherable, group of Eurasians. So there was no pattern extant. In David’s words, there is the occasional European with some anomalies, but these are *blips that usually don't even get them past the last Frenchmen on the MDS plot*.

DavidW is very confident about his approach in that, *this haplotype matching software doesn't seem to make mistakes* (DavidW, personal communication, 16 March 2011).

Perhaps at some point these plots will tell us about each segment’s migrational history so that in effect each segment will tell its own story. This task will be easier with a larger selection of segments, and clearer signals in the analysis via more reference samples. As noted, the segments in the author’s other study of this subject (those of chromosome 8 and particularly chromosome 18) were distinctive enough to be labelled “Beringian” by DavidW, and to fit within recent academic studies which use the same terminology for a group of Native Americans who migrated to Southwestern Ontario.

Posth et al. published an article entitled, “*Reconstructing the Deep Population History of Central and South America*” (Cell, 175, 2018), pp. 1-13). They re-analyzed the data by authors such as Scheib et al. (2018) and found that there was no apparent contribution of the Eastern North American Group (“Ancient Southern Ontario”) to the present - day genomic spectrum of South Americans. They in fact give the Southern Ontario group (apparent ancestors of the Wendat – Huron or Algonquins) their own migration (Ancestral – B) which split from the group that made up the early migrations to Western North America and South America (Ancestral – A) sometime between 17,500 and 14,600 years ago. Doubtless there was some later mixture in North America between the A and B groups but to what extent is unknown. The Clovis sample is classified with the A group, which was also the predominant group seen to date in early South America, but this Clovis input appears to have largely disappeared there. This is of some importance when we later integrate this academic finding with the data pertaining to the author. The A and B “split” is represented in the article in the following illustration. While the maternal segments on chromosomes 8 and 18 conform to the description of “Ancestral – B”, the paternal segment on chromosome 10 would appear to emerge from among the more general “coastal route” group “Ancestral – A”.

Graphical Abstract



Origin of Segment on Chromosome 10: The author’s father was born in Canada, but both of his parents were born in East Anglia (Norfolk and Lincolnshire), England. The only ancestor who could be considered as a “likely candidate” for having Native American ancestry is the great great grandmother of KF, Maria Hannah (MILLER) WORRILL. She was married to a British soldier in 1795 in Quebec City, Canada. Their only surviving child was Rev. Thomas WORRILL (1796 Quebec City, Quebec, Canada to 1873 Selby, Yorkshire, England). In his lengthy obituary (*Primitive Methodist Magazine*, 1874, p.304) it was reported that, “*His father was an Englishman, but his mother was an American lady.*”

Conclusion: It is worth noting that when the above testing was completed it was state of the art. However, the author did not have the FTDNA and Ancestry test data for his sister and father, both of whom display considerably more Native American percentages. Doubtless if this data had been submitted to Dr. McDonald and DavidW there would have been more segments labelled “Beringian” or “Amerindian” in their testing. Therefore, we must “make do” with the author’s only paternal NA segment to be flagged in both testing methods – one which, unfortunately, struggles hard to tell its own story beyond the generic “Amerindian”.

Dr. David K. Faux

20 May 2023