

A Y-Chromosome Signature of Polygyny in Norman England

Michael R. Maglio

A thirty-seven marker short tandem repeat (STR) genetic analysis of Y-chromosomes reveals an unnoted modal haplotype showing a significant association with surnames claimed to have descended from the Norman dynasties and allied with William, Duke of Normandy, during his conquest of England. This suggests that such phylogenetic prevalence is a biological record, supports the reliability of early genealogies and illustrates the link between power and polygyny in European society.

There are no documented living direct male-line descendants of William the Conqueror for testing purposes. A standard process for common ancestor haplotype analysis compares y-DNA results from similar surnames with well documented genealogies. The identification of William's haplotype is complicated due to the lack of documented genealogies and the adoption of surnames primarily occurring after his lifetime. There is no commonality among the surnames adopted by William's extended clan. There was a tendency for the surnames to be toponyms, derived from hereditary lands (Green 2002). The practice of polygyny added to the variety of surnames. The wealthy could afford to have both a wife and multiple mistresses (Betzig 1995), often siring more illegitimate offspring than legitimate. This same wealth increased the probability of successfully propagating the haplotype belonging to the line of nobility from Rollo to Henry I.

To determine a haplotype, a survey of an extended Norman population of allied surnames was completed (Graf 2010, Sykes 2000). Surname selection was based on William's companions during the Battle of Hastings, many who were his kinsmen, Norman allies who were rewarded with English land and surnames that were the result of polygyny. Similar research for the the U₁' Ne'ill haplotype started with a geographical selection and then a subsequent reduction by historical surnames (Moore et al

2006). The Genghis Khan research featured a geographical population only (Zerjal et al. 2003). The Norman selection includes twenty-seven surnames, 3,800 records and 6 common European haplogroups (Y Chromosome Consortium 2002). The surnames tested: Bartelott, Beaumont, Bruce, Clifford, Corbett, D'Arcy, Devereaux, Gifford, Hereford, Lindsay, Molyneaux, Montgomery, Mortimer, Mowbray, Neville, Norman (for origin), Norton, FitzOsbern, Pearsall, Ramsey, Spencer, St. Clair, Stewart, Sutton, Talbott, Umfreville and Warren.

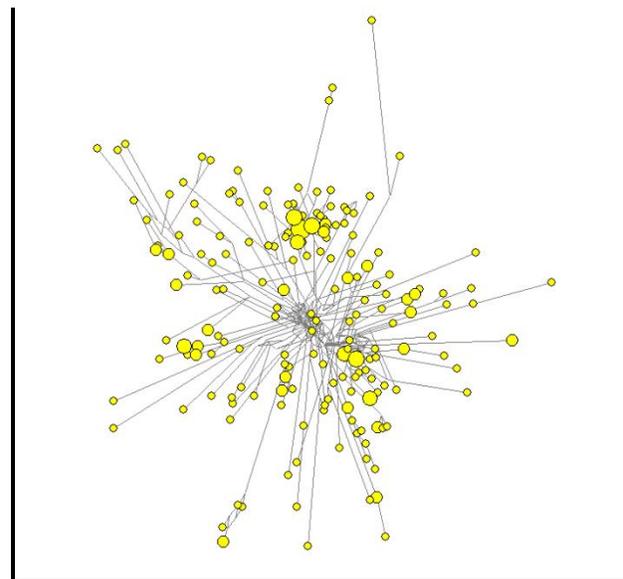


Figure 1 MJ network of Y DNA from haplogroup I1 with Norman dynasty surnames (n = 222). Note sub-clusters representing unique surnames and the absence of a coherent central cluster.

The resulting set was further reduced to those records that had the following 37 markers tested: *DYS393, DYS390, DYS19, DYS391, DYS385a, DYS385b, DYS426, DYS388, DYS439, DYS389i, DYS392, DYS389ii, DYS458, DYS459a, DYS459b, DYS455, DYS454, DYS447, DYS437, DYS448, DYS449, DYS464a, DYS464b, DYS464c, DYS464d, DYS460, Y-GATA-H4, YCAIIa, YCAIIb, DYS456, DYS607, DYS576, DYS570, CDYa, CDYb, DYS442 and DYS438.*

Haplotype data from this analysis is available in [Table 1](#), [Table 2](#), [Table 3](#), [Table 4](#), [Table 5](#) and [Table 6](#).

The analysis of records within each haplogroup to determine relationships across surnames shows a lack of correlation and eliminates groups E1b, G2a, I2, J and R1a.

Haplogroup I1, while showing relationships across eight surnames, did not form a coherent median-joining cluster (fig. 1). The time to most recent common ancestor (TMRCA) on the unique haplotypes within

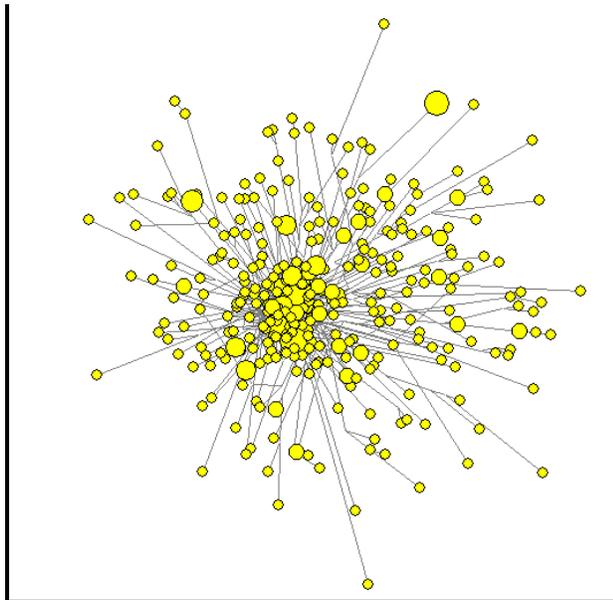


Figure 2 MJ network of 37-STR marker Y DNA haplotypes sampled from Conqueror allied surnames (n = 375). Each circle represents a unique haplotype, with size proportional to frequency. Sampling shows a coherent cluster.

this group (n = 29) is estimated to be 1,250 years ago, predating Rollo.

The remaining haplogroup, R1b, shows interrelationships across 25 of the 27 surnames and forms a coherent cluster (fig. 2) consistent with a common origin. Compare the baseline MJ network sampled from 2,600 randomly selected R1b records from the British Isles showing multiple clusters (fig. 3).

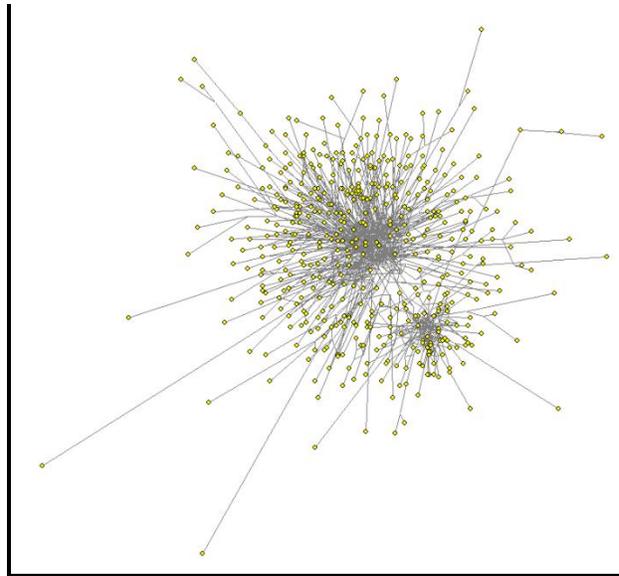


Figure 3 Baseline MJ network of random British Isles Y DNA from haplogroup R1b (n = 481). Sampling shows two distinct clusters.

Filtering the allied surname R1b records by the first 12 markers results in a segmentation of 471 haplotypes. One haplotype outweighs the others with 8.5% of the records and aligns with the Atlantic Modal Haplotype (AMH). Half of the first 12 markers have fairly high mutation rates, making them poor filters. Filtering by the first 12 “slow” mutating markers (Zhivotovsky 2004) results in 140 haplotypes and one haplotype which predominates with 43% of the records. These markers become the basis for the William the Conqueror Modal Haplotype (WCMH 37 marker haplotype - 13-24-14-11-11-14-12-12-12-13-13-29-17-9-10-11-11-25-15-19-29-15-15-17-17-11-11-19-23-15-15-17-17-36-37-

12-12). The SNP for this haplotype appears to be downstream from R-P312.

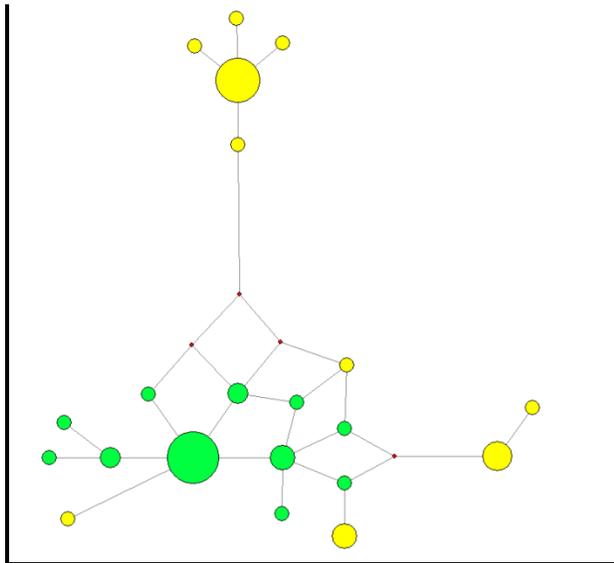


Figure 4 MJ network of Y DNA sampled from Conqueror allied surnames (n = 48) featuring the WCMH as its modal haplotype and having a coherent cluster (green circles) accounting for over half of the sample.

Calculating the time to most recent common ancestor (TMRCA) across 21 of the allied surnames of the 27 total (n = 152) supports an origin of ~1,080 years ago (95% confidence).

Genealogical evidence dating back 1,000 years can be sparse as well as fictitious. Randomly selecting surnames from the British Isles gives a scattershot of results without coherence. Selection based on genealogy, as anecdotal as it may be, results in a coherent cluster of individuals whose common ancestor lived between the times of Rollo and his 3rd great grandson, William. Surname adoption and polygyny combined for a wide spread of names. Dynastic wealth, while not a guarantee, paved the way for reproductive success and the transmission of this Norman haplotype. The following surnames (Bartelott, Beaumont, Bruce, Clifford, Corbett, D'Arcy, Devereaux,

Gifford, Molyneaux, Montgomery, Mortimer, Norton, FitzOsbern, Pearsall, Ramsey, Spencer, St. Clair, Stewart, Talbott, Umfreville and Warren) united with the WCMH have a strong Y DNA correlation to William the Conqueror.

Acknowledgements

I thank all of the DNA donors who have made their results publically accessible for review. Special thanks to Whit Athey and Dean McGee for making their DNA analysis websites available and Steve St. Clair and his website for pointing me in the right direction.

Web Resources

- Fluxus Engineering, <http://www.fluxus-engineering.com/sharenet.htm> (for NETWORK)
- St. Clair Research: Family Stories – William, <http://www.stclairresearch.com/content/storiesConqueror.html>
- Whit Athey's Haplogroup Predictor, <http://www.hprg.com/hapest5/hapest5b/hapest5.htm>
- Y-Utility: Y-DNA Comparison Utility, http://www.mymcgee.com/tools/yutility.html?mode=ftdna_mode

References

- Bandelt HJ, Forster P, Rohlf A (1999) Median-joining networks for inferring intraspecific phylogenies. *Mol Biol Evol* 16:37–48
- Betzig L (1995) Medieval monogamy. *J Fam Hist* 20:181–216
- Graf OM, Zlojutro M, Rubicz R, Crawford MH (2010) Surname distributions and their association with Y-chromosome markers in the Aleutian Islands. *Hum Biol.* 2010 Dec;82(5-6):745-57

- Green JA (2002) *The Aristocracy of Norman England*. Cambridge University Press
- Moore, LT, McEvoy B, Cape E, Simms K, Bradley DG (2006) A Y-Chromosome Signature of Hegemony in Gaelic Ireland. *Am J Hum Genet*, 78:334–338.
- Sykes B, Irven C (2000) Surnames and the Y chromosome. *Am J Hum Genet*. 2000 Apr;66(4):1417-9
- Y-Chromosome-Consortium (2002) A nomenclature system for the tree of human Y-chromosomal binary haplogroups. *Genome Res* 12:339–348
- Zerjal T, Xue Y, Bertorelle G, Wells RS, Bao W, Zhu S, Qamar R, Ayub Q, Mohyuddin A, Fu S, Li P, Yuldasheva N, Ruzibakiev R, Xu J, Shu Q, Du R, Yang H, Hurles ME, Robinson E, Gerelsaikhan T, Dashnyam B, Mehdi SQ, Tyler-Smith C (2003) The genetic legacy of the Mongols. *Am J Hum Genet* 72:717–721
- Zhivotovsky LA, Underhill PA, Cinniog˘lu C, Kayser M, Morar B, Kivisild T, Scozzari R, Cruciani F, Destro-Bisol G, Spedini G, Chambers GK, Herrera RJ, Yong KK, Gresham D, Tournev I, Feldman MW, Kalaydjieva L (2004) The effective mutation rate at Y chromosome short tandem repeats, with application to human population divergence time. *Am J Hum Genet* 74:50–61