Tribes of Britain Analysis

Thank you for requesting our *Tribes of Britain* analysis. We have now compared your Y-chromosome results with thousands of genetic signatures from Britain, Ireland, continental Europe and Scandinavia.

We are pleased to tell you that, following these comparisons, we have identified your Y-chromosome as being of probable ***Norse Viking*** origin. We arrived at this conclusion by matching the details of your Y-chromosome signature against a reference database which contains details of different Y-chromosomes and their geographical distribution. From these comparisons we can infer that your Y-chromosome belongs to a group which is found frequently in regions like Orkney, Shetland, the Outer Hebrides and Iceland, known from historical records to have been settled by Norse Vikings. It is less common in other parts of Britain with no history of Norse settlement, being virtually absent in parts of Wales and Ireland distant from the sea. The few examples of Norse Viking chromosomes found in southern England are probably descended from the Norman conquest of 1066. Normans were themselves the descendants of Norse and Danish Vikings who settled in northern France only a hundred years earlier, in the 10th century.

The Viking Age began in Britain with the sacking of the monastery at Lindisfarne, off the coast of Northumbria in 793 AD, and was followed by an attack on the St Columba's Church at Iona two years later. These assaults heralded a continuous and turbulent period of Norse cultural and political influence that lasted until the fifteenth century. What triggered the explosive expansion of Scandinavians from their homeland after a long period of self-sufficient isolation on the northern margins of Europe is unclear, but it is probably connected with the pressure on scarce agricultural land caused by an increasing population. This was exacerbated by the rules of inheritance, which transferred land title to the eldest son, compelling younger brothers to seek their fortune abroad. The means of their expansion was a mastery of the seas achieved by advanced construction of the 'dreki', or dragon ships, capable of long-distance voyaging on the storm-tossed northern oceans.

The Vikings soon dominated the routes from Norway 'west over sea' to Shetland, Orkney and the Hebrides and on to Ireland, where they established trading posts at Dublin, Waterford, Wexford and Limerick. Though there is no disguising the evidence that the early Viking raids were extremely violent and rapacious (the name '*Viking*' comes from the Old English for pirate, itself probably derived from the Norse 'viken', meaning "men of the fjords"), the search for somewhere to live soon began to replace the quest for loot and glory.

At first there was fierce resistance to the invaders but before long alliances, often sealed by marriage, were formed between Norse and Celtic lords. Eventually the

centralised power of Norway itself declined as lords in thrall to the Norse court were defeated by local uprisings. They were eventually expelled from Ireland after the High King, Brian Boru, defeated the Viking armies at the battle of Clontaf in 1014. After a succession of land and naval battles, the Norse were finally driven from the west of Scotland and the Hebrides in the 12th century by *Somhairle mac Gillebride*, also known as Somerled, whose descendants went on to form the great Clan Donald. Norse control eventually came to an end in 1472 when the Isles of Orkney and Shetland reverted to Scottish sovereignty as part of the dowry of Margaret, bride of James III.

It is very likely that your ancestor was involved in these power struggles, though on which side it is impossible to be sure from the genetics alone. Neither can we tell whether your ancestor settled in Britain peacefully or not, though you can be certain that, whoever he was, he braved a dangerous journey into the unknown when he left his homeland. He must have been successful and fathered sons, but whether by Celtic or Viking women we cannot tell. Through sons and grandsons, his Y-chromosome has been passed down virtually unaltered through time to you, where it lives on today in every cell of your body. Requiring no written records for its transmission, your Y-chromosome is a message from the past. It is truly your genetic legacy. If you have sons, it will continue its journey into the future through them.

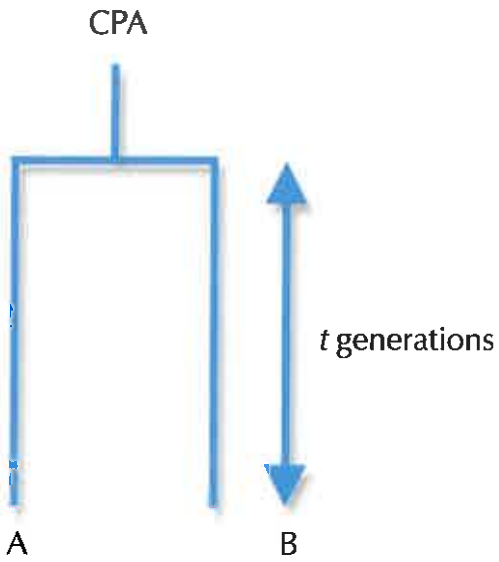
You can discover more about your ancestors and your Y-chromosome through the Oxford Ancestors website (www.oxfordancestors.com) including the opportunity to contact others with the same or similar genetic signatures by clicking on 'DNA Connections' You may also like to read Professor Bryan Sykes' latest book *Blood of the Isles*, which explores the genetic origins of Britain and Ireland based on his recently completed ten-year survey. *Blood of the Isles*, published in the US as *Saxons, Vikings and Celts,* can be found in bookshops and signed copies can be obtained via our website.

Thank you for your interest in Oxford Ancestors and congratulations on discovering more about your ancient ancestry.

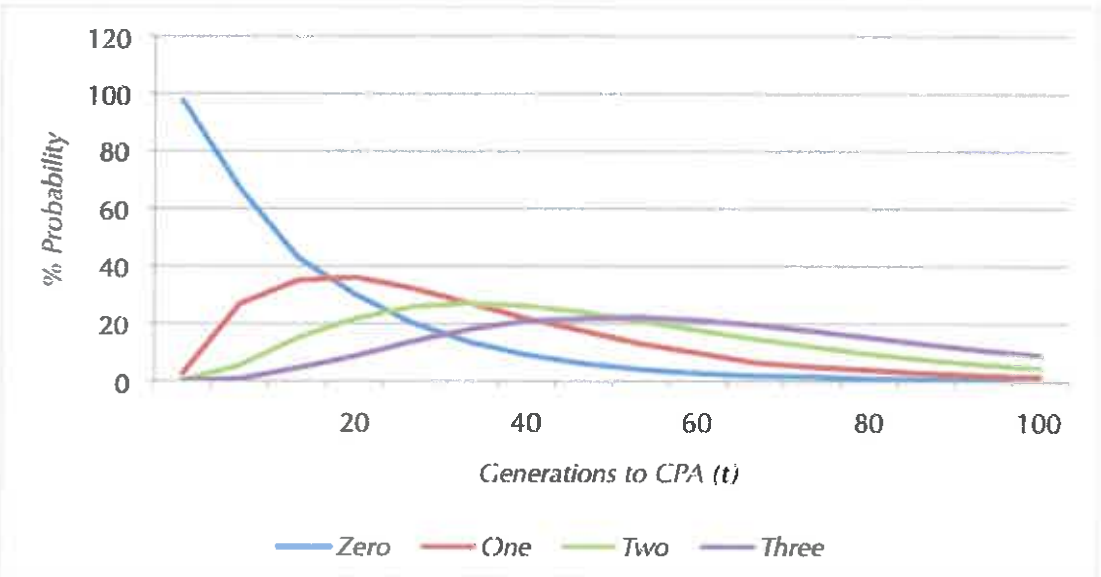
Please note that the interpretations supplied with your *Tribes of Britain* analysis are based on the assumption that your paternal ancestry can be traced to Britain or Ireland. The interpretations based on your Y-chromosome result give what we consider to be the *most likely* identity of the origin of your paternal ancestor or the historical group to which he belonged when he first reached these shores.

Y CHROMOSOMES AND THE POISSON DISTRIBUTION

Rare random events like Y-chromosome mutations follow what is called a Poisson distribution. This is a statistical tool widely used to plot and predict the characteristics of events of this kind, such as following the decay over time of radioactive atoms or, famously, the number of men in the Prussian Army kicked to death by a horse each year during the nineteenth century. For Y-chromosomes it is used to estimate how long ago the men that carry them last shared a patrilineal ancestor.



Here two men, A and B, are separated from their most recent common paternal ancestor (CPA) by *t* generations of descent. In the graph below we have plotted how *t* can be estimated by comparing the two Y-chromosome signatures.



The graphs plot how the probabilities for *t* change over time in cases where two Y-chromosomes differ by zero, one, two or three mutations in the Oxford Ancestors 15 marker set. Y-chromosomes differing by more than three mutations are unlikely to have a CPA within the last 1000 years and are not illustrated.

The number of generations (*t*) back to the CPA is plotted along the bottom while the axis on the left shows the probability, as a percentage, for each value of *t*. These graphs are plotted from the Y-chromosome mutation rate using the Poisson statistic.

The blue line follows the distribution of t where two Y-chromosomes are identical, with zero mutational differences. If these chromosomes belonged to two brothers, when t=1, the chances of their being exactly the same across the fifteen marker set is almost 100% (actually 97.5%). Following the blue line, the probability declines until, after twenty generations from the CPA, the chances of the two Y-chromosomes matching exactly falls to about 30%. After that it continues to decline until, after 100 generations, it is very close to zero.

The red line follows the distribution of *t* when there is one mutational difference between the two Y-chromosomes. This starts off at 2.3% when t =1, that is after one generation, then climbs to a maximum value of 37% after 15 generations then falls away. The green and purple lines illustrate the values for t when the Y-chromosomes being compared have two and three mutational differences respectively.

Another way of using the graphs is to find out when the probabilities for *t* reach their maximum values. You might want to do this, for instance, where you know the genetic signature of two Y-chromosomes and want to find the likeliest value for *t*. For identical Y-chromosomes, traced by the blue line, it is at 0 generations and declines steadily after that. But even after 50 generations, over 1000 years ago, there is still a small residual probability (3%) that no mutations have occurred on either line of descent and the chromosomes still match each other exactly at all fifteen markers. For Y-chromosomes with one mutational difference, the likeliest value for t is 20 generations after which the probabilities slowly decline. For two mutations the most probable value for *t* is 35 generations while for chromosomes differing by 3 mutations the most likely value is 55 generations.

The shapes of the curves are also instructive. As the number of mutations between two Y-chromosomes increases, the plots become increasingly flat. This means that the confidence in the accuracy of *t* diminishes as the mutational differences between the two Y-chromosomes increase.

This scope for inaccuracy is an unavoidable consequence of the random nature of genetic mutation of the Y-chromosome. Neither is the accuracy of the estimate improved by using more markers, which tends to flatten the curves even more. Consequently, although the Poisson distribution is a useful guide to the behaviour of mutations over time, we do not recommend using genetic differences between Y-chromosomes alone to fix the time of a common paternal ancestor.