

**Y-CHROMOSOME GENETIC TESTING AS AN ELEMENT OF A
KIPLING ONE-NAME STUDY**

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TITLE

Y-CHROMOSOME GENETIC TESTING AS AN ELEMENT OF A KIPLING ONE-NAME STUDY

ABSTRACT

Foundations are laid for a reconstruction of the family tree(s) of the Kipling surname using the DNA/documentary dual approach of Pomeroy (2009, 2010). DNA evidence is also gathered to cast additional light on the origins of the family containing the author and poet Rudyard Kipling.

Census data is used to compile a database of male Kiplings in 1911. Using various data sources, these are then traced back in time to a set of as few as possible common ancestors. Tracing forward in time, BMD data is used to link to Kiplings alive today.

A variety of routes, including social electronic media, are used to establish contact with living male Kiplings who are then invited to provide a DNA sample for testing. Invitations are, where possible, selective to ensure coverage of as many different ancestral family groups as possible in the time available.

Y- chromosome DNA results are compared over at least 30 markers and relationships between the ancestral groups conjectured by the predicted haplogroup and the number of allele matches.

Conclusions about the presence of and time to common ancestors are drawn and the implications for existing family trees discussed. The hypothesis of single origin proposed in Hey and Redmonds is critically examined.

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NOMENCLATURE

BMD – Birth, marriage and death.

NPE – Non-Paternal Event

SNP – Single Nucleotide Polymorphism

STR – Single Tandem Repeat

TMRCAs – Time to Most Recent Common Ancestor

Some technical genetic terms are used in this paper with the specific meanings described below:

- Autosomal – A DNA test which examines DNA inherited from all ancestral lines
- Haplotype – The values a particular person's y-DNA exhibits at a given set of STR markers
- Haplogroup – A broad group of people with similar haplotypes.
- Deep clade – A DNA test which examines the presence or absence of particular SNPs to place participants into specific haplogroups, and so potentially draw conclusions as to the population groups of which their distant ancestors formed part going back many millennia.

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1. INTRODUCTION

The first reference to the Kipling surname is in regnal year 3 of Edward III (1330/1) in the manor rolls of Lartington in Romalldkirk parish in the North Riding of Yorkshire, where there is mention of a William de Kyplyng.¹ There is a further reference in the Cotherstone (also in Romalldkirk parish) rolls in 13 Hen IV (1411/12) to, presumably, a subsequent William Kipling.² Manorial roll entries and a will of John Kipling (“to be buried at Romalldkirk”) in 1542 precedes a large number of entries in the Romalldkirk parish register (from 1579) and those of neighbouring parishes.^{3 4}

In 1577, a Robert Kyplyn was married at St Botolph’s, Aldgate, London and a Bryan Kipling sailed to Massachusetts on board the *Plough* in 1631.^{5 6}

By 1881, the name is still predominantly found in the North Riding of Yorkshire and Durham, although is also by then well-established in the USA, Canada and Australia.^{7 8}

The Kipling name is generally considered to have derived from the lower Swaledale hamlet of Kiplin (sometimes Kipling), written as Chipeling in Domesday Book.^{9 10} A

¹ Plantagenet-Harrison, G. H. de S. N. (1876) *The History of Richmondshire (Wapentake of Gilling West)*. London and Aylesbury: Hazell, Watson and Viney. p379

² Ibid. page 362

³ Archdeaconry of Richmond wills. West Yorkshire Archive Service. RD/AP1 53/2

⁴ Romalldkirk parish registers (transcriptions). North Yorkshire Records Office.

⁵ Register of St Botolph, Aldgate. 30 Jun 1577. Available on-line at Ancestry.co.uk. <http://search.ancestry.co.uk/Browse/view.aspx?dbid=1624&path=City+of+London.St+Botolph%2c+Aldgate.1558-1625.509&sid=&gskw=&cr=1>. Last accessed 14 July 2012.

⁶ Banks, C. E. (1885) *Colonel Alexander Rigby : A Sketch of his Career*. Page 38. USA: Privately printed. Transcription available on-line at Internet Archive. http://www.archive.org/stream/colonelalexander00bank/colonelalexander00bank_djvu.txt. Last accessed 14 July 2012

⁷ PublicProfiler gbnames. Available online at gbnames.publicprofiler.org. Last accessed 14 July 2012.

⁸ 1880 US Census, 1881 Canadian Census. Available online at Ancestry.co.uk. Last accessed 13 July 2012

⁹ Hay, D. and Redmond, G (2002) *Yorkshire Surnames and the Hearth Tax of 1762-1673* (Borthwick Paper No. 102). York: Borthwick Institute of Historical Research, University of York. Page 17

possible alternative source sometimes mentioned is Kiplingcotes in the East Riding of Yorkshire, although apart from a 1516 will of a Roger Kyplyng of Holderness (and another Holderness will in 1587), no early occurrences of the name in the East Riding have been found.¹¹

The most well-known bearer of the name is the author and poet Rudyard Kipling (1865-1936), whose ancestry has only been traced back four generations by traditional methods.¹²

Considerable research using traditional genealogical methods has been carried out, mostly unpublished, usually of particular family groups, although no complete Kipling one-name study has been attempted.

This project has the main objective of using y-chromosome DNA haplotype comparisons, in conjunction with paper-based research methods, to establish the foundation for a full Kipling one-name study. In particular, it aims to answer the questions:

- What is the smallest number of common male ancestors to which living Kiplings can confidently be mapped using traditional genealogical techniques?
- Can y-DNA evidence add to or diminish support for existing but unproven hypotheses about the linkages between these common ancestral groups?
- Is there support for the tentative hypothesis in Hay and Redmond that the Kipling name originates from a single common male ancestor or is there more support for multiple origins?¹³
- What, if anything, can be said about the earlier family history and deeper paternal genetic origins of Rudyard Kipling?

¹⁰ *Great Domesday Book*. National Archives. Folio 309v

¹¹ Yorkshire Archeological Society. Listing of Wills in the York registry.

¹² Ankers, A. R. (1988) *The Pater*. Otford: Pond View Books. Page viii.

¹³ Hay, D. and Redmond, G (2002) *Yorkshire Surnames and the Hearth Tax of 1762-1673* (Borthwick Paper No. 102). York: Borthwick Institute of Historical Research, University of York. Page 17.

Only a limited number of single-name y-DNA studies have yet been carried out and reported on. This project will add to the broad database of such studies, including additional experience on more and less successful methods of identifying and recruiting candidates for testing.

It will also be of interest to those with Kipling ancestry and to the wider audience interested specifically in the family background of the author Rudyard Kipling.

It will also advance the author's personal experience and skill in both traditional and new genealogical techniques.

2. REVIEW

The use of DNA comparisons in genealogy is a recent development, even more so in its application to single surname studies. The literature in the field is therefore relatively sparse, and what has been written is perforce recent. Even so, the pace of development of commercially available DNA testing means that even quite recently written material might be out of date in some respects.

The available literature can usefully be analysed in three categories. Firstly, material which presents the wider background of human population genetics, both from a biological and an anthropological approach. Secondly, material oriented at genealogists and the uses which may be made of DNA testing. Finally, material specifically oriented at the organisation of a DNA-led genealogical study.

Turning to the first category, a very recent publication is *Human Population Genetics* by John H. Relethford.¹⁴ This book sets out the main theories of genetics against the specific background of human genetics, which contrasts with that of the standard textbooks in the field such as *Principles of Population Genetics* by Hartl and Clark which is set against the background of animal genetics in general.¹⁵ Relethford also eschews some of the more complex mathematics of Hartl and Clark, without oversimplifying. He presents the theory of mutation, which underlays y-chromosome and mitochondrial genealogical uses and includes a number of case studies of interest to genealogists including the colonisation of Polynesia and genetic admixture in African-American populations.

The Seven Daughter of Eve by Bryan Sykes although written for the popular market, provides a very useful insight into the early days of DNA testing to establish links between individuals across the generations. The main focus is on mitochondrial DNA, as one might anticipate from the title, but illustrates nicely the development over millennia of a haplotree from a single source and how population group migration has led to the genetic diversity we see today.¹⁶

¹⁴ Relethford, J H (2012) *Human Population Genetics*. Hoboken, NJ: John Wiley & Sons Inc

¹⁵ Hartl, D.L. and Clark, A.G. (2007) *Principles of Population Genetics*. 4th Edition. Sunderland, MA: Sinauer.

¹⁶ Sykes, B. (2001) *The Seven Daughters of Eve*. London: Transworld Publishers

A similar book, although somewhat less personally anecdotal, is *The Scots: A Genetic Journey* by Moffat and Wilson.¹⁷ This examines the waves of incomers to Scotland over the centuries and uses DNA comparisons, mainly y-chromosome, together with archaeological, linguistic and historical evidence to shed light on the origins of the population today.

Moving on to material specifically produced for genealogists, *Surnames, DNA and Family History* by Redmonds, King and Hey is mainly a work on the origins of surnames in England and Wales, on to which has been added an explanation of y-chromosome genetics and the ability of testing to support or contradict the hypothesis of the single origin of a particular name.¹⁸ It provides some examples of actual DNA y-chromosome studies, although only four pages are devoted to single name studies. *Family History in the Genes* by Chris Pomery has the advantage of being written by the organiser of one of the more long-standing single-name projects in the UK and is written more for the amateur family historian than for the academic genealogist.¹⁹ It provides an overview of a number of ‘success stories’ and concludes with a short chapter on how to organise a DNA project, drawing on the author’s own experience.

Amongst published papers, ‘What’s in a name? Y chromosomes, surnames and the genetic genealogy revolution’ by King and Jobling provides a useful introduction to the use of DNA testing for surname projects, although as one might expect with an author in common, there is some overlap with the later book by Redmonds, et al mentioned earlier.²⁰ ‘Estimating the Time to the Most Recent Common Ancestor for the Y chromosome or Mitochondrial DNA for a Pair of Individuals’ by Bruce Walsh establishes the mathematics around the probabilities associated with STR marker mutations, leading to a method for computing a best estimate and range for the time to a common ancestor of two differently-haplotyped individuals (y-chromosome or mitochondrial).²¹

Single name projects predominantly use STR alleles for comparison. However haplogroup projects typically search for differentiating SNPs, causing deep clade family history studies

¹⁷ Moffat, A. and Wilson, J.F. (2011) *The Scots: A Genetic Journey*. Edinburgh: Birlinn Limited

¹⁸ Redmonds, G., King, T. and Hey, D. (2011) *Surnames, DNA and Family History*. Oxford: Oxford University Press.

¹⁹ Pomery, C. (2007) *Family History in the Genes*. Richmond: The National Archives

²⁰ King, T.E. and Jobling, M.A. (2009) What’s in a name? Y chromosomes, surnames and the genetic genealogy revolution. *Trends Genet.* 25(8): 351-360

²¹ Walsh, B. (2001) Estimating the Time to the Most Recent Common Ancestor for the Y chromosome or Mitochondrial DNA for a Pair of Individuals, *Genetics* 158 : 897-912

and academic population studies to overlap. Reports on a variety of broader and narrower haplogroup studies are accessible via the FTDNA website. For example, members of the R1b-U152 project have access to a library of relevant papers and results, such as ‘A Short Essay about the U152 Haplogroup’ by Tibor Feher.²²

A recent publication which specifically addresses the ways in which modern electronic media can be used to organise and publicise family history DNA projects is *DNA and Social Networking* by Debbie Kennett, herself the organiser of a number of international DNA projects.²³ As well as non-recombinant DNA testing, Kennett explains the uses of autosomal DNA SNPs for providing evidence for recent family relationships other than along the strict male and female lines. Fully half the book systematically examines all significant forms of electronic media, serving both as a comprehensive checklist of possibilities and as a sequence of tip sheets should a particular approach be considered appropriate.

A number of papers focus specifically on the organisation of DNA-assisted single surname projects. In the *Journal of One-Name Studies*, Meates passes on the benefit of personal experience in ‘Some tips for establishing a DNA Project for your one-names study’.²⁴ This work is carried forward by Pomery in two linked papers in the *Journal of Genetic Genealogy*, ‘The Advantages of a Dual DNA/Documentary Approach to Reconstruct the Family Trees of a Surname’ and ‘Defining a Methodology to Reconstruct the Family Trees of a Surname Within a DNA/Documentary Dual Approach Project’.^{25 26} In the former, the author argues that in a country where extensive transcribed and searchable BMD and census data is available on-line, such as the UK, it is efficient to carry out a surname reconstruction using both documentary evidence and y-chromosome STR testing, as a considerable economy of scale (and cost) results relative to the alternative approach of testing all comers with the target surname, as only one or two tests will be required of any group credibly linked together by documentary means. In the latter paper, Pomery establishes a structured approach using the

²² Feher, T. (2010) *A Short Essay about the U152 Haplogroup*. Available online: <http://www.familytreedna.com/public/R1b-U152/default.aspx?section=results>. Last accessed 28 Apr 2012

²³ Kennett, D. (2011) *DNA and Social Networking*. Stroud: The History Press.

²⁴ Meates, S.C. (2009). Some tips for establishing a DNA Project for your one-name study. *Journal of One-Name Studies*. Vol 9, Issue 3, 8-10.

²⁵ Pomery, C. (2010) The Advantages of a Dual DNA/Documentary Approach to Reconstruct the Family Trees of a Surname. *Journal of Genetic Genealogy* 6(1).

²⁶ Pomery, C. (2010) Defining a Methodology to Reconstruct the Family Trees of a Surname Within a DNA/Documentary Dual Approach Project, *Journal of Genetic Genealogy* 5(2).

dual approach, from conception to completion. He suggests that the approach is reasonably feasible for a surname with up to 5000 current holders. The *Journal of Genetic Genealogy* is important source of relevant background for all types of DNA-related work.

Irvine, in 'Towards Improvement in y-DNA Surname Project Administration', focuses more on an analysis of the different techniques used by DNA-based surname projects., including the use of modal haplotypes, triangulation, the penetration of testing into the total population and the differing approaches to classification of close matches (for which the author proposes a solution based on FTDNA's TiP facility.²⁷ Further useful analytical techniques in projects, particularly ones with larger volumes of data, are presented in 'The Use of Correlation Techniques for the Analysis of Pairs of Y-Chromosome DNA Haplotypes (Parts I and II)'.²⁸ Amongst other tools, the author proposes an approach for establishing the order in which different haplotypes break away from the original.

The FTDA website also contains a range of explanations of how genetic distance is calculated and about the peculiarities of some markers, including DYS389 and DYS464 where solutions for properly integrating results for these markers into genetic distance calculations are provided.²⁹

Finally, turning specifically to the Kipling name, the only published pedigree is that which links the Kipling family of Newhouses, Romalldkirk, into the Powell family (the family of Robert Baden Powell, the hero of Mafeking).³⁰ A number of other partial Kipling trees have been made accessible via Ancestry.com or other genealogical websites, including one by Michael Hansell of the family of Rudyard Kipling.³¹ Unpublished work includes an extensive collection of notes and tree fragments compiled by Dennis and Vivienne Middleton and a list of over 1200 Kipling births and marriages compiled by Brian Kipling and others.

²⁷ Irvine, J.M. (2010) Towards Improvements in y-DNA Surname Project Administration, *Journal of Genetic Genealogy* 6(1).

²⁸ Howard, W.E. (2009) The Use of Correlation Techniques for the Analysis of Pairs of Y-Chromosome DNA Haplotypes (Parts I and II). *Journal of Genetic Genealogy* 5(2).

²⁹ *Family Tree DNA* (2012) Available online: www.familytreedna.com Last accessed 3 June 2012

³⁰ Powell, E (1896). *The Pedigree of the Family of Powell*. London : William Clowes & Sons.

³¹ Hansell, M. *Kiplings of Lythe and North Yorkshire*. Available online: <http://trees.ancestry.co.uk/tree/16326564/family/familyview>. Last accessed 10 June 2012

3 METHODOLOGY

Identification Of Potential Candidates

A number of different routes were adopted to identify potential candidates for testing:

1. The first approach was to a number of individuals already known to be involved in researching part of the Kipling name group. They were either already known to the author or were identified by a search on genealogical websites such as Ancestry or Genes Reunited.³² E-mail messages were sent, expressing an interest in exchanging research findings and introducing the testing prospect. In some cases, these contacts did not lead to any testable male Kiplings. In one case, they led to more than one through secondary contacts.
2. Next, specifically for the sub-group containing Rudyard Kipling, the descendents of Kipling's grandfather were identified using census returns and UK BMD records, leading fortunately to a direct line male descendant for whom no death was recorded. A successful search for that individual's present address was made by 192.com and a letter was written setting out the aims of the project. This elicited a supportive response and a DNA test was subsequently completed.
3. A more general search on 192.com listed around 1000 Kiplings, with addresses and telephone numbers. Many others were identified via Linked-in and Facebook. However, it was recognised that it would not be possible whether in time or money terms simply to contact all of these people. A more structured approach was therefore required. This is described in the next section.
4. Finally, a limited random contact exercise was undertaken in the latter stages of the project.

It was recognised at an early stage in the project that it would be most productive to obtain at least one DNA sample from as many different sub-groups as possible, defining sub-group here as any group which had not yet been linked by conventional genealogical means. To do this would require the ability to link a potential candidate into the relevant sub-group. A three-stage process was adopted to do this, centred on the 1911 English census (this being the most recent available).

³² Genes Reunited website. Available online at www.genesreunited.co.uk. Last accessed 21 July 2012.

Stage 1 involved copying the results of a search for the Kipling name (and credible variants) from Findmypast.co.uk into an Excel spreadsheet. This resulted in 1040 individuals. The census was then interrogated for each individual and a family number allocated to each individual in the same family, with details of the oldest Kipling males in the family (or that there was none) noted, as well as key data including place of birth and age. This led to 370 families. The resulting database is attached as Appendix A.

At stage 2, traditional genealogical methods were used to identify the oldest male ancestor of as many of these families as possible. BMD and census records were mainly used back to 1837/41, after which parish records (sourced mainly from the International Genealogical Index, Durham Records Online, Nottinghamshire Family History Society and existing research) were used to go back further.^{33 34 35}

The final stage was to use BMD records on Findmypast (with actual certificates obtained to clear ambiguities) to link potential candidates back to the 1911 families and hence to the sub-groups.³⁶ There was not time to identify all of the current day descendants of the 1911 families, so the process was most often used in reverse to determine if a 'likely' candidate was worth approaching. A 'common-sense' approach was adopted to identifying likely candidates.

Linked-in was a particularly useful source of likely candidates, as its mainly business-oriented user base might prima facie be considered to fit the demographic profile of those quite likely to be interested in genealogy (male, middle aged and middle class).³⁷ Sometimes, a Linked-in user's profile contained sufficient information to trace the individual via a Google search and obtain an e-mail address. In other cases, the used of Linked-in's message service enabled messages to be sent (for a fee).

³³ FamilySearch.com. International Genealogical Index. Available online: <https://www.familysearch.org/igi/>. Last accessed 14 July 2012.

³⁴ Durham Records Online. Available on-line: www.durhamrecordsonline.com. Last accessed 14 July 2012.

³⁵ *Viewer Pack 2011-2102*. CD ROM. Nottinghamshire Family History Society.

³⁶ Findmypast. Available online: www.findmypast.co.uk. Last accessed 14 July 2012.

³⁷ Linked-in. Available online: www.linkedin.com. Last accessed 14 July 2012.

192.com provides postal addresses, telephone numbers and usually an age range.³⁸ It was decided that cold-calling would be unlikely to be welcome, so an introductory letter was sent to likely candidates.

Facebook has a much younger user profile, and it was not considered that those who appeared under thirty would be likely to be good responders.³⁹ Less information was also generally available about each individual. A very poor response rate was obtained from Facebook messages even to older users.

Linked-in contacts in particular were not restricted to the UK and, in the end, three candidates were from overseas (2 USA and one South Africa).

The design of the initial message was carefully considered. In particular, it was necessary to weigh-up whether an initial mention of DNA testing would concern more potential candidates than it would intrigue. For those already familiar with family history, it was placed up front. For others, it was only mentioned as a possibility later in the message. A website was also constructed (www.genealogy.kipling.me.uk) to which prospects were referred for more information including links to commercial DNA testing sites.

As the project progressed, newsletters were produced to keep participants and other supporters informed. Earlier editions of the newsletter were used to help attract later candidates, with the ability to compare DNA to that of Rudyard Kipling mentioned as an additional attraction.

DNA Testing

Initially, Ancestry was selected as the test provider because of the familiarity of the Ancestry brand with those involved in documentary genealogy.⁴⁰ Also, one test result in the name of Kipling was already reported by Ancestry but none by other providers. The 46 marker test was chosen as testing a sufficient number of markers at an acceptable cost.

Seven participants were tested at Ancestry. However, it later became clear that Ancestry offered limited scope for further investigation, especially deep clade testing or autosomal

³⁸ 192.com. Available online: www.192.com. Last accessed 14 July 2012.

³⁹ Facebook. Available online : www.facebook.com. Last accessed 14 July 2012.

⁴⁰ Ancestry DNA. Available online: <http://dna.ancestry.com/>. Last accessed 14 July 2012.

DNA testing, should either be required and that Family Tree DNA (FTDNA) did offer this flexibility.⁴¹ The tests results already carried out at Ancestry (apart from one where contact was lost with the testee and permission could not be obtained) were uploaded to FTDNA and future participants were tested using FTDNA's 37 marker test.

Ancestry's 46 marker test is, for most participants, only a 43 marker test, as it includes the rarely-present markers DYS19b, 464e and 464f. There also an incomplete overlap between Ancestry's 43 markers and FTDNA's 37, with only 32 markers being shared in common.

One participant from each of the two main groups which were by then being seen in the early results provided an additional sample to FTDNA, and an upgrade test was carried out, to fill the missing five of 37 markers. These DNA samples were then also available for further testing at FTDNA.

Analysis of Results

The testing laboratory's prediction of the broad haplogroup of each participant was used.

Genetic distance between participants sharing a common haplogroup were calculated pairwise using all markers in common (32, 37 or 43). Genetic distance was based on the stepwise model, apart from markers DYS464, where the infinite allele model was used. There were no DYS389 mismatches in those sharing a common haplotype, so no adjustments were necessary for possible double counting of a mismatch.

The modal haplotype was identified for each haplogroup and a network diagram constructed to show the most likely relationships between the test participants.

Test results were also fed into Dean McGee's Y-DNA Utility⁴² and the output used to support calculate genetic distance and estimate TRMCA. It was recognised that through not testing the same markers for all participants, the results from the utility would need treating with care.

⁴¹ Family Tree DNA. Available online: <http://www.familytreedna.com/default.aspx>. Last accessed 14 Jul 2012.

⁴² McGee, D. Y-DNA Utility. Available online: <http://www.mymcgee.com/tools/yutility111.html#GeneticDistance>. Last accessed 24Jun 2012

4 RESULTS

The table below shows the first 25 lines of the spreadsheet capturing the 1911 families. The complete spreadsheet forms Appendix 1 to this report.

NAME	YOB	Age	Sex	Reg. District	County	Fam#	Occupation	Residence	Birthplace	County	Sub-group of lead male	Ancestry
KIPLING, Mabel	1866	45	F	Easthampstead	Berkshire	1	Matron	Wellington College	Richmond	Surrey	F	
KIPLING, Annie May	1910	1	F	Chesterfield	Derbyshire	2						
KIPLING, Evelyn	1906	5	F	Chesterfield	Derbyshire	2						
KIPLING, Jarvis	1881	30	M	Chesterfield	Derbyshire	2	Miner	Brimington	Eckington	Derbyshire	Notts	s Harry 1863, s Jervis 1821
KIPLING, Georgiana	1874	37	F	Chesterfield	Derbyshire	2						
KIPLING, Reginald	1905	6	M	Chesterfield	Derbyshire	3						
KIPLING, Cecil	1903	8	M	Chesterfield	Derbyshire	3						
KIPLING, Kathleen	1901	10	F	Chesterfield	Derbyshire	3						
KIPLING, Gladys	1899	12	F	Chesterfield	Derbyshire	3						
KIPLING, Nellie	1896	15	F	Chesterfield	Derbyshire	3						
KIPLING, Robert	1893	18	M	Chesterfield	Derbyshire	3						
KIPLING, William	1891	20	M	Chesterfield	Derbyshire	3						
KIPLING, Nellie	1869	42	F	Chesterfield	Derbyshire	3						
KIPLING, William	1863	48	M	Chesterfield	Derbyshire	3	Gardener	Chesterfield	Egmanton	Notts	Notts	s Robert 1835, s George 1786
KIPLING, Fred	1890	21	M	Chesterfield	Derbyshire	4	Colliery Horseman	Killamarsh	Scaforth	Lincs	NPE	s Charles, s Martha
KIPLING, Harry	1884	27	M	Chesterfield	Derbyshire	5	Coal Miner	Bolsover	Eckington	Derbyshire	Notts	s Harry 1863, s Jervis 1821
KIPLING, Mary Elizabeth	1884	27	F	Chesterfield	Derbyshire	6	DS	Eckington	Letwell	Yorks	F	
KIPLING, Ann	1845	66	F	Chesterfield	Derbyshire	7	Widow	Eckington	Eckington	Derbyshire	F	
KIPLING, Liza	1827	84	F	Chesterfield	Derbyshire	8	Mother-in-Law	Eckington	Ewinstow	Notts	F	
KIPLING, Arthur William	1901	10	M	Glossop	Derbyshire	9						
KIPLING, Agnes Harriet	1865	46	F	Glossop	Derbyshire	9						
KIPLING, Matthew	1856	55	M	Glossop	Derbyshire	9	Insurance Clerk	Glossop	Lartington	Yorks	Pitcherhouse	s John (1830) s William (1797)
KIPLING, William	1845	66	M	Glossop	Derbyshire	10	Bootmaker	Glossop	Wehnam	Notts	Notts	s Joseph (1799/1802) s William (
KIPLING, Donald Seager	1892	19	M	Barnstaple	Devonshire	11						
KIPLING, Sarah Jane	1863	48	F	Barnstaple	Devonshire	11	Widow	Ilfracombe	Honiton	Devon	Arkendale	s Jonathan 1854, s Robert 1812, f

Fig 1. 1911 Census; Kipling data and ancestry notes

A description of each of the sub-group named in the penultimate column forms Appendix 2. Nomenclature was selected to identify a particular place or person associated with that group (e.g. 'Rudyard').

The table below shows the county of residence of the 1040 Kiplings identified in the 1911 census.

1911 Residence	Number	%
Durham	365	35%
Yorkshire	267	26%
Nottinghamshire	40	4%
Northumberland	40	4%
London/Middlesex	80	8%
Lancashire	62	6%
Other (<5%)	186	18%
	1040	100%

Fig 2. 1911 Census; Kipling entries analysed by County of residence

Of the 375 families or individuals, 83 consisted solely of females (mainly young single women working as servants). It proved possible to trace the ancestry of all but of 11 of the remaining families containing at least one male, allocating each either to one of 26 sub-groups not known to be illegitimate, to one of the two sub-groups with recorded long-standing illegitimacies or to 12 more recent illegitimacies.

Recruitment

The table below explains how participants were recruited.

Group identifier	Recruitment method of participant
Barningham	Self
Brough	Initial identification on Linked-in, then Google name to get e-mail address
Capt. Robert	Member of my own profession
Dean	Father of female 'Kipling' family researcher identified via tree on and contacted via Ancestry.com
Gilling (2 part.)	Both known to 'Pitcherhouse' through previous research, who then contacted them
Greystock	Relative of female 'Kipling' family researcher identified via tree on and contacted via Ancestry.com
Missionary	Identified on SA website, 192.com address look-up and postal invitation
Notts	Initial identification on Linked-in, then Google name to get e-mail address
Pitcherhouse	Google for 'Kipling' family researchers
Rudyard	Trace of descendents, 192.com address look-up and postal invitation
Stackholm	Initial identification on Linked-in, then send Linked-in e-mail
Staindrop (2 part.)	Both known to 'Pitcherhouse' through previous research, who then contacted them

Fig 3. Recruitment method of each participant

In total, 14 male Kiplings were recruited for DNA testing, representing 12 of the 26 families (and almost exactly 50% of the male Kiplings in the 1911 census not known to have NPE ancestry).

In addition, the Kipling observed to have already taken a test at Ancestry had a predicted haplogroup of R1a. Following contact, the individual concerned reported a family tale of relatively recent illegitimacy, which the test appears to confirm as the individual would otherwise have fallen into the Greystock group.

DNA SNP matching analysis

All participants fell into just two haplogroups, I1 and R1b, hence only two genetic distance tables were required. The first table in each case shows the number of mismatches, the second table show the number of markers compared.

R1b Group results

R1b	Gilling (1)	Rudyard	Gilling (2)	Brough
Barningham	1	1	1	3
Gilling (1)		2	0	1
Rudyard			2	2
Gilling (2)				1

R1b	Gilling (1)	Rudyard	Gilling (2)	Brough
Barningham	43	43	43	37
Gilling (1)		43	43	32
Rudyard			43	32
Gilling (2)				32

Fig 4. STR test results. R1b Pairwise mismatches and comparisons

Commentary:

1. There was an exact 43 marker match between the two participants from the Gilling group. This is not unexpected as documentary evidence showed them as 5th cousins.
2. Barningham is closest to the modal haplotype for the group.
3. Barningham and Brough differ by 2 in one value of the marker CDY, which was not tested for Gilling or Rudyard.
4. No differences of more than 1 were observed at any other marker.
5. No differences were observed at DYS389 or DYS464.

The network diagram below (Fig. 5) has been constructed (using Microsoft Word drawing tools) to show the most likely relationship between the R1b participants deducible from the evidence available. Relevant mutations are shown in red.

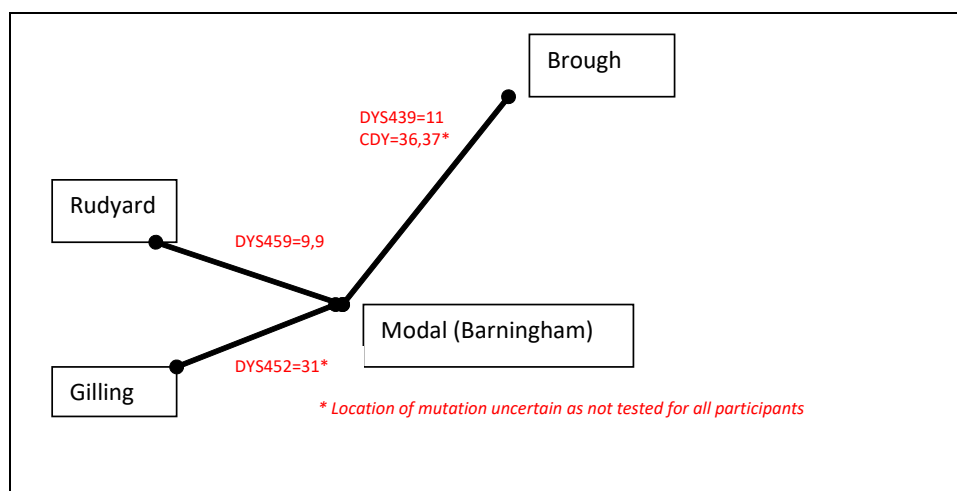


Fig 5. Possible relationship of R1b group, derived from DNA test results

Marker	DYS439	DYS452*	DYS459	CDY*
Value	12	30	9,10	37,38

(Values are identical at all other markers)

Fig 6. Kipling modal R1b haplotype, derived from DNA test results

It is possible from Fig 5. to postulate that some genetic distances might be greater than derived by simple pairwise comparisons. For example, Brough and Gilling are likely to have a distance of 4 rather than 1, as only one of the three mutations identified as likely to separate them (including the double mutation in CDY) was actually tested for both participants. The R1b results from Dean McGee's utility were:

Genetic Distance						
ID	modal	Brough	B-ham	Rudyard	Gilling2	Gilling1
modal	111	1	1	1	1	1
Brough	1	37	2	2	1	1
B-ham	1	2	76	1	1	1
Rudyard	1	2	1	43	2	2
Gilling2	1	1	1	2	43	0
Gilling1	1	1	1	2	0	43
	Related	Probably Related	Possibly Related			
- Hybrid mutation model is used						
- Values on the diagonal indicate number of markers tested						

Time to Most Recent Common Ancestor (Years)					
ID	Brough	B-ham	Rudyard	Gilling2	Gilling1
Brough	37	330	420	300	300
B-ham	330	76	240	240	240
Rudyard	420	240	43	360	360
Gilling2	300	240	360	43	120
Gilling1	300	240	360	120	43
	0-270 Years	300-570 Years	600-870 Years	900-1170 Years	
- Infinite allele mutation model is used					
- Average mutation rate varies: 0.0044 to 0.0054, from FTDNA derived rates					
- Values on the diagonal indicate number of markers tested					
- Probability is 80% that the TMRCA is no longer than indicated					
- Average generation: 30 years					

Fig 7. SNP test results. R1b McGee Y-DNA Utility output

The genetic distances appear even closer for Brough and Barningham, as McGee appears to apply the infinite allele model to CDY. These results are also likely overstate the relationship between some individuals both because of the 'pairwise' comparison issue mentioned above and because no information on most distant non-common ancestor is not used to calculate the TRMCA.

II Group Results

<i>II</i>	P'house	S'drop(1)	Capt. R	S'drop(2)	Missionary	Stackholm	Notts	Greystock
Dean	6	7	5	8	19	22	5	6
Pitcherhouse		5	1	4	29	23	2	5
Staindrop (1)			4	1	18	21	4	3
Capt. Robert				3	17	20	1	2
Staindrop (2)					17	20	3	2
Missionary						28	29	26
Stackholm							23	20
Notts								7

<i>II</i>	P'house	S'drop(1)	Capt. R	S'drop(2)	Missionary	Stackholm	Notts	Greystock
Dean	43	43	43	43	32	32	32	32
Pitcherhouse		43	43	43	37	37	37	37
Staindrop (1)			43	43	32	32	32	32
Capt. Robert				43	32	32	32	32
Staindrop (2)					32	32	32	32
Missionary						37	37	37
Stackholm							37	37
Notts								37

Fig 8. STR test results. II Pairwise mismatches and comparisons

As mentioned above, pairwise comparisons will underestimate the genetic distance in some cases where mutations are identified in markers not tested for all participants.

The genetic map in Fig X below is likely to give a more complete picture.

Commentary:

1. Missionary and Stackholm (shaded) clearly have no common ancestors since surnames became fixed with either each other or with the other group. Documentary investigation has subsequently shown Stackholm to descend from a 1779 NPE.
2. With the possible exception of Dean, the remaining groups are likely to share a relatively recent common ancestor, having genetic distances of between 1 and 4. Dean's closest genetic difference is 5.
3. The two Staindrop participants are known to be 7th cousins.
4. Excluding 'Missionary' and 'Stackholm', all individual marker mismatches were of size 1 except for Dean, which had a mismatch at one YCAII marker of 2 with the others.

A similar genetic map has been constructed. Where markers evidencing a mutation have not been tested for all participants, it has been assumed to occur as far as possible from the mode.

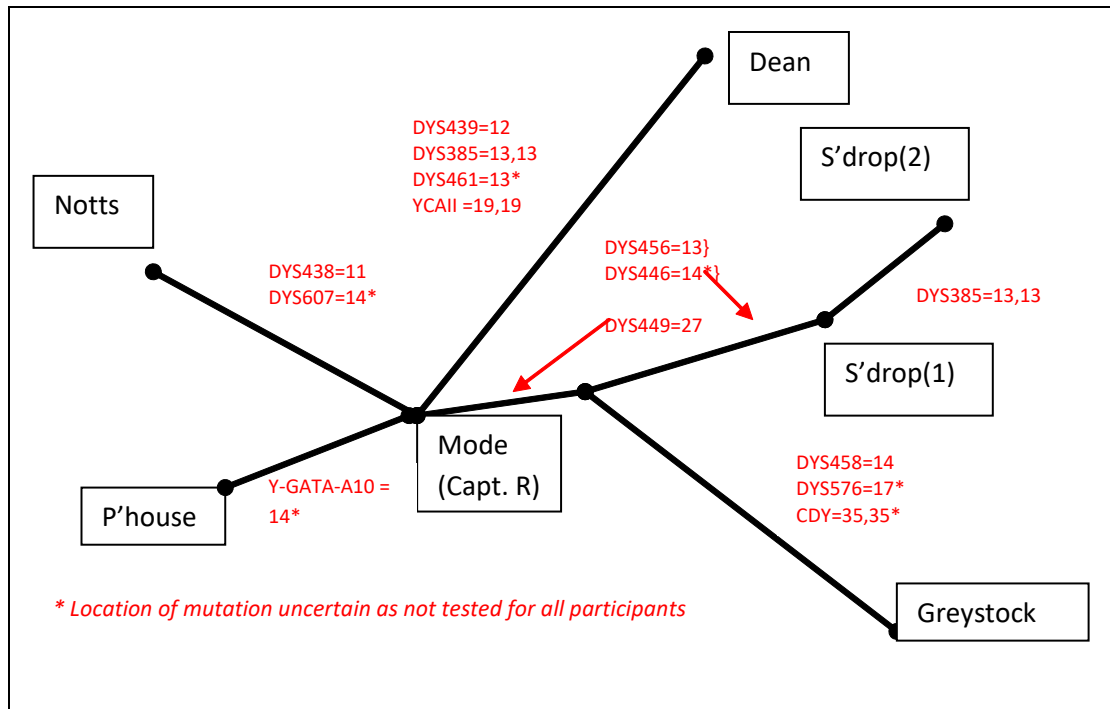


Fig 9. Possible relationship of II group, derived from DNA test results.

Marker	DYS385	DYS438	DYS439	DYS446*	DYS449	DYS456	DYS458	DYS461*	YCAII
Value	13, 14	10	11	13	26	14	15	12	19,21
Marker	Y-GATA-A10*	CDY*	DYS607*	DYS576*					
Value	15	36,36	15	16					

(Values are identical at all other markers)

Fig 10. Kipling modal II haplotype, derived from DNA test results

The I1 results from Dean McGee's utility were (excluding Missionary and Stockholm):

Genetic Distance								
ID	modal	Sdrop-2	Notts	P-house	Sdrop-1	G-stock	C-Robt	Dean
modal	48	4	2	1	3	5	0	4
Sdrop-2	4	43	4	5	1	3	4	6
Notts	2	4	37	2	3	7	1	4
P-house	1	5	2	48	4	5	1	5
Sdrop-1	3	1	3	4	43	2	3	7
G-stock	5	3	7	5	2	37	2	5
C-Robt	0	4	1	1	3	2	43	4
Dean	4	6	4	5	7	5	4	43

Time to Most Recent Common Ancestor (Years)								
ID	modal	Sdrop-2	Notts	P-house	Sdrop-1	G-stock	C-Robt	Dean
modal	48	570	330	210	450	630	120	570
Sdrop-2	570	43	660	660	240	540	570	780
Notts	330	660	37	330	540	840	300	660
P-house	210	660	330	48	570	630	240	660
Sdrop-1	450	240	540	570	43	420	450	900
G-stock	630	540	840	630	420	37	420	780
C-Robt	120	570	300	240	450	420	43	570
Dean	570	780	660	660	900	780	570	43

Related	Probably Related	Possibly Related
FTDNA's Interpreting Genetic Distance for 12 Markers		
FTDNA's Interpreting Genetic Distance for 25 Markers		
FTDNA's Interpreting Genetic Distance for 37 Markers		
FTDNA's Interpreting Genetic Distance for 67 Markers		
FTDNA's Interpreting Genetic Distance for 111 Markers		

- Hybrid mutation model is used
- Values on the diagonal indicate number of markers tested

Fig 11. SNP test results. I1 McGee Y-DNA Utility output

Similar cautions to those for R1b apply regarding the matters not factored into the above results apply.

Unexpectedly, FTDNA identified a match of Stockholm with a test result under the name of Pinkney. This relatively rare name was the maiden surname of the mother of the Sarah Kipling whose illegitimate child began this line. This suggests that the father might have been a cousin or uncle of Sarah.

Deep Clade Results

The R1b cluster is of the Atlantic Modal Haplotype, the modal version of R1b (based on six markers) in the UK and much of Atlantic Europe⁴³. FTDNA 'deep clade' analysis of the DNA sample of one R1b participant, 'Barningham', resulted in a terminal SNP of U152 (testing negative for 'downstream' SNPs M126, M160, L2 and L4).

Haplogroup I1 is, unfortunately, as yet much less differentiated by identified SNPs. FTDNA predicted haplogroup is I1-M253. Tests were carried out on one I1 participant (Pitcherhouse) and was negative for SNPs M21, M227, P259 and L22, leaving the group as I1* until further differentiating downstream SNPs are identified and can be tested.

⁴³ Campbell, K.D. (2007) Geographic Patterns of Haplogroup R1b in the British Isles – Deconstructing Openheimer. *Journal of Genetic Genealogy* 3(2).

5 CONCLUSIONS

Single origin hypothesis

The main conclusion that can be drawn from this project is that current Kipling males who are not associated with a known NPE fall into two completely unrelated clusters when STR haplotypes are compared. One is of haplotype R1b and the other I1. Both clusters have documentary evidence that shows no separation by NPE for at least 300 years, possibly longer. It cannot be precluded, however, that additional shared haplotypes would have been found if a higher proportion of the groups had been tested.

Within each cluster, the members are closely related, marginally less so for 'Dean' in the I1 cluster. Only one participant, with documentary evidence back to the beginning of the 19th century, was neither the result of a known NPE nor closely matched to one cluster or the other.

This leaves open whether the family was of single origin, as the documentary evidence might on balance suggest, with an early NPE leading to two lines both of which prospered, or whether the name was separately adopted by two genetically unrelated individuals whose lines have prospered.

Documentary evidence links all but seven⁴⁴ of the 26 groups to ancestors in the upper Teesdale region. DNA results were obtained for three of the seven (Greystock, Notts and Rudyard) and all confirm a genetic link to Teesdale groups, making it increasingly likely that the name had a single geographical, if not y-DNA, origin.

The most common haplogroup was I1, which is particularly prominent in Scandinavia and, in the UK, and is often taken as indicating a Viking or other Scandinavian origin of the male line in question⁴⁵. There is in Sweden a Kipling Berg farm which has been around since at least the mid 17th century⁴⁶, suggesting a possible similar development in that country of the name.

⁴⁴ David, Ebenezer, Greystock, Lincoln, Missionary, Notts and Rudyard

⁴⁵Manco, J. (2011) New Vistas on the Distant Past – The Story of I. Website. <http://www.buildinghistory.org/distantpast/haplogroupi.shtml>. Last accessed 12 June 2012.

⁴⁶ Kiplingeborg website. www.kiplingeborg.se. Last accessed 11 June 2012

Methodology

Initial recruitment into a testing project like this can be swift where there are a number of existing family history researchers who can easily be contacted via genealogical websites and who may in turn have other contacts. They are also likely to have an enthusiasm for and awareness of genealogical uses of DNA tests.

After that, recruitment can be more difficult. Despite establishing Kipling projects on FTDNA and Ancestry, setting up a Guild of One-Name Studies project and constructing a website, no unsolicited requests to participate were received⁴⁷. Linked-in proved to be the best mechanism for recruitment, although not via its facility to send messages to members which generated only one participant. Rather, individuals, such as academics and businessmen, were identified through Linked-in and then a targeted Google search was carried out which often identified an email address enabling these individual to be contacted directly. An experiment to make contact via Facebook messaging met with no success.

One problem with a name like Kipling, which will be shared by some other names, is that most internet searches, unless very specifically designed, produce results for famous individuals or commercial brands sharing the name (Rudyard Kipling, his son John Kipling and the Kipling luggage brand in this case). Even a search for “James Kipling” produced examples of lists of authors where (Henry) James immediately preceded (Rudyard) Kipling!

It is hoped that these remarks will be of assistance to others considering a similar exercise.

⁴⁷ Guild of One-Name Studies website. Available online: www.one-name.org/. Last accessed 14 July 2012.

Rudyard Kipling

A secondary objective of this project was to add to documentary knowledge about the ancestry of Rudyard Kipling. Two significant results have been obtained.

Firstly, a close match has been obtained between a y-chromosome STR-based haplotype of a documented relative of Rudyard and three other Kipling family groups, some with a longer documented history. Whilst the relationship of the haplotypes and number of samples obtained is insufficient to draw firm conclusions on the exact nature of the relationships between these four groups, it can nevertheless be concluded that Rudyard's family share a male line ancestry with three other Kipling families, all of which are associated with upper Teesdale area of the UK.

Secondly, the 'deep clade' results of 'Barningham', R-U152* (aka R1b1a2a1a1b3*), because of the slow mutation rate of SNPs relative to STRs and their uniqueness, will also be the haplogroup of the other R1b participants and of Rudyard. The U152 mutation is currently the subject of a number of studies⁴⁸ and its presence has been observed particularly in the Alpine regions of Switzerland, parts of France and Northern Italy which overlap to an extent with the historic territories of the late bronze and Iron Age Halstatt and La Tene Celtic cultures. The mutation may well have moved with the Celts westward from there, although quite possibly arriving in England indirectly and more recently via the Danes or Angles. TRMCA calculations amongst U152+ individuals indicate that the original mutation may have occurred over 11,000 year ago⁴⁹.

Of course, it needs to be born in mind that the unbroken male line DNA formed only a minuscule part of Rudyard's total genetic makeup and that it can have almost certainly had only an insignificant influence on his character or talent.

⁴⁸ Faux, D. K. (2011) *Y-Chromosome marker S28/U152 Haplogroup R-U152 Resource Page*. Available online at http://www.davidkfaux.org/R1b1c10_Resources.pdf. Last accessed 10 June 2012

⁴⁹ Ibid. Page 2

Recommendations for future work

Increasing the number of markers tested for selected participants, for example to FTDNA's 67 markers, as well as feeding in information about most distant non-common ancestors will improve the calculated probability of common ancestry or NPE since surnames became fixed.

Of the untested groups, 'Melsonby' is the largest and it would significantly increase penetration for a test result to be obtained. Male descendants of each 1911 male member of the group should be traced via BMD records and, if possible, extended invitations to participate. Similar steps should be taken for other groups in decreasing order of significance. It ought also to be possible, given time, to link all male English post 1911 BMDs to one or more of the family groups, which would also provide supporting evidence of those male lines thought to have ended during the 20th century.

Recently, Ancestry has produced a new transcription of the 1911 census and this could be compared with Appendix 1 to identify any transcription errors by FindMyPast.

The study could also be formally extended outside the UK, using US censuses from 1910 to 1940 and the 1911 Canada census in particular, linking each Kipling found to one of the UK groups (or to a new group). False leads may arise, as 'Kipling' was adopted by a number of US immigrant families as an attractive Anglicisation of their name (e.g. of Keplinger).

Hansell shows that a male line of descent from Rudyard Kipling's great-great-uncle George Kipling persisted to the start of the 20th century (in Whitby) and further BMD investigation shows that it has continued to today. If a DNA sample can be obtained, this can confirm the result for the 'Rudyard' group and also support the documentary evidence for the Kiplings of Whitby to be related to Rudyard.

Past research by Brian Kipling and others⁵⁰ has shown that a John Kipling, most likely of the 'Barningham' group, sired a number of male children with two native American women whilst employed by the Hudson Bay Company in the 18th century and that descendants named Kipling or Keplin persist to this day, especially in Manitoba and

⁵⁰ Red River Ancestry website. <http://www.redriverancestry.ca/KIPLING-JOHN-1724.php>
Last accessed 11 June 2012.

North Dakota. Obtaining a y-DNA sample from one of this group could validate a most interesting line of descent.

Further comparisons can be made with existing or future large-scale studies of the distribution of different I1 haplotypes around Europe, which may provide more insight into the distant origins of the I1 Kiplings. The opportunity should be taken to test for any new SNPs identified as making a material subdivision in the I1* group in Western Europe.

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