Using Three Strands of Research to Recreate Briese Surname Lineages

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Preface

People become interested in genealogy in an effort to understand better who they are, as well as why and how they find themselves in a particular place and circumstance. It helps establish a better sense of identity. Although our ancestry is multi-stranded, many people attach a special importance to the surname lineage, which in western culture is the paternal line. However, we need to keep in mind that this too has two strands – genetic and cultural. The genetic strand informs our hard-wired physical and biological traits, while the cultural strand carries down the more fluid and subtle inputs of the behaviours, circumstances and values of a long line of ancestors. We are ultimately the product of both nature and nurture.

In most cases, these strands are tightly interwoven – in the paternal line, the surname defines both cultural and genetic strands. However, this is not always the case. Events such as adoption, use of the maternal surname, extra-marital paternity etc can cause a separation of the strands. After such an event, a person and their descendants could continue with the original surname and cultural strand, but a different genetic one – i.e. there has been a patrilineal disjunct. The reverse can also occur, e.g. an adoption could lead to a genetic strand from the original surname joining with another cultural strand.

Such disjuncts can be surprisingly frequent – for instance, in the old German church records, children born of unmarried mothers kept their mothers' surnames. The Germans also added the word "uneheliche" (illegitimate) to such birth records and, from those listed in the Briese Surname database, they made up 2 to 4% of the total. This means that, over 10 generations, the cumulative chance of a patrilineal disjunct occurring may be as high as 1 in 3. Thus, it is not surprising that surname lineages may have several genetic strands, while maintaining a common cultural origin. As we shall see, some patrilineal disjuncts may remain hidden until revealed by genetic genealogy. Fortunately, today, people are less judgmental and such genetic/cultural admixture is viewed more as enriching the history of a surname rather than some misconceived idea of surname purity.

I decided to write this paper after reading a summary of the 2021 society member survey [1], which indicated that the majority of members do not have a DNA project, that many who do have either done little with it or don't know where to start and that there is even outright antipathy to the use of DNA in genealogical research. Hopefully, my own experiences with the Briese Surname Project may show how genetic studies can complement and add value to more traditional genealogical research. Like our ancestry itself, genealogy is a multi-stranded field of research.

Background

The Briese Surname Project [2] has amassed a large database of records, based on traditional genealogical research, largely through on-line birth, death and marriage records. This has been sufficient to show both where the surname originated and how it has subsequently spread to form geographic clusters within the home range of Prussia and beyond through emigration to parts of the New World [3]. Like many such projects, it also posed as many questions as it answered.

As an illustration, one of the homeland clusters of the Briese surname is Deutsch Krone district (Kreis) in West Prussia. Of all the Brieses born before 1850 with known birthplaces, 25% were born in Kreis Deutsch Krone. Moreover, most emigration of Brieses from Prussia to the New World (Australia, Brazil, Canada and USA) took place in the latter half of the 19th century and 50% of male emigrants (potential sources of continuing surname lineage) were from Deutsch Krone [2]. Clearly, this region is important to an understanding of the origins and dispersal of the Briese surname. Unfortunately, this part of West Prussia was also the scene of heavy fighting between German and Russian forces during the latter stages of World War II and, in the aftermath, German populations were expelled and scattered. While local churches kept extensive records of births, deaths and marriages, many were destroyed in the conflict. As a consequence, genealogical research is difficult.

While available evidence suggests that the Briese surname in Prussia has a single toponymic origin dating from the 14th-15th century [3], when surnames were adopted, traditional paper record-based genealogy has left us with many separate lineages of from 3 to 8 generations. The question of whether and how they might merge towards a single common ancestor remains unanswered. To overcome this impasse, the Briese Surname Project reached out to genetic genealogy and, in 2010, established a Briese Surname DNA Project on FamilyTreeDNA [4,5].

Research Strands and Result

It can be difficult to attract participants to a DNA study - concern over privacy of genetic data, the cost of testing or just a general disinterest in genealogy being factors. To date, 14 males bearing the Briese surname have had their Y-DNA tested (Table 1) and the results reported here for this group, plus a further three linked to these by paper records, are based on three separate strands of evidence, one traditional and two genetic.

Table 1. Data sets used to create the Briese surname lineage (blanks indicate data not yet obtained). See below for explanation of terms.

Person / Data Sets	B1 Cluster											Other Brieses		
	AU01	AU03	US03	AU06	US02	US01	AU04	DE01	US04	US05	AU02	US06	US07	CA01
BMDR records[a]	6	3	5	3	5	2	3	2	5	3	5	2	4	5[b]
STR37[c]	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑
STR67	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑			
STR111	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑				
BigY SNP[d]	☑	☑	☑	☑	☑	☑	☑	☑	☑	☑				

a. BMDR = birth, marriage, death and residence records, and the number indicates the number of generations from person tested to oldest known ancestor (tester = 0)
b. Paper record lineage is cultural not genetic
c. STR refers to the short tandem repeats tested by FamilyTree DNA, and the numbers 37, 67 and 111 indicate the number of markers tested. Participants can opt for increasingly sensitive levels of testing.
d. Big Y SNP refers to the highest level of Y-DNA testing conducted by FamilyTree DNA, where single nucleotide polymorphisms are detected and up to 700 STRs analysed for mutations.

Paper records – the traditional method of genealogical research is to trace a person's ancestry back through life-stage records (birth, death, marriage, residence etc). Provided it is done diligently, it provides absolute evidence of ancestry. However, paper records often do not go back more than a few hundred years, may contain gaps or may be missing altogether. Where present, such records are the most useful for determining relationships in recent times. In the Briese Surname Project, this was done by searching on-line databases such as Family Search, Ancestry, Geneanet and My Heritage. Importantly, because transcriptions of records are not perfect, databases were verified against original records, where these had been digitised and were also available on-line. Public family trees on these sites were found to be useful for more recent lineages, but often ascribed more distant ancestors incorrectly to particular lineages and hence also required verification.

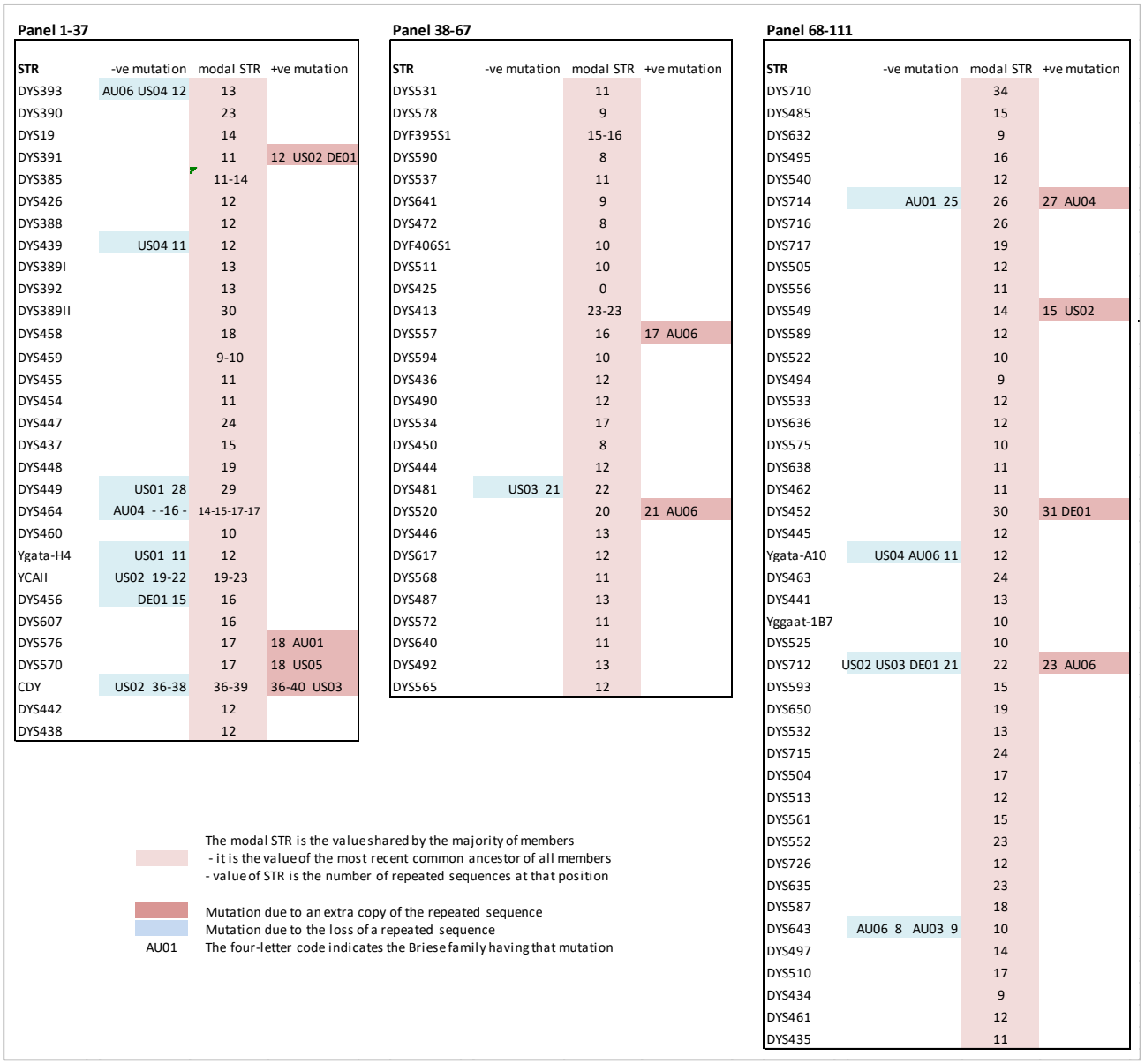
- Short Tandem Repeats (STR) – these occur when a short sequence of base-pairs (2-13) is repeated several times within the Y-chromosome. Mutations lead to copies of this sequence being added to or subtracted from the DNA region. This means that the number of repeats can vary from person to person and, while unrelated people may have the same number for an individual STR, the pattern of such differences over multiple STRs can be used to measure the degree of genetic relatedness. The more STRs tested, the greater is the degree of accuracy in determining the relationship. STRs are therefore probabilistic, not absolute, in determining relationships. Moreover, as repeats can be subtracted as well as added, and mutation rates vary between them, their accuracy diminishes with time. They are useful, though, in determining genetic relationships in the medium-term, back to the time when most surnames originated in Europe (20-24 generations) and are thus an important genealogical tool. Based on measured mutation rates, STRs can be used to estimate the time to the most recent common ancestor of a pair or group of persons.

- Single nucleotide polymorphisms (SNP) – these are mutations that occur at a single base-pair of the Y-chromosome DNA (in humans, the Y chromosome has 58 million base-pairs). The rarity of individual mutations means that a descendance tree constructed from these can be considered absolute and the age of an SNP can be estimated from known mutation rates. Once an SNP is confirmed, the group of persons sharing that mutation become members of a haplogroup (named for that SNP mutation). Subsequently, new mutations within that haplogroup can be used to identify daughter haplogroups. Thus, an SNP descendance tree tends to grow from its base towards more recent times. As a consequence, it has been considered useful for determining relationships with absolute accuracy in distant or pre-genealogical time (i.e. before the origin of surnames). However, with the explosion in testing for and discovering SNPs, the identification of new haplogroups is now being pushed forward to the surname period.

The best way to study ancestral relations is to combine all three sets of evidence, which can take a family tree from the distant past to the present.

Fig. 1. Visualisation of Short Tandem Repeat (STR) data
(results based on 11 tests - 1 STR37, 1 STR67 and 9 STR111).

FamilyTreeDNA results show individual STR haplotypes as a set of numbers associated with a marker on the Y-chromosome. The number tells us how many times a short DNA sequence has been replicated in that region. This figure shows the modal STR haplotype in pink (the set of marker values that is most common amongst group members) and indicates where mutations have occurred, either by adding a new copy of the replicated sequence or losing it. By definition, the modal haplotype is also the haplotype of our common ancestor, as all mutations can be traced back to it. In the Briese B1 cluster, only 18 of the 105 markers have mutated, 15 of these are unique and only five have multiple mutations (11 in all). Of these multiple mutations, only three sets are shared – for DYS391, both US02 and DE01 = 12; for DYS393, both AU06 and US04 =12; and for DYS712, TRB and WB2 = 21. This possibly indicates a common ancestor, but as STR mutations can be reversed, it is not certain. In the case of DYS712, the marker has been measured to have a fast mutation rate (0.0164) and so is less reliable, whereas DYS391 and DYS393 have much lower mutation rates (0. 0021 and 0.0018 respectively, or roughly once every 500 generations), meaning that it is more likely the mutation occurred only once and that AU06 and US04 share a common ancestor, as do US02 and DE01.



Panel 1-37

STR	-ve mutation	modal STR	+ve mutation
DYS393	AU06 US04 12	13	
DYS390		23	
DYS19		14	
DYS391		11	12 US02 DE01
DYS385		11-14	
DYS426		12	
DYS388		12	
DYS439	US04 11	12	
DYS389I		13	
DYS392		13	
DYS389II		30	
DYS458		18	
DYS459		9-10	
DYS455		11	
DYS454		11	
DYS447		24	
DYS437		15	
DYS448		19	
DYS449	US01 28	29	
DYS464	AU04 - -16 -	14-15-17-17	
DYS460		10	
Ygata-H4	US01 11	12	
YCAII	US02 19-22	19-23	
DYS456	DE01 15	16	
DYS607		16	
DYS576		17	18 AU01
DYS570		17	18 US05
CDY	US02 36-38	36-39	36-40 US03
DYS442		12	
DYS438		12	

Panel 38-67

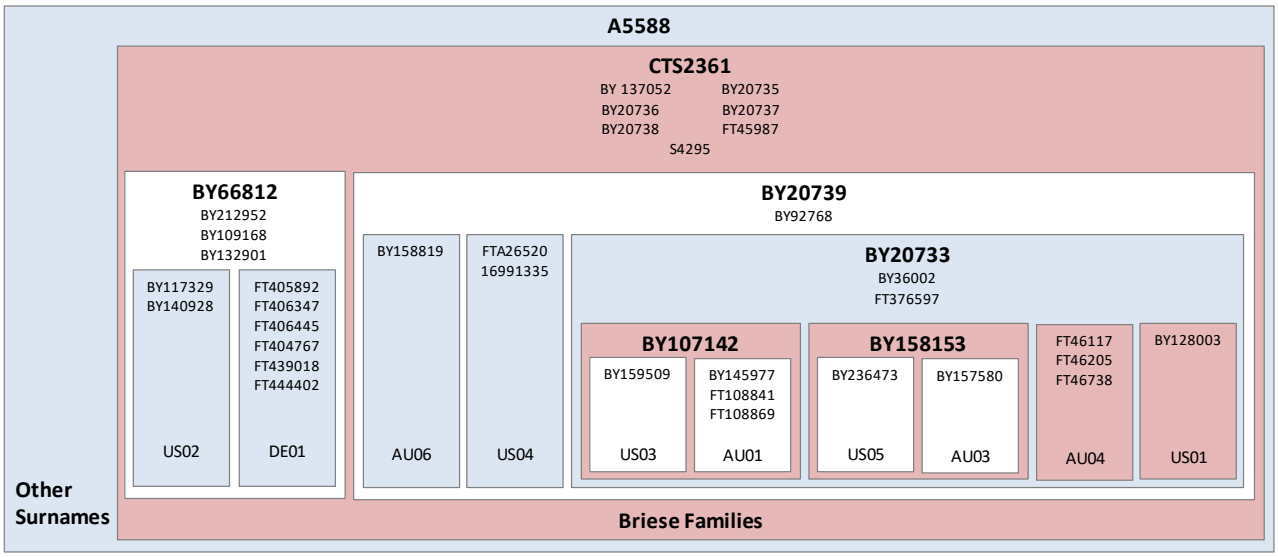
STR	-ve mutation	modal STR	+ve mutation
DYS531		11	
DYS578		9	
DYF395S1		15-16	
DYS590		8	
DYS537		11	
DYS641		9	
DYS472		8	
DYF406S1		10	
DYS511		10	
DYS425		0	
DYS413		23-23	
DYS557		16	17 AU06
DYS594		10	
DYS436		12	
DYS490		12	
DYS534		17	
DYS450		8	
DYS444		12	
DYS481	US03 21	22	
DYS520		20	21 AU06
DYS446		13	
DYS617		12	
DYS568		11	
DYS487		13	
DYS572		11	
DYS640		11	
DYS492		13	
DYS565		12	

Panel 68-111

STR	-ve mutation	modal STR	+ve mutation
DYS710		34	
DYS485		15	
DYS632		9	
DYS495		16	
DYS540		12	
DYS714	AU01 25	26	27 AU04
DYS716		26	
DYS717		19	
DYS505		12	
DYS556		11	
DYS549		14	15 US02
DYS589		12	
DYS522		10	
DYS494		9	
DYS533		12	
DYS636		12	
DYS575		10	
DYS638		11	
DYS462		11	
DYS452		30	31 DE01
DYS445		12	
Ygata-A10	US04 AU06 11	12	
DYS463		24	
DYS441		13	
Yggaat-1B7		10	
DYS525		10	
DYS712	US02 US03 DE01 21	22	23 AU06
DYS593		15	
DYS650		19	
DYS532		13	
DYS715		24	
DYS504		17	
DYS513		12	
DYS561		15	
DYS552		23	
DYS726		12	
DYS635		23	
DYS587		18	
DYS643	AU06 8 AU03 9	10	
DYS497		14	
DYS510		17	
DYS434		9	
DYS461		12	
DYS435		11	

Fig. 2. Visualisation of Single Nucleotide Polymorphism (SNP) data.

The lists of codes are individual mutations, and those shared by a common ancestor are grouped in nested boxes. The code in bold is the one used to identify a named haplogroup (which contains a minimum of 2 people). For example, US03 and AU01 have a few unique mutations, but share BY107142 indicating common ancestry. Similarly, AU03 and US05 share haplogroup BY158153. AU04 and US01 do not have either of these ancestors, but all five share the common ancestor of BY27033 …. and so on. Based on the lineage of haplogroups, AU01 would be identified as A5588>CTS2361>BY27039>BY27033>BY107142.



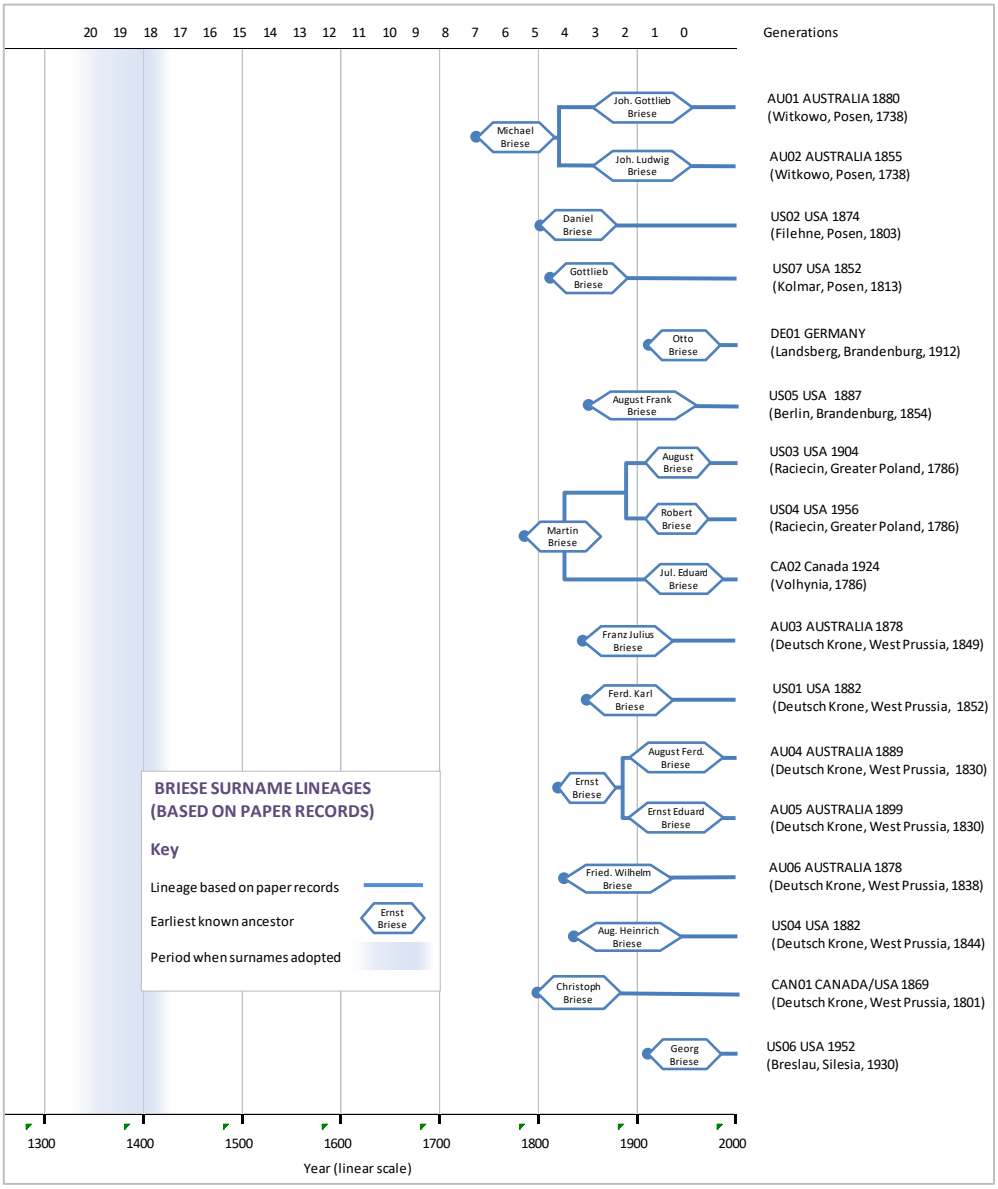
Results from paper records

Most of the Briese families involved in the current study are emigrant families, having moved from their Prussian homeland to either North America or Australia in the 19th or early 20th centuries. As mentioned earlier, many came from the Deutsch Krone district in West Prussia, where the birth, marriage and death records were kept by the two main evangelical churches in the towns of Lueben and Neugolz [6]. Lueben records survive for the period 1757-1837 and 1860-1874. Thus, while the names of many early Brieses are known, unfortunately many of the emigrant Brieses were born during the gap period of 1838-1859. This makes it difficult to connect family lines from present to past. The situation for Neugolz / Clausdorf is worse, as only birth records exist for a very short period from 1860-1869, other records having been lost during World War II.

To illustrate this, a summary of lineages, derived from paper records for the set of DNA-tested and linked Brieses, is shown in Fig. 3. While each lineage has several branches in more recent times, Fig. 3 only shows the main trunks. The records cover from 2-6 generations and individual lineages go back as far as 1738 and as little as 1930. Moreover, only four of the 17 lineages could be merged using paper records, leaving 13 unresolved lineages from five separate regions in Prussia. There is also a gap of at least 12 generations between the period when the Briese surname was adopted and the earliest known ancestor. Clearly, this leaves many questions unanswered and Fig. 3 shows the limitations of paper records in developing a comprehensive family tree.

Fig. 3. Briese surname lineages for 17 families determined from birth, death and marriage records.

The names of the earliest ancestors are shown in boxes. Lineages are coded for privacy and indicate the country where most descendants live and emigration year (where relevant). The bracketed information is the location of the earliest known ancestor and the year of his birth. The blue region shows the period when the surname would have been adopted.



Results from genetic studies

From the first two comparisons, the Y-DNA data began to show the relationship between previously unconnected families and, with the current 14 data sets, a detailed picture of the pattern of descendance of the 13 unresolved lineages has emerged. The genetic distance (a measure of the number of different mutations between pairs of testers) can be determined from STR data. This reduced the number of lineages from 13 to 3 distinct groups that separated long before surnames were adopted, one (B1) containing 11 of the lineages and the other two (B2 and B3), a single lineage each. Based on known mutation rates, STRs can also be used to estimate when the time to the most recent common ancestor [7]. In the case of group B1, the common

ancestor of the 11 lineages lived around 1500 AD, not long after the period of surname adoption in this area.

Here, the power of SNPs came into play, as they can identify with certainty the mutations that defined group B1 and subdivisions within it. B1 itself belongs to the haplogroup R-U106, which formed around 5000 years ago and is centred on Northern Europe. SNPs describe how the 11 lineages within group B1 merged back to their single ancestor (Fig. 4). Thus, B1 was defined as haplogroup R-CTS2361, which contained two daughter haplogroups, BY20739 and BY66812. Haplogroup BY20739 contains a further daughter haplogroup, BY20733, which itself is subdivided into haplogroups BY107142 and BY158153. Genetic studies had linked all 11 lineages and shown a pattern of descent through this hierarchy of haplogroups (Fig. 4).

Critically, haplogroup R-CTS2361 has proved unique to the Briese surname, supporting the hypothesis of a single origin. While lineages B2 and B3 pre-dated surname adoption, which could suggest multiple origins of the name, both have been shown by DNA evidence to have had patrilineal disjuncts, where the genetic strand associated with another surname merged into the cultural and name-bearing Briese lineage. Lineage B2 also shows the other type of disjunct, where an adoption led to a genetic Briese strand merging into another surname's cultural strand. From demographic evidence, both these lineages are associated with the B1 grouping.

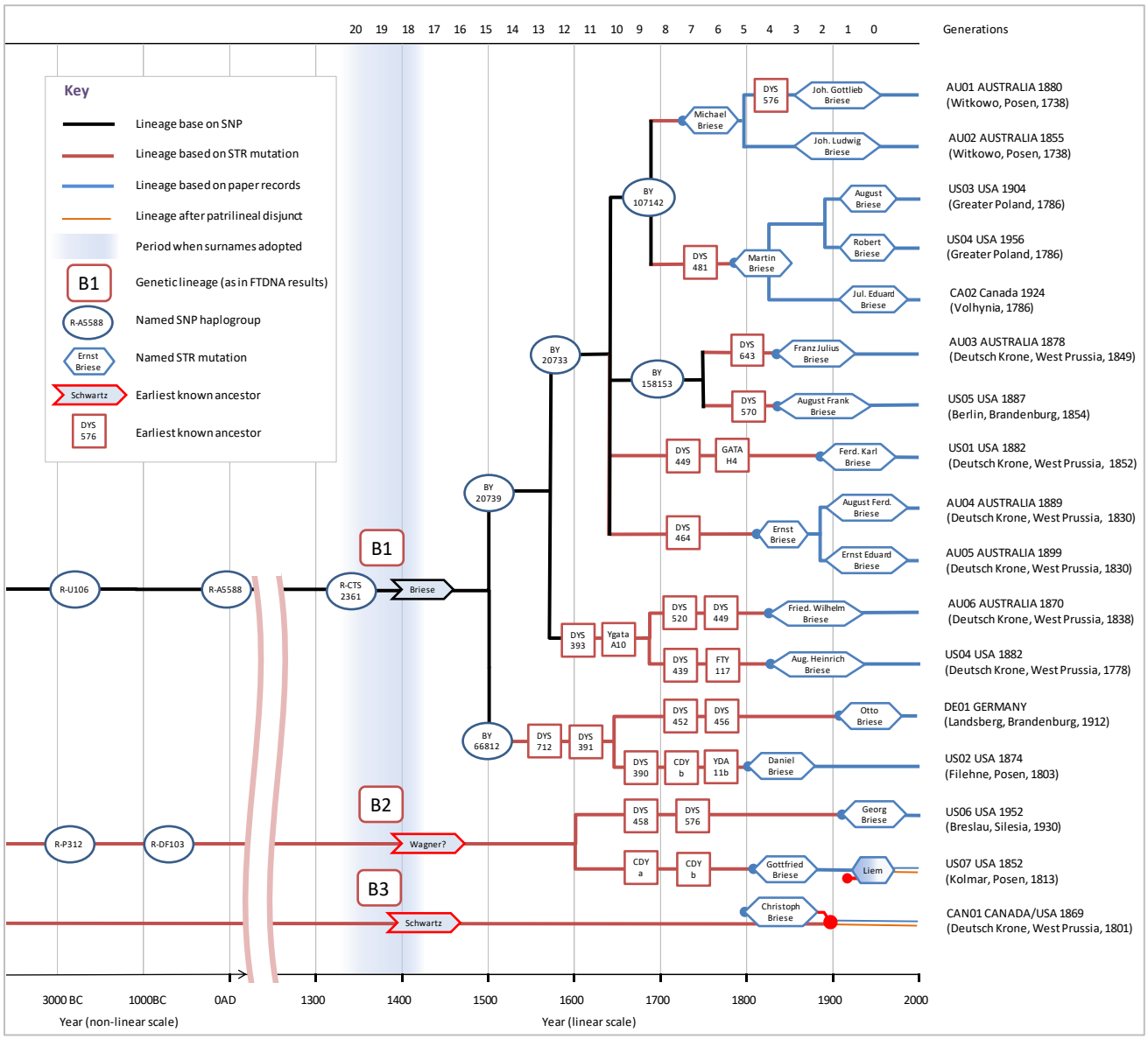
As STR and SNP mutations occur independently, STR mutations are further able to resolve patterns of descent. Lineages within an SNP-defined haplogroup which share some of their STR mutations as well as having distinct ones, most likely share a more recent common ancestor within that group. Thus, a lineage can be further split. This is the case with three pairs of lineages within haplogroup BY66812, BY20739 and BY107142, respectively (Fig. 4).

As is the case with Haplogroup R-CTS2361, the age of the daughter haplogroups could be determined from the number of STR mutations, leading to a tree that shows not only the pattern, but the approximate dateline of descent (Fig. 4). While not providing actual names for our ancestors, the analysis of STR and SNP DNA data in combination with paper genealogical records have shown clearly how the Briese B1 families are related.

The data become even more interesting when a demographic component is added. The earliest subdivision of the Briese B1 lineage, suggests a geographic split in the 16th century, with the 2 members of haplogroup BY66812 centred around Landsberg in Brandenburg and the remaining 11 lineages of haplogroup BY20739 having a strong connection to Deutsch Krone in West Prussia, some 100km to the east. These locations correspond to distinct density clusters of the Briese surname from paper records [3]. Descendants of the daughter haplogroup BY107142 within the Deutsch Krone cluster could not be traced back to that region on paper, but the genetic data and known eastwards migration patterns of German settlers in the 18th and 19th centuries [11] indicate that they must have emigrated from Deutsch Krone to their later locations in Posen and Greater Poland, respectively, and further to Volhynia (current-day Ukraine).

In conclusion, the importance of genetic data to this surname study cannot be understated. While not providing actual names for our ancestors, the analysis of STR and SNP DNA data in combination with paper genealogical records has taken an unconnected set of lineages to a comprehensive and dated family tree from which we can start to make inferences about the demography of the surname as well as its origin.

Fig. 4. Briese surname lineage based on genetic and paper records (see notes after figure for more detailed explanation).



Notes for Fig. 4

1. Surnames in Germany were adopted slowly during the late middle ages (1250 -1500 AD) and it is not possible to say when a particular name arose. For the purposes of this figure, I am assuming that ”Briese” began in the late 1300s. The Briese surname project database gives a median generation time of 32 years, and this period allows a convenient 20 generations between the origin of the name and now. The time-scale for the figure is based on this generation time and known STR and SNP mutation rates per generation.
2. There are three distinct genetic lineages – B1, B2 and B3. They could represent three separate adoptions of the surname by unrelated people, but the genetic evidence indicates that there has been a patrilineal disjunct after adoption of surnames, as B2 is genetically close to the Wagner surname and B3 is genetically close to the Schwartz surname. In the latter case, paper records provide some additional support for this. Here the Briese surname (cultural strand) continues with the Schwartz Y-DNA genetic

strand. In addition, in B2, an adoption has led to the Briese Y-DNA genetic strand continuing with the Liem surname (cultural strand).

3. Lineage B1 contains a group of 14 Briese families – 14 with paper BMD records (blue), 11 with STR genetic data (red) and 10 with SNP genetic data (black) – that can be traced back to a single origin. From the most common place of origin of the group members, this has been split into two sub-lineages, the Deutsch Krone cluster (12 families) and the Landsberg cluster (2 families).
4. The blue lines show how paper records trace back from the present, the black line show how SNP data pushes forward from the past and the red lines show how STR data fills in the blanks in between. The ultimate description of our ancestry would be when SNP (black) and paper records overlap to produce an absolute and complete lineage.
5. Each black oval represents an SNP mutation, which defines the haplogroup of the same name, i.e. if, within an existing haplogroup, there are at least two members with a new mutation that no-one else in the group has, then they form a new daughter haplogroup. Thus, the SNP tree grows forward from ancient times toward the present. Haplogroups may also have several mutations unique to themselves, and the number of these can be used to determine their age. When this study first commenced, the youngest haplogroup to which the Briese lineages belonged was A5588, which formed around 3000 years ago. In 2016, when the first project members had their DNA analysed for SNPs, the big discovery was an SNP mutation called CTS2361 that is so far unique to the Briese surname. It arose around 600-700 years ago, i.e. just before we assume the Briese surname was adopted in eastern Germany. With more members testing, haplogroup CTS2361 has now formed five daughter haplogroups, BY66812, BY20739, BY20733, BY158153 and BY107142 (each with more than one member). Thus, members of the last group are identified as A5588>BY20738> CTS2361>BY20739>BY20733>BY107142. Below this, single members have unique SNPs, which if found in another member of that haplogroup would split the group even further.
6. FamilyTreeDNA carry out STR analysis in blocks, STR37 (markers 1-37), STR67 (also has markers 38-67), STR111 (also has markers 68-111) and BigY (also has markers 112-700, which is part of the BigY SNP test). As a base, having the Briese surname and testing for STR37 is sufficient to determine if a family belongs to the cluster. However, to find out with certainty the relationships within the cluster, more STR or even SNP testing is needed. STR analysis is only useful within 20 generations from the present, but this is the period of surnames.
7. In the figure, red squares represent STR mutations and, although the lineages derived from them are not absolute, they help understand the period in between known SNP mutations and known paper records. For example, AU06 and US04 share the STR mutations DYS393 and YgataA10, which suggests that they have a common ancestor.

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