

Preliminary Phylogenetic Analysis of Briese Family Relationships

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Summary

A comparison was made of the STR markers on the Y-chromosome of six individuals bearing the surname Briese. Based on paper records, two of these individuals were known to be related, but relationships could not be determined for others. The genetic study showed that four of the six did have a common ancestor and suggests that a cluster of related Briese families lived in the Deutsch Krone area of West Prussia in the 18th century. A fifth individual, originating from a different geographic region, Meseritz in Posen, was more distantly related, while the sixth was not related at all. While not providing proof, these findings agree with the hypothesis that the Briese surname originated as a “place name” that was initially adopted by unrelated people. Genetic genealogy can help to determine relationships between emigrant Briese families and those remaining in Germany. More individuals from Briese families with known origins are needed to participate in this study to confirm and enlarge on these preliminary findings.

Introduction

The Briese surname¹, as considered here, is of German origin. It is a “place name”, that is when people began adopting surnames in the 15th and 16th centuries, they took the name of the place where they lived. The Briese surname is most common in former regions of Prussia, from Brandenburg through to East Prussia. This area has many towns and villages bearing the name Briese, Briesen, or variants of this and these are likely sources of the surname. More detail of the origins of the name can be found elsewhere¹.

The “place name” origin of the surname would suggest that unrelated people could initially have adopted the name Briese. As families grew and moved, it is hypothesised that this would lead to clusters of related family groups, differentiated from other such clusters, but all bearing the surname Briese. Classical genealogical research indicates that such geographic Briese clusters existed in the late 18th and 19th centuries in Brandenburg, West Prussia, East Prussia, Pomerania and Posen (see Table 1). However, subsequent internal movement, emigration overseas and displacement due to war has destroyed much of this demographic pattern.

During the 19th century, a number of Briese families emigrated from these areas to North America, Australia and Brazil. Many of the descendants of these families are now interested in discovering their family roots and whether their Briese family is related to other Briese families. Paper records provide some answers, but in many cases, these are missing, have critical gaps, or do not go back far enough to provide the evidence needed. As both the surname and the Y-chromosome are passed down the male lineage of a family, genetic genealogy provides a complementary approach that can help unravel the answers to these questions.

This study² is an attempt to describe the phylogenetic relationships between people bearing the surname Briese, based on a comparison of genetic markers on male Y-DNA. Such a study could also clarify conjecture on the origins of the Briese name.

Table 1. Regions of Prussia where the Briese name occurs most frequently in 18th and early 19th century records.

Province	District
Brandenburg	Landsberg/Warthe
Brandenburg	Lebus
East Prussia	Gerdauern
East Prussia	Roessel
Pomerania	Neustettin
Posen	Meseritz
Posen	Czarnikau
Posen	Schwerin
West Prussia	Deutsch Krone
West Prussia	Flatow

Methods

To date, six individuals with the surname Briese have contributed Y-DNA samples for analysis. These individuals descend from families that migrated to North America and Australia and, in all but one case, can trace their family back to a specific location in Prussia. Genetic analyses were carried out by FTDNA (Family Tree DNA)³, a commercial firm offering genetic testing for genealogical purposes. The recommended test for 37 STR (short tandem repeat) markers on the Y-chromosome was used, as the 12- and 25-marker sets offered are insufficient to determine relationships as accurately as required.

Individuals participating in this study are identified here by a 6-letter code to protect privacy. The code also identifies the location of the place where the earliest known ancestor of each individual (see Table 1). An example of an individual data set of 37 STR markers is shown in Table 2.

Table 1. Explanation of the geographic identity code (all regions are former parts of Prussia).

First letter =Province (Provinz)	Next two letters = District (Kreis)	Last two letters = town or village
P Posen	Me Meseritz	Me Meseritz
	Wi Witkowo	Po Potrzymowo
W Westpreussen	DK Deutsch Krone	Ap Appelwerder
		Ng Neugolz
U Prussia (region unknown)		

N.B a final number distinguishes individuals originating from the same location, where required
e.g. P-WiPo1 = Posen, Witkowo, Potrzymowo, person 1

Table 2. An example of the data obtained from the FamilyTreeDNA analysis of 37 Y-DNA markers.

Name	Paternal Ancestor Name	Haplogroup	DYS393	DYS390	DYS19	DYS391	DYS385	DYS426	DYS388	DYS439	DYS389i	DYS392	DYS389ii	DYS458	DYS459	DYS455	DYS454	DYS447	DYS437	DYS448	DYS449	DYS464	DYS460	Y-GATA-H4	YCAII	DYS456	DYS607	DYS576	DYS570	CDY	DYS442	DYS438
DTB	Michael Briese, b.c. 1738, d. Potrzymowo, Posen	R1b1a2a1a1a4	13	23	14	11	11-14	12	12	12	13	13	30	18	9-10	11	11	24	15	19	29	14-15-17-17	10	12	19-23	16	16	18	17	36-39	12	12

The six sets of 37 markers were initially subjected to McGee's on-line Y-DNA Comparison Utility⁴ to produce a matrix indicating the number of generations to the most recent common ancestor and a matrix of genetic

distances (the total number of differences, or mutations, between two sets of results). The analyses were based on the infinite allele mutation model with a mutation rate of 0.0054 per generation (the average value derived from all FTDNA data). The genetic distances were further analysed by the Kitsch program of Phylip⁵ (version 3.69), a freeware package of phylogenetic software. This program used the Fitch-Margoliash distance matrix method (with molecular clock) to produce a tree showing the phylogenetic relationships of the six individuals and, by inference, their families. Individuals W-WiPo1 and W-WiPo2 are known to be related with 4 and 5 generations separation, respectively, from their most recent common ancestor. This was used to calibrate the results, by adjusting the outcome probability to reflect this known point. The tree was shown on two scales, one showing the indicative number of generations back to the point when family lineages separated, and the other showing a calendar year time-line, which gives an idea of when such separation occurred. This time-line is based on a generation time of 30 years, which was found to accurately reflect the time scale for the two known related individuals.

Results

Genetic distances between pairs of Briese individuals are shown in Table 3. According to the FTDNA interpretation of genetic distance⁶, a distance of 1 indicates a tight relationship, 2-3 indicates that they are related, 4 indicates a probable relationship, 5 a possible relationship and 6 or more suggests relationships may pre-date the time when people in Europe adopted surnames.

Table 3. Matrix of genetic distances between pairs of Briese individuals (1-3 = related, 4-5 = probably related)

ID of person	P-WiPo1	P-WiPo2	W-DKNg	W-DKAp	P-MeMe	U
P-WiPo1		1	1	2	4	15
P-WiPo2			2	3	5	15
W-DKNg				3	5	15
W-DKAp					6	16
P-MeMe						18
U						

Given that P-WiPo1 and P-WiPo2 are from the same family originating from Potrymowo, Posen, it is not surprising that the genetic distance is so close (=1). This family has been in Australia since 1855. However, these two are also genetically close (distances = 2-3) to the two individuals originating from Deutsch Krone, Westpreussen (W-DKNg and W-DKAp). The family of W-DKNg emigrated to Australia and the family of W-DKAp emigrated to the USA. No connection had been found between these three families in paper records (births, deaths and marriages), but the y-DNA evidence demonstrates that they have a relatively recent common origin. The times to the most recent common ancestor of pairs of individuals (Table 4) indicate that were part of a common family about seven generations ago.

P-MeMe, originating from Meseritz, Posen, and now based in the USA, is genetically more separated from this group (distances = 4-6) and, when individual pairs are considered, borders on the limit of what FTDNA considers evidence for a relationship. However, the results need to be interpreted in terms of the overall pattern of genetic distances (see Fig. 1). The phylogenetic tree in Fig. 1 suggests that the split between the Meseritz family and the others occurred around 15 generations ago, i.e. in the 1500s.

The last individual, from a family that emigrated to the USA, but of unknown origin (other than Prussia), is clearly unrelated to the other five in genealogical time, showing very large genetic separation from them (distances = 15-18).

Table 4. The number of generations back to the most recent common ancestor for pairs of Briese individuals. The 4 generations to the common ancestor of P-WiPo1 and P-WiPo2 is known to be correct and was used to calibrate other values.

ID of person	P-WiPo1	P-WiPo2	W-DKNg	W-DKAp	P-MeMe	U
P-WiPo1		4	4	7	12	50
P-WiPo2			7	10	15	50
W-DKNg				10	15	55
W-DKAp					18	55
P-MeMe						64
U						

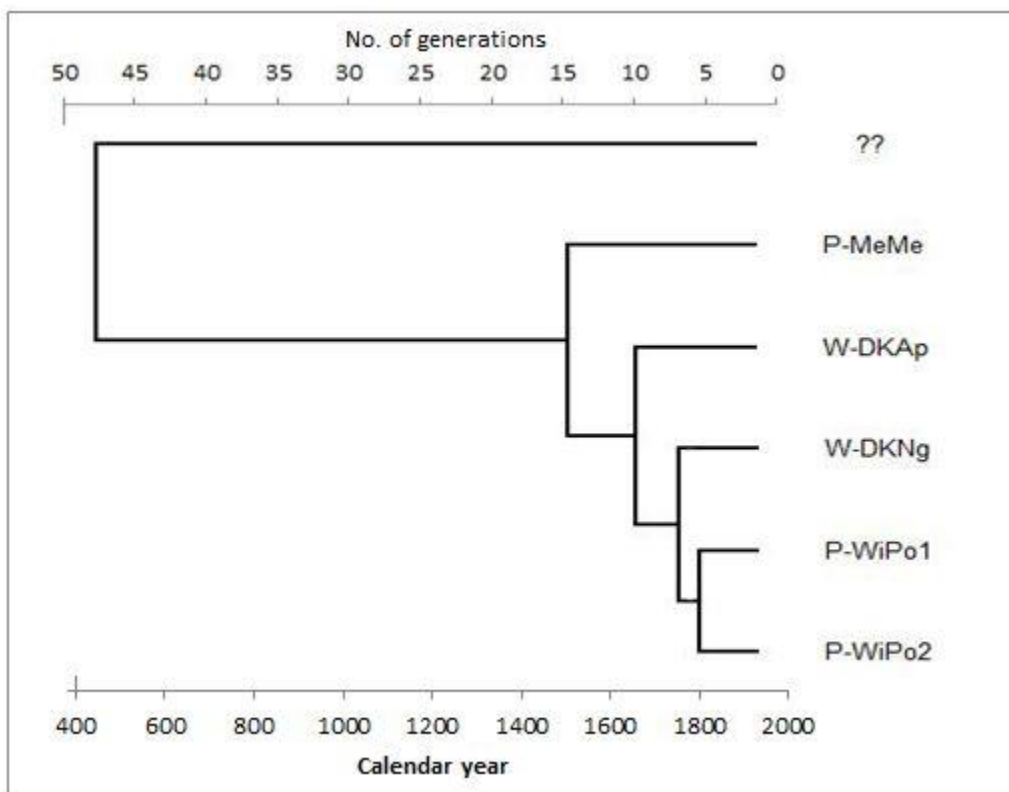


Fig. 1. Phylogenetic relationships of six Briese individuals from five separate “families”. Each individual is identified by a code indicating the place where their earliest known ancestor was born or lived (see methods). The top axis shows the number of generations before now (based on a 30-year generation period) and the bottom axis is the calendar year.

Discussion

A sample size of six is small and, as a result, findings should be viewed as indicative. That said, the results have shown that genetic studies can make an important contribution to genealogy. They show that four of the individuals, two from Potrzykowo, Posen, and two from Deutsch Krone, West Prussia (from the villages of Appelwerder and Neugolz, respectively), belong to a related cluster of Brieses, which was not demonstrable from paper records. The Y-DNA data also indicates that the common ancestor lived in the late 1600s or early

1700s. Church records from the Lüben Evangelical Parish⁷ show that there were a large number of Brieses in the Deutsch Krone district, as far back as the mid 1700s . By contrast, the related Briesie family from Potrymowo is the only one in the Czerniejewo Evangelical Church Records⁷. This suggests that the family may have emigrated to that area from Deutsch Krone just prior to the dates of surviving paper records.

The individual originating from Meseritz also appears to be related to the Deutsch Krone cluster, but more distantly, dating back perhaps to the 1500s. Given the large number of Briesie records in the Meseritz church book⁶ in the 18th and 19th century, it seems likely that this region comprises a distinct cluster of Briesie families. Further testing of individuals originating from Meseritz is needed to verify this. The Deutsch Krone Brieses could originate from Meseritz, or both clusters might originate from a common ancestor who lived in another region. Again more samples are needed.

As for the unrelated individual, there are two possibilities; 1) he is descended from an ancestor who independently took on the name Briesie when surnames were being adopted, or 2) the surname lineage and genetic lineage have become disjunct at some stage during the generations elapsed (e.g. in the case of adoption). As before, more samples might provide evidence that this is an independently-originating and unrelated group of Briesie families, as might be expected when the surname is derived from a place name.

These results demonstrate that genetic genealogy is able to prove (or disprove) relationships between families where paper records are missing. Several families from the Deutsch Krone area, other than those mentioned here, emigrated to Australia and North America and Y-DNA comparisons of their members should show how they are related. Broader sampling of Briesie families from other areas should also be able to show whether the different clusters have originated independently or not. In the latter case, it should be able to show the patterns in related family clusters of a diverging lineage from a distant common ancestor. More sampling is needed to clarify the relationships within family clusters and also between Briesie families originating from different geographic regions.

Notes and references

1. Why is the family tree a silver birch? The meaning of the Briesie name
http://gang-gang.net/briesegenealogy/histories/pdf_files/briesename.pdf (David Briesie)
2. Briesie surname project <http://www.familytreedna.com/public/briesie/default.aspx>
3. Family Tree DNA website <http://www.familytreedna.com/>
4. McGee's Y-DNA Comparison Utility for FTDNA
http://www.mymcgee.com/tools/yutility.html?mode=ftdna_mode (D. McGee)
5. Phylip phylogeny inference package <http://evolution.genetics.washington.edu/phylip/general.html> (J. Felsenstein)
6. If two men share a surname, how should the genetic distance at 37 Y-chromosome STR markers be interpreted?
<http://www.familytreedna.com/faq/answers.aspx?id=9#922> (Family Tree DNA)
7. From microfilmed records sourced in the Family Search Catalog and on-line resources of FamilySearch.org
<https://familysearch.org> (Church of Jesus Christ of the Latter Day Saints)

