

# Z305

Variance-based foundation: 1048 BC +/- 901 years

# Provisional top-level phylogeny of the Y-DNA R-DF98 "Kings' Cluster"

## DESCRIPTION

Using differences in the Y-chromosome DNA of people matching this group, we have reconstructed the family tree of the Saxon royal household back to antiquity.

This chart shows the most-ancient structures in the tree, covering the latest of our pre-historic roots. Some speculation is given in their origins and details about the uncertainties in obtaining the dates of their foundation.

These structures are not necessarily fixed, but represent our best guess as to how the structure of DF98 maps out. In time, groups may split up, merge, or move up or down the tree structure as we get more information. Aside from genealogical and historical interests, these structures help us focus future testing on the branches and individuals who need it most. General recommendations for further testing for existing members are given for each "clan" in their descriptions. Individual recommendations can be given upon request.

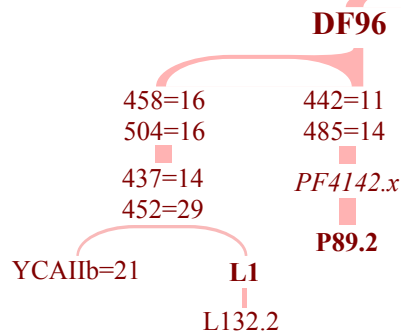
The dates given here are very approximate, but include reasonable estimates for all sources of error. These dates are given as "confidence intervals"; e.g., we can be 95% sure that a date lies within the 95% confidence interval, based on the data we have.

## SOURCE DATA, ANALYSIS & INFORMATION

Y-DNA tests sourced from Family Tree DNA U106 and other projects and from Y-Search and semargl.me. Only 67 and 111 marker data are used for finding dates but <67 marker data have been used to aid structure finding. Further details are given on the next page.

Pink connectors denote relationships based on differences in DNA. Light blue connectors denote relationships linked by geography and/or surnames, or by recorded speculative histories; Blue connectors shown complete and well-known paper trails to given dates.

Compiled 01 November 2013  
Dr. Iain McDonald



## DF98 "The Kings' Cluster"

### Age

**Most-recent common ancestor for Kings' Cluster**  
Best estimate (50%): 478 BC  
68% confidence (16-84%) the MRCA was born between: 738BC - 222BC  
90% confidence (5-95%) the MRCA was born between: 893BC - 66BC  
95% confidence (2.5-97.5%) the MRCA was born between: 970BC - 7AD

There are two main methods for determining the age of a group of individuals: the infinite alleles Bayesian method developed by Walsh et al. (2001, Genetics, 158, 897) and the variance-based method of Nordvedt et al. (2008, Jour. Gen. Gen., 4, 96). They each have their drawbacks. The infinite alleles model does not take into account back mutations or several sequential mutations in a lineage. The variance-based method does not take into account multi-step mutations. Corrections can be applied: for the infinite alleles model, a percentage correction for a given number of generations can be added; for the variance-based method, those STRs with known multi-step mutations can be removed. This results in an answer that is at least consistent with the uncertainties involved and probably only differs due to the bounding constraints applied to the infinite alleles model. We have taken a weighted average of the two methods for our final results. Full results are:

Variance-based method (affected by multi-step mutations)  
Multi-step markers removed: 182BC - 46AD (95%)  
Also removed 441, 411, 712, 1090C - 13AD (95%)  
+/-, and (DYS641, 1257C, 207AD) (95%)  
Best estimate: 675 BC (274-year correction)

Infinite alleles Bayesian method (affected by multiple back mutations)  
Final estimate: 402C - 46AD (95%)  
Rounded by paper trails and Z305 variance-based age  
Adapted 2% +/- correction for back/multiple mutations  
(based on Monte-Carlo simulation of a 70-generation pop., a typical line will have ~2 back & 1 multiple mutation)  
Corrected: 742BC - 70BC (95%)  
Best estimate: 399 BC (477-year correction)

**Defining mutations:**  
DYF395s1=16-16  
DYS557=15

### Speculative origin

The age of the cluster cannot be constrained much better than the first millennium BC, though there is a peak in probability close to the middle of that millennium and it is almost certainly older than Roman invasions of northern Europe. The geography of the cluster (see later pages) has the most-diverse (highest-variance) population within a few hundred miles of Frankfurt. The combination of the two would place the foundation of the cluster in either the Hallstatt or La Tene cultures. We know there was a core region of La Tene influence to the north of Frankfurt, which arose around 450BC with the overthrow of the Hallstatt power structure. While the La Tene culture was disparate, lacking in nobility, a major power base seemed to operate at Glauberg in Hesse. Were DF98 able to be linked to the La Tene culture, which is a purely speculative suggestion, we can explain its rapid diversification into different groups as follows. Polybius, Livy and other Greco-Roman writers noted incursions by northern tribes to Sudra and 320 BC. These are now believed to be a result of over-population, which we expect to be driven by a population boom. DF98 would then have expanded rapidly, creating the broad tree structure we see.

The La Tene culture suffered from the spread of Germanic cultures from the north and the Roman Empire from the south. The effect on DF98 is not clear, though the number of groups with several mutations not seen outside them suggests the population underwent a contraction in numbers and possible dispersion.

A resurgence in later times, particularly among well-tested Britons, may be attributable to migrations from Europe. Distribution in the British Isles avoids the Scottish Highlands, Wales, Cornwall and parts of the Rep. of Ireland. This suggests a mixture of Anglo-Saxon, Norman and possibly Danish Viking migrations brought DF98 to England, eastern Scotland and subsequently Ireland.

### Notes on sub-structure

Substructure within a group is usually defined by SNPs. The SNPs that define the older structure within DF98 are not yet known. With certain groups, like the Kings' Cluster, sufficient time passes between one group's foundation and another to build up some defining STR mutations. While groups with many shared STR mutations exist within DF98, the population explosion shortly after DF98's foundation has meant that not enough time passed between the DF98 founder's birth and the establishment of the main groups for many identifiable STR mutations to take place. Structure clearly exists within DF98 at a high level, but it is fast-mutating STR markers that are unreliable tracers. The structure that we show is what we believe the most-likely interpretation to be.

A large portion of the cluster have the mutations DYS607=14 and DYS552=25. Clearly these markers define a large sub-cluster. However, both markers are volatile, with (back) mutations expected in 9% of cluster members over the existence of DF98: i.e. around 18 members should mutate into or out of the sub-cluster on one of the markers. However, only one or two should mutate into/out of the cluster on both markers. At the moment, we are assuming that DYS552 mutated first, as it is found in more of the cluster, despite having a similar mutation rate. Testing DYS552 requires an 111-marker upgrade.

## L128? (DYS534=16)

An ancient group with a sequential hierarchy, typical of a population which has been stable over the last 2000 years. This group contains the SNP L128 and its daughter SNP L127.2. While we may only expect a small fraction of individuals within this group to be L128+, should a commercially test for it become reliably available, this group of people should consider testing for L128.

I have defined this group by DYS534=16, as it seems the largest encompassing mutation. It is not clear that all those with 534=16 arise from the same mutation, but we must assume this until further tests prove otherwise. The group's structure is not wholly clear and would benefit from more members testing to 111 markers. DYS459=9-9 probably provides the next level of structure, with DYS444=13 below that. However, each of these mutations has probably occurred more than once within the group. Many of the remaining ambiguities will be resolvable with 111 marker upgrades.

Geographically, this group is diverse, having spread as far as Norway. Members are known to the south of Frankfurt. In the UK, members may congregate in East Anglia and the Saxon counties.

**Most-recent common ancestor**  
Best estimate (50%): 200 BC  
68% confidence (16-84%) the MRCA was born between: 506BC - 77AD  
90% confidence (5-95%) the MRCA was born between: 720BC - 236BC  
95% confidence (2.5-97.5%) the MRCA was born between: 828BC - 309AD  
(infinite alleles method, assumes 20 +/- 6% correction for invisible mutations)

## Ancient Germans

Though probably a young cluster overall, this is among the most-distantly related sub-clusters in the others. They share none of the mutations at DYS607, 552 and 534 of the other groups. This makes them important in uncovering its origins.

It appears likely that this small cluster, which is strongly German and congregates near Frankfurt on the east bank of the Rhine, has moved little since its origin, possibly occupying the south-eastern side of the original distribution. I strongly recommend upgrading to 111 markers and confirming DF98.

The youth of this cluster is surprising. As always, the dates are very uncertain and a great many things were happening in this period. However, perhaps the most striking was the collapse of the Roman Empire. This group may have expanded through a Germanic population expansion that may have happened afterwards during the "Migration Period".

**Most-recent common ancestor**  
Best estimate (50%): 563 AD  
68% confidence (16-84%) the MRCA was born between: 371AD - 739AD  
90% confidence (5-95%) the MRCA was born between: 241AD - 840AD  
95% confidence (2.5-97.5%) the MRCA was born between: 176AD - 886AD  
(infinite alleles method, assumes 12 +/- 6% correction for invisible mutations)

## DYS552=25

This largest group may represent the northern side of the DF98 expansion. It may be larger because it avoided the later Roman constriction of the Germanic/Celtic tribes which may have affected the DF98 southern expansion.

**Most-recent common ancestor**  
Best estimate (50%): 316BC  
68% confidence (16-84%) the MRCA was born between: 538BC - 141BC  
90% confidence (5-95%) the MRCA was born between: 667BC - 30BC  
95% confidence (2.5-97.5%) the MRCA was born between: 727BC - 21AD  
(infinite alleles method, assumes 21 +/- 5% correction for invisible mutations)

## Dutton & Bowes clans

The whole of DYS552=25, DYS607=14 may be a single lineage, or may be two separate clans under DYS552=25.

### Bowes clan

An old group, this "clan" includes the Pope family, who are thought to trace back to Belgium. As other clans, this group is dominated by the British testing bias. There is not sufficient information to deduce their origins, save the fact that they may have a northerly bias within the larger Cluster.

**Most-recent common ancestor**  
Best estimate (50%): 158 BC  
68% conf. int. (16-84%) for MRCA: 710BC - 281AD  
90% conf. int. (5-95%) for MRCA: 1138BC - 513AD  
95% conf. int. (2.5-97.5%) for MRCA: 1370BC - 615AD  
(20 +/- 8% correction for invisible mutations)

### Dutton clan

The Classical history of this clan is unclear. There is an unusual early link to Sudra, the easternmost known member, which sets the MRCA date for this clan. After this, it appears to have been a small population for the next thousand years, before expanding into a small but significant British population. The Dutton and Warburton surnames are historically linked to a Norman knight, Odard de Dutton. The MRCA timescale of the closely-related members of this group implies a Norman-era origin, hence we surmise that the two tested lines here are those descending from Odard.

**Most-recent common ancestor**  
Best estimate (50%): 197 BC  
68% conf. int. (16-84%) for MRCA: 707BC - 554AD  
90% conf. int. (5-95%) for MRCA: 1138BC - 513AD  
95% conf. int. (2.5-97.5%) for MRCA: 1094BC - 762AD  
(20 +/- 8% correction for invisible mutations)

## DYS607=14

This is the largest group within the Kings' Cluster which we can put together with great confidence, sharing both the 552 and 607 mutations. They are centred much more to the north and west of the population locus at Frankfurt, and may represent an early expansion in this direction. They generally stay to the north of the Limes Germanicus, and have a much lower percentage of continental testers, possibly indicating a large, early migration to Great Britain.

**Most-recent common ancestor**  
Best estimate (50%): 172AD  
68% confidence (16-84%) the MRCA was born between: 29AD - 321AD  
90% confidence (5-95%) the MRCA was born between: 63BC - 404AD  
95% confidence (2.5-97.5%) the MRCA was born between: 106BC - 442AD  
(infinite alleles method, assumes 16 +/- 5% correction for invisible mutations)

## DYS511=11 and/or DYS533=11

Many of the 607=14, 552=25 group fall into the three clans below. The Jarman and Donald/Beckwith clans have 511=11, the Donald/Beckwith and Wettin lines have 533=11. The Jarman line has 533=13, i.e. a mutation in the other direction. The question remains at to whether we are looking at two mutations of DYS511 or DYS533, or a back mutation in one of these markers in one of the lineages. Currently, the age of this group is inseparable from its parent, the 607=14 group, however the DYS511 pairings have a much younger MRCA than the DYS533 pairings. This makes it more probable that the DYS511 group is the real one, but it then becomes unclear where the Wettin group fits in.

**Most-recent common ancestor**  
Best estimate (50%): 114AD  
68% confidence (16-84%) the MRCA was born between: 81BC - 296AD  
90% confidence (5-95%) the MRCA was born between: 210BC - 403AD  
95% confidence (2.5-97.5%) the MRCA was born between: 273BC - 452AD  
(infinite alleles method, assumes 17 +/- 5% correction for invisible mutations)

## Norton clan

The exact age and scope of this cluster is difficult to pin down. The 464-444 sub-cluster within the clan appears to have a higher age than the clan itself, which could indicate that we do not have the correct structure for the upper parts of the clan. (In which case the MRCA is liable to be slightly older). Geographically, this cluster is hard to pin down. The inclusion of Kolb suggests that this cluster originated near the foundation point of DF98.

The high percentage of German families and German names suggests a predominantly Germanic background. A number of STRs in the 111-marker upgrade are used for membership. Inclusion relies heavily on these markers, and testing them is liable to reveal the true structure. I strongly recommend upgrading to 111 markers and confirming DF98. Test consider Full Genomes, Geno 2.0 and Chrom2.

**Most-recent common ancestor**  
Best estimate (50%): 582AD  
68% confidence (16-84%) the MRCA was born between: 405 - 743AD  
90% confidence (5-95%) the MRCA was born between: 285 - 835AD  
95% confidence (2.5-97.5%) the MRCA was born between: 225 - 877AD  
(infinite alleles method, assumes 13 +/- 4% correction for invisible mutations)

## Graham clan

The large number of common mutations and lack of clear structure in the group suggests a rapid spread from a single, relatively young source. Members of the cluster are easily identifiable by the 3-step mutation to DYS617=9.

Within the UK surnames are in northern and western areas. The age of the cluster implies an origin from a single Norman migrant to Britain, but the inclusion of Washbaugh suggests that there is a German component of this clan. Weschbach as a surname localises slightly north of Frankfurt.

There have been few upgrades to 111 markers in this group, which would help pin down ages and structure.

**Most-recent common ancestor**  
Best estimate (50%): 967AD  
68% confidence (16-84%) the MRCA was born between: 803 - 1110AD  
90% confidence (5-95%) the MRCA was born between: 687 - 1191AD  
95% confidence (2.5-97.5%) the MRCA was born between: 627 - 1227AD  
(infinite alleles method, assumes 13 +/- 4% correction for invisible mutations)

## Wilder-Koch clan

While it is clear that a large sub-group exists within the Cluster, and that the indicated families are likely part of it, it is difficult to pin down an exact structure to the cluster, which makes dating it hard. It is quite possible that the cluster is older than is indicated here. The reason for this would be that this clan spread and diversified fairly early in the history of the Cluster, before many mutations had begun to build up.

The Germanic names concentrate towards the north of the Cluster's area, suggesting this may have been an early migration of DF98 north toward Denmark. The age and geography of the cluster suggests either a Danish or Anglo-Saxon descent for at least some of the English names within the cluster. Ordering of some of the early lines is difficult to determine and 111-marker upgrades are recommended for more lines.

**Most-recent common ancestor**  
Best estimate (50%): 680AD  
68% confidence (16-84%) the MRCA was born between: 412 - 898AD  
90% confidence (5-95%) the MRCA was born between: 212 - 1017AD  
95% confidence (2.5-97.5%) the MRCA was born between: 105 - 1070AD  
(infinite alleles method, assumes 11 +/- 4% correction for invisible mutations)

### DYS511-11

**Most-recent common ancestor**  
Best estimate (50%): 449AD  
68% confidence (16-84%) the MRCA was born between: 192AD - 673AD  
90% confidence (5-95%) the MRCA was born between: 8AD - 799AD  
95% confidence (2.5-97.5%) the MRCA was born between: 87BC - 856AD  
(infinite alleles method, assumes 13 +/- 4% correction for invisible mutations)

### DYS533-11

**Most-recent common ancestor**  
Best estimate (50%): 54AD  
68% confidence (16-84%) the MRCA was born between: 189BC - 276AD  
90% confidence (5-95%) the MRCA was born between: 355BC - 404AD  
95% confidence (2.5-97.5%) the MRCA was born between: 439BC - 462AD  
(infinite alleles method, assumes 16 +/- 5% correction for invisible mutations)

## Jarman clan

The youth of this cluster and ambiguous (Germanic/English) surnames suggests they represent branches of a larger cluster which mostly remained in Germany until at least post-Norman times. This cluster appears to have DYS511=11 but are mutated up to DYS533=13, rather than down to 11. They lack sufficient information to make an educated guess of a geographical origin, but show slowly-branching substructure typical of a stable population over the last 1000 or so years.

**Most-recent common ancestor**  
Best estimate (50%): 806AD  
68% confidence (16-84%) the MRCA was born between: 383AD - 1116AD  
90% confidence (5-95%) the MRCA was born between: 33AD - 1271AD  
95% confidence (2.5-97.5%) the MRCA was born between: 164BC - 1336AD  
(infinite alleles method, assumes 10 +/- 3% correction for invisible mutations)

## Donald & Beckwith clan

This pair of clans is in good shape, thanks to significant efforts to upgrade to 111 markers. It has both DYS511=11 and DYS533=11. It is not clear how closely these two groups are linked, as they only appear to share one extra mutation (DYS452=29). They probably separated shortly after their last link to their neighbouring "clans". The lack of German names may suggest a largely British origin, representing an early (Roman?) migration to the Isles. However, there are large sections of history missing from both clans that need to be filled in by new testers which may make this picture clearer.

**Most-recent common ancestor**  
Best estimate (50%): 70AD  
68% confidence (16-84%) the MRCA was born between: 182BC - 297AD  
90% confidence (5-95%) the MRCA was born between: 353BC - 429AD  
95% confidence (2.5-97.5%) the MRCA was born between: 439BC - 489AD  
(infinite alleles method, assumes 16 +/- 5% correction for invisible mutations)

### Donald sept

This is a young group within this clan, with five closely-related families sharing a probable post-Norman origin. Donald and Hadden have known roots near Aberdeen. Bess and Lawrence have no known origin, but their surnames localise at the opposite end of the country in Devon. The exact origin of these families is unclear, as is their geographical bissection. It is clear that they are a result of the rapid expansion of a family existing only a century or two before the adoption of surnames.

### Beckwith sept

This is probably a fairly old group within its clan, though there are few testers during its pre-Norman-era period. In this sept (as in the whole clan) there is a strong northern bias, with a definite concentration in Anglicised Scotland and north-eastern England. There are a number of closely-related testers, indicating the expansion of the family perhaps a few centuries before surnames were adopted.

We are continuing to search for proof of the Beckwith line of descent, which will come from other Beckwith testers.

## Wettin Royal clan

Though most of this family is British in origin, we know that the Wettin royal line began in Saxony around 1000 years ago. Most of this clan are related sometime during the Middle Ages, likely towards the earlier end of the dates given below. One interpretation of this is that they are descended from the Saxon chieftains which existed in the British Isles shortly after the Anglo-Saxon migrations to Britain.

It is difficult to accurately determine relationships within the main cluster. This is consistent with a period of population stagnation in between the circa Roman-era expansion of the last major structures within DF98 and the Middle-Ages expansion of this clan. The later expansion may be linked to the Saxon and/or Wettin rise to power during this time.

Geographically, it is hard to pin down a location for this clan's origin, due to lack of German surnames other than Wettin who are closely associated. Given the age of the clan and the proximity of the Wettin origin in the Harz mountains to other DF98 members, it is reasonable to surmise it was somewhere around there.

Though many of the lines closest to the Wettins are in good shape through 111-marker upgrades, I strongly recommend this upgrade to those on the left-hand side of the group. We continue to search for members of the House of Wettin to pin down mutations to points in history.

**Most-recent common ancestor**  
Best estimate (50%): 1000AD  
68% confidence (16-84%) the MRCA was born between: 882AD - 1108AD  
90% confidence (5-95%) the MRCA was born between: 803AD - 1169AD  
95% confidence (2.5-97.5%) the MRCA was born between: 763BC - 1197AD  
(infinite alleles method, assumes 10 +/- 3% correction for invisible mutations)



