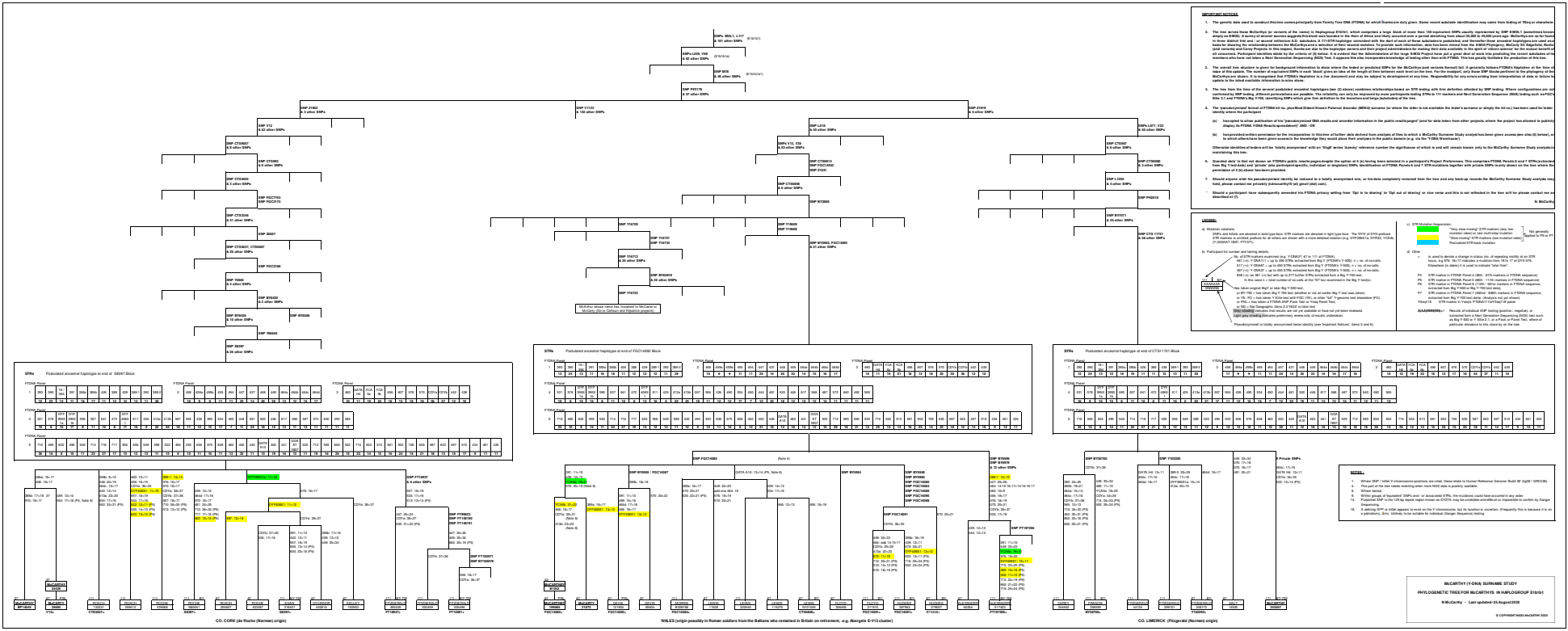
IMPORTANT NOTICES
1. The genetic data used to construct this tree comes principally from Family Tree DNA (FTDNA) for which Surname was duly given. Some record duplicate identification may come from testing at 'Ring or elsewhere.
2. The tree arrives from McCarthys (or variants of the name) in Haplogroup R1b1a1, which comprises a large block of more than 100 equivalent SNPs usually represented by SNP S4538.1 (sometimes known simply as S4538). A survey of several dozens suggests this block was founded in the Horn of Africa and likely accrued over a period stretching from about 20,000 to 30,000 years ago. McCarthys are so far found in only a few of the 100+ SNPs that have been identified within the block. Most of the latter are known only from a single family and are therefore not shown on the tree. Instead, they are listed in the accompanying table for allowing the McCarthy surname to be confidently tested to the appropriate selection of their ancestral matches. To provide such information, data has been mined from the S4538 Phylogeny, McCarthy DC Haplotest, Ruvos (and variants) and Carey Projects. In this respect, thanks are due to the haplotype owners and their project administrators for making their data available in the spirit of 'citizen science' for the mutual benefit of all concerned. Participant identities abide by the criteria of (i) below. It is evident that the Administrators of the large S4538 Project have put a great deal of work into predicting the recent subclades of the members who have not taken a Next Generation Sequencing (NGS) Test. It appears this also incorporates knowledge of testing other than with FTDNA. This has greatly facilitated the production of this tree.
3. The current tree structure is given for background information to show where the tested or predicted SNPs for the McCarthys (and variants thereof) fall. It generally follows FTDNA's Haplotree at the time of issue of this update. The number of equivalent SNPs in each 'block' gives an idea of the length of time between each level on the tree. For the mediaeval, only those SNP blocks pertinent to the phylogeny of the McCarthys are shown. It is recognised that FTDNA's Haplotree is a fine document and may be subject to development at any time. Responsibility for any errors arising from interpretation of data or failure to update to the latest available information is mine alone.
4. The tree from the time of the several postulated ancestral haplotypes (see (2) above) combines relationships based on STR testing with firm detection afforded by SNP testing. Where configurations are not confirmed by SNP testing, different permutations are possible. The reliability can only be improved by more participants testing STRs to 111 markers and Next Generation Sequence (NGS) testing such as FGC's Elite 3.1 and FTDNA's Big Y700. Identifying SNPs which give fine definition to the branches and twigs (subclades) of the tree.
5. The 'pseudonymised' format of FTDNA kit no. plus Most Distant Known Paternal Ancestor (MDKA) surname (or where the latter is not available the leader's surname or simply the kit no.) has been used for lineal identity where the participant:
(a) has opted to allow publication of his "pseudonymised DNA results and ancestor information in the public results pages" (and for data taken from other projects, where the project has allowed its publicly display its FTDNA 'Y-DNA Results spreadsheet)" AND / OR
(b) has provided written permission for the incorporation in this tree of further data derived from analysis of this to which a McCarthy Surname Study analyst has been given access (see also (6) below); or to which others have been given access to the knowledge they would place their analyses in the public domain (e.g. via the "Y-DNA Warehouse").
Otherwise identities of testers will be 'totally anonymised' with an 'Orgill' series 'dummy' reference number the significance of which is and will remain known only to the McCarthy Surname Study analysts in maintaining this tree.
6. Guarded data' is that set down on FTDNA's public results pages despite the option at 5 (a) having been selected in a participant's Project Preferences. This comprises FTDNA Panels 6 and 7 STRs (inclusive) from Big Y test data and 'private' (aka participant-specific, individual or singleton) SNPs. Identified Panels 6 and 7 STR mutations together with private SNPs tardily shown on the tree where their penetration of 5 (b) above has been provided.
7. Should anyone wish his pseudonymised identity be reduced to a totally anonymised one, or his data completely removed from the tree and any back-up records the McCarthy Surname Study analysts may hold, please contact me privately (rulmccarthy10 (at) gmail (dot) com).
Should a participant have subsequently amended his FTDNA privacy setting from 'Opt in to sharing' to 'Opt out of sharing' or vice versa and this is not reflected in the tree until he please contact me as described at (7).
N. McCarthy
LEGENDS
a) Mutation relations
SNPs and eSNAs are denoted in bold type face. STR markers are denoted in light type face. The "DYS" of DYS prefixed STR markers is omitted; prefixes for all others are shown with a more detailed notation (e.g. GYP2M3.1a, DYR22, YCA2a, GGAAT1B07, PP21**).
b) Participant kit number and testing details:
No. of STR markers examined (e.g. Y-DNA37, 67 or 111 of FTDNA);
561 (+); Y-DNA111 = up to 650 STRs extracted from Big Y (FTDNA's Y-SEQ); (+) = no. of mutations;
637 (+); Y-DNA111 = up to 700 STRs extracted from Big Y (FTDNA's Y-SEQ); (+) = no. of mutations;
657 (+); Y-DNA37 = up to 650 STRs extracted from Big Y (FTDNA's Y-SEQ); (+) = no. of mutations;
838 (+); as 561 (+) but with up to 277 further STRs extracted from a Big Y-700 test.
In this case n = (total number of no calls at the 137 loci examined in the Big Y tests).
"Has taken original Big Y" or later Big Y-500 test;
"Has taken Big Y-700" = has taken Big Y-700 test (whether or not an earlier Big Y test was taken);
or YE, FC = has taken Y Elite test with FGC (YE), or other "kit" Y-genome test elsewhere (FC);
FL = has taken a FTDNA SNP Pack Test or Ysay Panel Test;
or NG = Next Geographic Data 2.0 "NGS" or later test.
"Results awaited" = sample sent to lab but results not yet in or have not yet been reviewed.
Light grey shading indicates preliminary review only of results undertaken.
"Pseudonymised' or totally anonymised tester identity (see 'Important Notices', items 5 and 6).
c) STR Mutation frequencies:
"Very slow moving" STR markers (very low mutation rates) or non-multistep mutation
"Slow moving" STR markers (low mutation rates)
Not generally applied to PH or FT
Penalated STR back mutation
d) Other
+ is used to denote a change in status (no. of repeating motifs) at an STR locus, e.g.16+. "A+" indicates a mutation from 16 to 17 at DYS 576. Elsewhere (e.dele) it is used to indicate "later than".
PA STR marker in FTDNA Panel 4 (389i - 675 markers in FTDNA sequence)
PB STR marker in FTDNA Panel 5 (885i - 1116 markers in FTDNA sequence)
PR STR marker in FTDNA Panel 6 (1356 - 561a2 markers in FTDNA sequence, extracted from Big Y-700 test data; (Analysis not yet shown)
P7 STR marker in FTDNA Panel 7 (Annex 1680+ markers in FTDNA sequence, extracted from Big Y-700 test data; (Analysis not yet shown)
YDiag118 STR marker in Ysay's FTDNA117(old Panel 7)Panel
A(AAAAAAAAA)n Results of individual SNP testing (positive / negative), or extracted from a Next Generation Sequencing (NGS) test such as Big Y-500 or Y Elite 2.1, or a Pack or Panel Test, above of particular relevance to kits close by on the tree.
NOTES
1. Where SNP / InDel Y-chromosome positions are cited, these relate to Human Reference Genome 'Build 38' (hg38 / GRCh38).
4. This part of the tree needs revising when more NGS data is publicly available.
8. Where tested.
9. Within groups of 'equidistant' SNPs and / or associated STRs, the mutations could have occurred in any order.
14. Purported SNP in the 12th bp repeat region known as DYZ19, may be unreliable and difficult or impossible to confirm by Sanger Sequencing.
18. A defining SNP' or InDel appears to exist on the Y chromosome, but its location is uncertain. (Frequently this is because it is on a palindrome, (brm). Unlikely to be suitable for individual (Sanger Sequenced) testing.
McCARTHY (Y-DNA) SURNAME STUDY
PHYLOGENETIC TREEFOR McCARTHYS IN HAPLOGROUP E1b1b1
N McCarthy - Last updated-23 August2020
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STRs Postulated ancestral haplotype at end of S8297 Block
STRs Postulated ancestral haplotype at end of FGC14282 Block
STRs Postulated ancestral haplotype at end of CTS11721 Block
WALES (origin possibly in Roman soldiers from the Balkans who remained in Britain on retirement, e.g. Abergele EY12 cluster)
CO. CORK (ie Roche (Norman) origin)
CO. LIMERICK (Fitzgerald (Norman) origin)