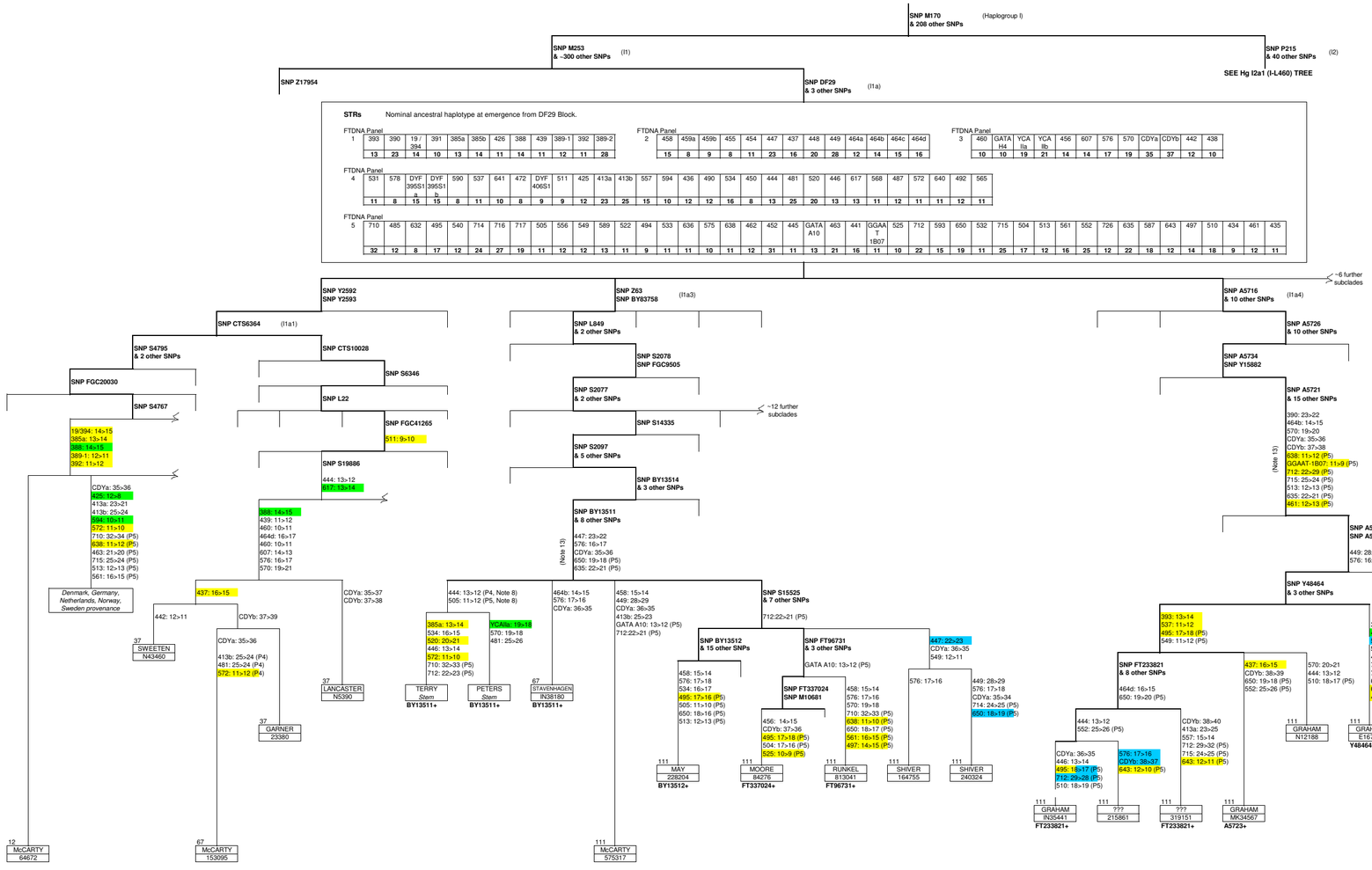
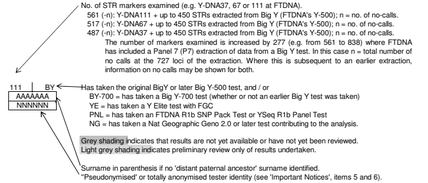


LEGEND:

a) Mutation notations

SNPs and InDels 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. DYF395S1a, DYR33, YCAIIb, (Y-)GGAAT 1B07, FTY371).

b) Participant kit number and testing details:



c) STR Mutation highlighting (frequencies revised February 2020 in accordance with Fig 4a at https://mccarthydna.wordpress.com/):

"Very slow moving" STR markers (very low mutation rates) or rare multi-step mutation
"Slow moving" STR markers (low mutation rates)
} Not generally applied to P6 or P7 (see (d) below).
Postulated STR back-mutation

d) Other

> is used to denote a change in status (no. of repeating motifs) at an STR locus, e.g 576: 18>17 indicates a mutation from 18 to 17 at DYS 576. Elsewhere (in dates) it is used to indicate "later than".

P4 STR marker in FTDNA Panel 4 (38th - 67th markers in FTDNA sequence).
P5 STR marker in FTDNA Panel 5 (68th - 111th markers in FTDNA sequence).
P6 STR marker in FTDNA Panel 6 (112th - 561st markers in FTDNA sequence, extracted from Big Y data).
P7 STR marker in FTDNA Panel 7 (562nd - 838th markers in FTDNA sequence, extracted from Big Y data).

A{AA}NN{NN}+/- Results of individual SNP testing (positive / negative), or extracted from a Next Generation Sequencing (NGS) test such as Big Y or Y Elite 2.1, or a Pack or Panel Test, where of particular relevance to kits close by on the tree.

IMPORTANT NOTICES

1. **The genetic data used to construct this tree comes principally from Family Tree DNA (FTDNA) for which thanks are duly given. Some recent subclade identification may come from testing at YSeq or elsewhere.**

2. **The tree serves those McCarthys (or variants of the name) in Haplogroup I1, that headed by SNP I-M253, with its numerous equivalents. An approximate ancestral haplotype at the time of emergence from the I-DF29 SNP 'Block' has been evaluated. For the fast mutating STR markers CDYa/b and DYS712 its allele values are nominal, but others may also be erroneous. This haplotype is nonetheless used as a basis for an indication of STR mutations which have occurred from this point down to the present day. To provide such information, data has been mined from the I1 Eastern Europe and I1-S4795 Projects and a variety of surname projects, including but not limited to those for the names Gardner, Graham, Lancaster, May, Peters, Shiver and Terry. 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 (5) below.**

3. **The overall 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 as it stood early in 2021. The number of equivalent SNPs in each 'block' gives an idea of the length of time between each level on the tree. For the mostpart, only those SNP blocks pertinent to the phylogeny of the McCarthys are shown. It is recognised that FTDNA's Haplotree is a live 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 rests solely with the Owners of this tree, the McCarthy Surname Study analysts.**

4. **The tree combines relationships based on STR testing with firm definition 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 2.1 and FTDNA's Big Y-700, identifying SNPs which give firm 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 tester's surname or simply the kit no.) has been used for tester identity where the participant or his kit manager**

   (a) **has opted in to allowing publication of his "pseudonymized DNA results and ancestor information in the public results pages"' (and for data taken from other projects, where the project has allowed to publicly display its FTDNA Y-DNA Results spreadsheet)' OR**

   (b) **has e-mailed to a McCarthy Surname Study analyst permission to display the output from the analyis of data from any source in the tree (see (6) and (7) below) OR**

   (c) **has made results available to others (e.g. depositions in the 'Y-DNA Warehouse') in the knowledge their analyses, identifiable with surname and / or kit number, would be placed in the public domain.**

   Otherwise identities of testers will be 'totally anonymised' with an 'XHgl-' series 'dummy' reference number known only to the McCarthy Surname Study analysts.

   - **Status of a participant's FTDNA privacy setting has been determined in a one-off exercise on or since 25 May 2018 (or for recent testers, at the time a kit has been added to the tree). Should a participant / kit manager wish the tree respect a subsequent alteration to the setting or indeed have a kit removed altogether and any back-up records held by the McCarthy Study analysts expunged, will he / she please request this by e-mail. (See (7)).**

6. **Despite the option at 5 (a) having been selected in a participant's FTDNA Project Preferences, certain data to which the McCarthy Surname Study analysts may have access, e.g. FTDNA Panels 6 and 7 STRs extracted from Big Y testing, results of testing elsewhere, may not be available, or readily available, in the public domain. Inclusion of output from analysis of such data on the tree requires e-mailed authorisation using an appropriate form of words which can be supplied to the participant or his kit manager. See (7) for contact details.**

7. **For the identity and contact details of the McCarthy Surname Study analysts responsible for this tree please go to** https://www.familytreedna.com/groups/mccarthy-surname-study/about.

NOTES : (Not all may currently be in use)

1. Where SNP / InDel Y-chromosome positions are cited, these relate to Human Reference Genome 'Build 38' (hg38 / GRCh38).
8. Where tested.
9. Within groups of 'equivalent' SNPs and / or associated STRs, the mutations could have occurred in any order.
13. Mutation(s) may have occurred further up the tree.
14. Purported SNP in the 125 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 palindromic arm). Unlikely to be suitable for individual (Sanger Sequence) testing.

McCARTHY (Y-DNA) SURNAME STUDY

PHYLOGENETIC TREE FOR McCARTHYS IN HAPLOGROUP I1 (I-M253)

Last updated - 04 March 2021