SNPs R-L21, R-FGC3218, R-L459, R-Z260 and R-Z290

SNPs R-DF13, R-CTS8221/Z2542

STRs Estimated ancestral haplotype for R-DF13 (values at CDYa and DYS 533 uncertain)

FTDNA Panel 1

393	390	19 / 394	391	385a	385b	426	388	439	389-1	392	389-2
13	24	14	11	11	14	12	12	12	13	13	29

FTDNA Panel 2

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	9	10	11	11	25	15	19	29	15	15	17	17

FTDNA Panel 3

460	GATA 1H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	17	36-37	38	12	12

Value assumed: 36

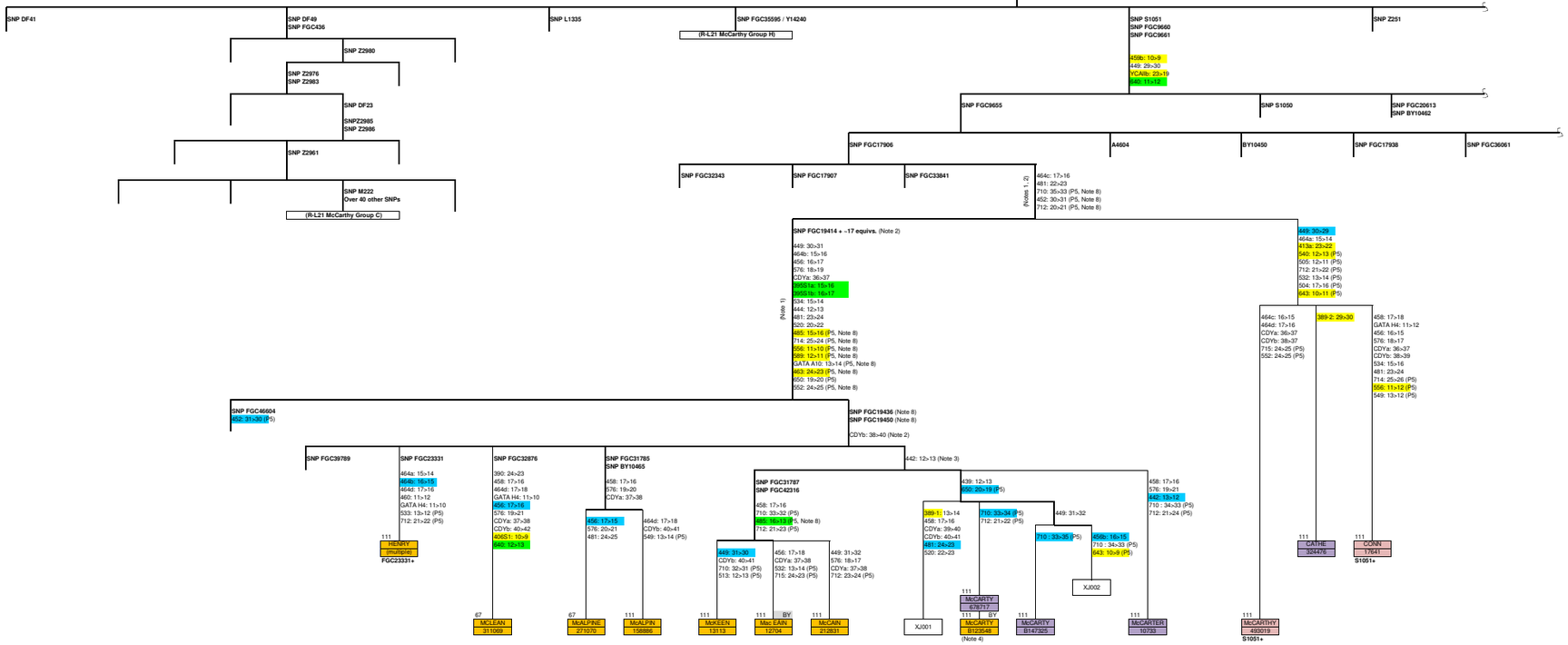
FTDNA Panel 4

531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12

FTDNA Panel 5

710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	GATA A10	463	441	GGAA T1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
35	15	9	16	12	25	26	19	12	11	13	12	11	9	12/13	12	10	11	11	30	12	13	24	13	10	10	20	15	19	13	24	17	12	15	24	12	23	18	10	14	17	9	12	11

Value assumed: 13



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:

No. of STR markers included in the analysis (e.g. Y-DNA37, 67 or 111 at FTDNA).

Has taken BigY-500 test,
or PNL = has taken a FTDNA SNP Pack Test or a YSeq [SNP] Panel Test,

111 BY
AAAAAAA
NNNNNN

Grey shading indicates that results are not yet available or have not yet been reviewed.
Light grey shading indicates preliminary review only of results undertaken.

Surname in parenthesis if no 'distant paternal ancestor' surname identified.
'Pseudonymised' or totally anonymised tester identity (see 'Important Notices' (below), items 5 and 6).

c) Validation of position on tree is indicated as follows:

Position determined by one or more terminal (i.e. most recent shared) SNPs indicated.

Postulated position based on positive test for a higher level SNP and STR mutations being similar to that of (an) other(s) who have tested the terminal SNP(s) shown (and sometimes name similarity).

Postulated position based on STR mutations being similar to that of (an) other(s) who have tested the terminal SNP(s) shown (and sometimes name similarity).

d) STR Mutation frequencies:

Very slow moving' STR markers (very low mutation rates) or very rare multi-step mutation
Slow moving' STR markers (low mutation rates)
Postulated STR back-mutation

e) Other

> is used to denote a change in status (the allele, or no. of repeating motifs) at an STR locus, e.g. 576: 18>17 indicates a mutation from 18 to 17 repeating motifs 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-500 test data, not yet used on this tree).

YSeq116 STR marker in Yseq's 'FTDNA111toYSeq116' panel

A(AA)NN(NN)$_{n+}$ Results of individual SNP testing (positive / negative) where an NGS test has not been taken, or taken from an NGS or Pack Test where of particular relevance to kits close by on the tree.

tbc To be confirmed (e.g by Sanger sequencing)

IMPORTANT NOTICES

1. **The genetic data used to construct this tree comes principally from Family Tree DNA (FTDNA). Some data may have come from testing at Yseq.**

2. **The tree is intended to serve 'R-L21 Group J' in the McCarthy Surname Study and show the probable pathway of its members' genetic ancestries from the time of SNP R-L21 (via R-S1051), along with their most recent common ancestry shared with those of other surnames. To provide such information, additional data has been mined from other projects displaying it in the public domain; 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. Haplotypes and terminal SNPs have been taken from the R-S1051 and the Hawke Projects.**

3. **The overall tree structure is based on the R-Z39589>S1051 section of Alex Williamson's Y-tree (http://www.ytree.net/) and FTDNA's Haplotree, for which thanks are duly given. Not all SNPs / subclades in these sources are necessarily shown and responsibility for any errors arising from interpretation of data or failure to update to the latest available information is mine alone.**

4. **The tree combines postulated relationships based on STR testing with firm definition afforded by SNP testing. Where configurations are not confirmed by SNP testing, different permutations are possible, particularly in the occurrence of more frequently occurring mutations such as those at DYS458, DYS576, CDYa/b, DYS710, DYS533 and DYS712. The postulation of back mutations is highlighted with blue background as indicated in Legend item (d). The reliability can only be improved by more participants testing STRs to 111 or 125 markers and Next Generation Sequence (NGS) testing such as FGC's Elite 2.1 and FTDNA's Big Y-500, 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**

   (a) has opted in to sharing his data in the public viewing of FTDNA's Y-DNA results (and for data taken from other projects, where the project has allowed to publicly display its FTDNA Y-DNA Results spreadsheet).*

   (b) has provided, where applicable, written permission for the incorporation in this tree of 'guarded' data not covered by (a) or to which others have been given access in the knowledge they would place their analyses in the public domain.**

   Otherwise identities of testers are 'totally anonymised' with an 'XG' series 'dummy' reference number the significance of which is and will remain known only to myself or my successor in maintaining this tree.

6. **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 I may hold, he is asked to contact me privately (mccarthygenATtiscaliDOTcoDOTuk).**

* **Each participant's status with respect to this option will have been determined in a one-off exercise between 15 and 22 August 2018. Should he have subsequently amended this from 'Opt in to sharing' to 'Opt out of sharing', he will please contact me as described at (6).**

** **e.g. STR information on FTDNA's Panel 6 and various SNP data extracted from a participant's Big Y-500 files to which I have been given access, or additional information derived from testing at Yseq.**

N. McCarthy

NOTES:

1. These SNP and STR mutations could have occurred in any order.

2. When the tree is more developed some of these mutations marked with this note may be moved to a higher level but in the case of SNPs not as far as the next SNP tier.

3. This mutation at DYS 442 may have occurred independently in the McCain and McCarter / McCarty lineages.

4. Positive for FGC19436/50 but negative for all other SNPs heading subclades under FGC19436/50 on this tree B. Where tested.

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McCARTHY (Y-DNA) SURNAME STUDY
POSTULATED PHYLOGENETIC TREE FOR SNP R-S1051
McCARTERS / McCART(H)YS (McCARTHY R-L21 GROUP 'J')

N McCarthy **22 August 2018**