SNPs R-L21, R-FGC3218, R-L459

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

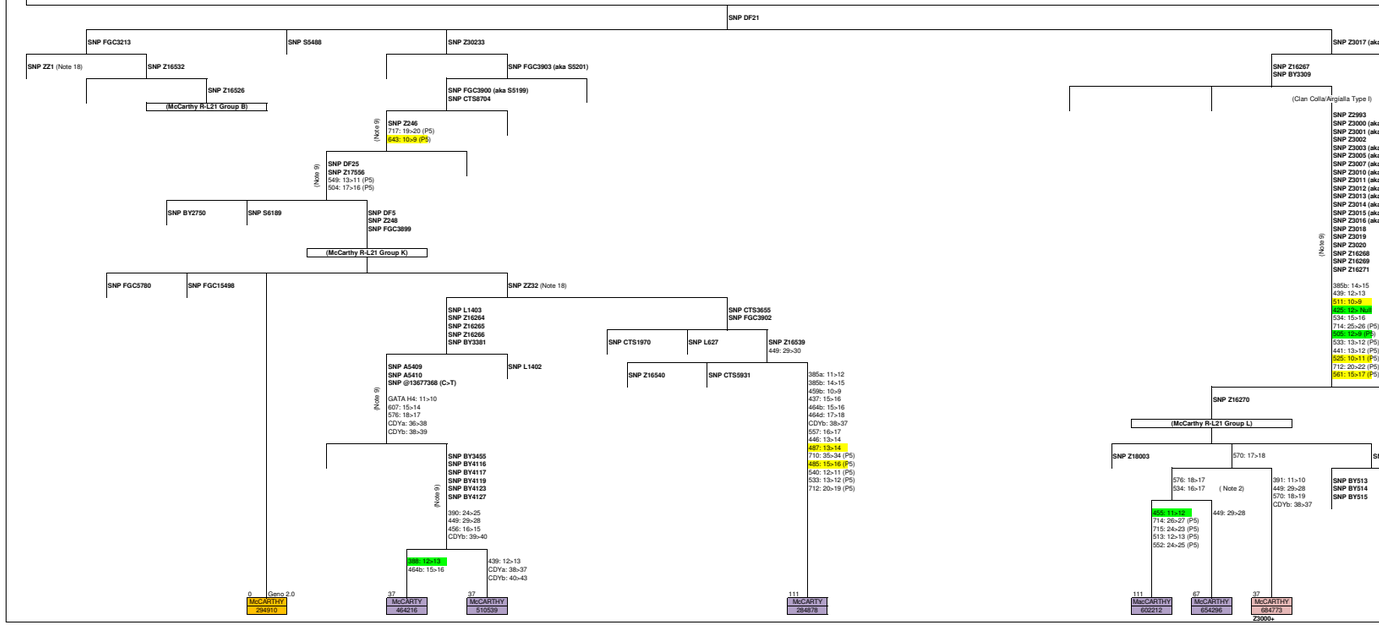
	FTDNA Panel											
3	460	GATA H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
	11	11	19	23	16	15	18	17	36/37	38	12	12

Value assumed: 36

	FTDNA Panel (where applicable)																							
4	531	578	395S 1a	395S1 b	590	537	641	472	406S 1	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 (where applicable)																																									
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	GGA AT 1B07	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 (and key to highlighting):

STR Mutations:

"Very slow moving" STR markers (very low mutation rates) or rare multi-step mutation
"Slow moving" STR markers (low mutation rates)
Postulated STR back-mutation where earlier mutation occurs on this tree

Participant kit number and testing details:

111 BY
AAAAAAA
NNNNNN

No. of STR markers included in analysis
"+6" indicates additional Genetree markers.
125 implies FTDNA's 111 plus Yseq's additional 14 (aka YSeq116).
Has taken BigY test,
or YE, FO = has taken Y Elite test with FGC (YE), or other "full" Y-genome test elsewhere (FO),
or PNL = has taken FTDNA's R1b-DF21 SNP Pack Test or Yseq's R1b-DF21 Panel Test,
or NG = Nat Geographic Geno 2.0 'NGS' or later test
Shading indicates that results are not yet available
Participant ancestral surname / kit no.

A(AA)NNN(NN)+/- Results of individual SNP testing (positive / negative) where an NGS test has not been taken.

Text in italics denotes alignment with recorded MacCarthy genealogies (see Fig.2 on McCarthyScrapbook website). Note: prior to Ceallachán of Cashel the phylogenetic tree is not consistent with ancient genealogical tracts.

>	Following a DYS number denotes a STR mutation, 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"
tbc	To be confirmed (e.g by Sanger sequencing)
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).
YSeq116	STR marker in Yseq's 'FTDNA111toYSeq116' panel

NOTES:

1. All SNP / InDel positions are referenced to human genome build GRCh37 / hg 19
2. Instead of being shown sharing the DYS 576 mutation with kit 602212, kit 654296 might alternatively be grouped primarily with kit 684773, sharing the DYS 449 mutation.
8. Where tested.
9. Within groups of SNPs and / or associated STRs, the mutations could have occurred in any order.
13. Some of these STR mutations 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.

IMPORTANT NOTICE

THIS TREE COMBINES POSTULATED RELATIONSHIPS BASED ON STR TEST DATA WITH FIRM DEFINITION AFFORDED BY SNP TESTING. THE LATTER WILL BE REGULARLY UPDATED TO INCORPORATE NEW INFORMATION.

WHERE CONFIGURATIONS ARE NOT CONFIRMED BY SNP TESTING, DIFFERENT PERMUTATIONS ARE POSSIBLE PARTICULARLY IN THE OCCURRENCE OF FASTER REPEATING STR MARKERS SUCH AS DYS 458, DYS 576, CDY, DYS 710, DYS 533 AND DYS 712 AND THE CONSIDERATION OF FEASIBLE BACK MUTATIONS.

THE RELIABILITY CAN ONLY BE IMPROVED BY MORE PARTICIPANTS TESTING STRs TO 111 MARKERS AND NGS TESTING, IDENTIFYING SNPs WHICH GIVE FIRM DEFINITION TO THE BRANCHES AND TWIGS (SUBCLADES) OF THE TREE.

McCARTHY (Y-DNA) SURNAME STUDY
POSTULATED PHYLOGENETIC TREE FOR McCARTHYs IN THE HAPLOGROUPS OF:
SNP DF5 (McCARTHY R-L21 GROUP 'K') and
SNP Z16270 (McCARTHY R-L21 GROUP 'L')

To be read in conjuction with analysis on the Results pages of the McCarthy Surname Study Project

(Ref: https://www.familytreedna.com/groups/mccarthy-surname-study/about/results)

N D McCarthy

28 July 2017

© COPYRIGHT NIGEL McCARTHY 2017

The high level SNP stucture on this tree is based on Alex Williamson's *The Big Tree* (http://www.ytree.net) and FTDNA's *Haplotree*. The intent of this tree is to show the probable pathway from the time of SNP R-L21 for McCarthys in R-L21 Groups K and L, and their most recent common ancestry with those of other surnames. Data on non-McCarthy testing has been taken from *The Big Tree* and from the R1b-DF21 Project's and other Surname Projects' Results tables to the extent necessary to place the R-L21 Groups K and L McCarthys. Thanks are due to Alex and to all those whose revelation of their test results has made this tree possible. (Any errors in interpretation