

(These Notes also serve the McCarty R-L21 Group B tree maintained independently as a subset of the R-Z16262 tree; see continuation at R-Z16266 on Sheet 3)

- Where SNP 1 (C>T) vs. C>G positions are cited, these relate to Human Reference Genome Build 38 (HG38) (GRCh38).
- Dates shown in the key diagram on this sheet 1 or on other sheets on the detailed tree in the boxed text of sheets 2,5 have been compiled using counts of all mutations, i.e. both SNPs (subject to certain qualifying restrictions) and FTDNA Panel 1,7 STR mutations. They are intended for guidance only. The start date for R-L21 (or rather the midpoint of the L21 block, comprising SNPs L21 and L405) is normally 2,500 B.C. (BCE), estimated from reported radiocarbon dating of ancient bones. This may be supplemented by more information from key. Chromosome, dates are estimates for the L402T mutation in the block in which such representative SNP occurs, i.e. for the most recent shared (or common) ancestor (MCA) of all who descend through subsequent branches. As explained in Note 4, this is not necessarily the SNP shown in the key diagram on this sheet 1 and could be an STR mutation or any other 'equivalent' SNP or I-04C within a block.
- Not used.
- Within blocks of 'equivalent' SNPs and/or associated STRs, the mutations could have occurred in any order.
- It is likely that the most marked role here participated in a Multiple Nucleotide Polymorphism (MNP). However, since it is much easier for SNP interpretation software to handle single base substitutions rather than complex mutations, they are usually treated as separate SNPs.
- (Not used)
- Recurrent mutations at least one other SNP1 (C>G) / FGC10265: Samples
- Where listed (or, for PE and PF, where cited):
- Placement of the mutation subject to further investigation.
- Repeat content. Needs Sanger Sequencing test to confirm.
- (Not used)
- SNP (or I-04C) may have occurred further up the tree but not as far up as the next level on which SNPs occur.
- Mutations may have occurred further up the tree.
- Polymorphic SNP within the 152 bp repetitive zone known as DY179 (20054914 to 20351654 (hg38)). Cannot be confirmed by Sanger Sequencing.
- In a sequence with over 90% similarity with another chromosome, only valid if phylogenetically consistent across two or more participants with other matching. Unlikely to be suitable for Sanger Sequencing testing.
- Presence of a sequence also found in other chromosomes but presented as consistent here, not suitable for individual (Sanger Sequencing) testing.
- May be difficult or impossible to confirm by Sanger Sequencing.
- The presence of polymorphic SNP AC16131, in a region 100% identical to that around position 1677649, inlets other than 708549 is related by FTDNA, however review of raw data BAM files has justified the configuration as shown on the tree, and this is now supported by the sharing of three STR mutations by the same kits.
- A defining SNP or I-04C appear to exist on the Y chromosome, but its location is uncertain. Frequently this is because it is on a palindromic area. Unlikely to be suitable for individual (Sanger Sequencing) testing.
- SNP occurs within a STR and may therefore be unreliable. May also have been identified but phylogenetically consistent where listed.
- As Note 18, but here the alternative occurrences are at the interface of two motifs counted within DY330. A third alternative at the base of two motifs.
- (Not used)
- Mutation evident from Big Y700 extraction only; Big Y700 extraction reported normal allele.
- Mutation evident from Big Y500 extraction only; Big Y700 extraction reported normal allele.
- Big Y700 indicates an allele of 11 at FTY145 but the mutation to 12 indicated by Big Y500 is phylogenetically consistent: see further up the tree.
- The allele at DY2560T frequently appears as 11 or 11 with subclades either the tree to 15 or 16 descent; they may be due to a problem measuring the allele, identification of mutations at this marker may therefore be suspect.
- FTY650 is rarely read, but when it is the allele may be reported as 8 or 16 or 16 when for different reads of the same samples (often from other relatives close to 16). This suggests a problem regarding 8 rather than 16 to 8 mutation.
- SNPs from 25606 down to 25611 are negative in DuffyM kit no. 17780 but shown in Druoid kit no. 21725; SNPs from 1362 down to 25613 are negative in both tests. The remaining SNP, I-04C from I-04C 25607 to SNP 22564T require further investigation in both kits.
- OT-076 is the latest reading marker, so whether OT-076 occurred independently or in a common ancestor can be ascertained by finding a clade of other shared mutations through leading to 11 STRs and/or I-04C testing such as Big Y.
- Additional based at Genemay, DY568: 20, DY6252:16-19-21, DY568: 18. Also tested at Genemay, with results consistent with those extracted from Big Y as shown here, were DY5653, 64 and 536.
- For further exploration of this section please refer to <https://www.familytreedna.com/groups/irish/mt/mt-dna-076/>
- 3000000 mutation results show a 12-11 mutation at DY542 while N16368 Dervny shows a non-value. While this may well occur from time to time (e.g. in haplogroup D10101), DY542 has a reputation as difficult to read. It is suspected that a return of 11 may be seen in some of the other Dervny(hg) kits when extended to 67 markers.
- Instead of showing the DY5607 15-16 mutation other kits currently show, kit 653862 may be placed closer to the Poles through a shared DY5504 10-14 mutation.

IMPORTANT NOTES

- The genetic data used to construct this tree comes principally from Family Tree DNA (FTDNA), Some data has come from testing at YSEQ. Any substantial SNP testing elsewhere will be as indicated by Legend item (b).
 - The tree serves the R-Z16262 and Subclades Project. Analysis has shown that SNP ZS4066 on Sheet 3 heralds the phylogeny of Carberry, Le Muxu(OT) kings of Cashel and Desmond. Their phylogeny has been moved to an independently managed McCarty Surname Study Tree (for McCarty R-L21 Group B). However the Notes, Legend and Timeline on this Sheet 1 are shared by both trees.
 - The tree shows the probable pathway of the paternal genetic ancestry of the project's members (and of the pre-2nd millennium ancestry of the Muxu(OT) kings of Cashel and Desmond) from the time of SNP R-L21 (via R-Z16262). To provide such information, additional data has been added a number of years from other projects displaying in the public domain. In this regard, Banks are due to the Haplogroup names and that project administrators for making their data available in the spirit of 'citizen science' for the mutual benefit of all concerned. Participant identities aside by the effort of (S) below. Projects from which haplotypes have been taken include but are not limited to Corcoran LeBlain, Irwin(OT), DNA, Davies, Penrhyn, R-DP1 and Subclades, L21 Post and those pertinent to the following surnames or variants thereof: Banks, Barry, Callahan, Campbell, Chisham, Cradock, Dempsey, Dunn, Domet, Dugan, Eubank(s), Gray, Griffin, Haney, Johnson, Kelly(s), Kennedy, Lyons, Martin, MacCormac, MacLaughlin, McCallan, McEaster, Miller, Murvell, Neenan, Ogan, O'Higgins, O'Mahony, O'Mara, O'Shea, Peck, Perry, Porter, Reane, Ross, Rusch, Sutherland, West
 - The overall tree structure is based on the R-DP1 section of Asia Williams's Ytree (<https://www.ytree.com/>) 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 rests solely with the author of this tree. Haplogroup data noted principally in the R-DP1 and Subclades Project's DNA Results spreadsheet has been used to give an idea of the probable ancestral association with the initial branches of these other DP1 subclades. These are speculative, particularly with respect to the levels in the hierarchies at which STR mutations occurred. There are no data to the Administrators, past and present, and participants of the R-DP1 & Subclades Project.
 - The tree combines relationships based on STR testing with fine 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 or 125 markers and Next Generation Sequence (NGS) testing such as FGC's, Ilika 2.1 and FTDNA's Big Y700, identifying SNP which give fine definition to the branches and help subclades of the tree.
 - The 'autosomal' form 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 is or the kit manager
 - (a) has opted to allow publication of his 'autosomal' DNA results and ancestor information in the public results page; and/or the data from other projects, where the project has allowed a publicly display its FTDNA Y-DNA Results spreadsheet; OR
 - (b) has allowed a slight McCarty permission to display the output from the analysis of data from any source in the tree (yes or no) and (c) (not used)
 - (d) has made results available to others (e.g. depositions in the 'DNA Workshop') in the knowledge that analyses, identifiable with surnames and/or kit number, would be placed in the public domain.
- Otherwise identities of testers will be 'totally anonymised' with '3E' unless 'Surname' identifier number occurs only to the R-Z16262 and Subclades Project Administrators.
- * Status of a participant's FTDNA privacy setting has been determined to a single extent or as either 2016 (or for recent additions at the time it 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 R-Z16262 and Subclades Project Administrators, will be asked please request they e-mail: (See 7).
- 6 Despite the option at 5 (a) having been selected in a participant's FTDNA Project Surnames, certain data which the R-Z16262 and Subclades Project Administrators 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 explicit authorization using an appropriate form of words which can be supplied to the participant or their kit manager. See (7) for contact details.
- 7 For the identity and contact details of the R-Z16262 and Subclades Project Administrators please go to <https://www.familytreedna.com/groups/r-z16262-and-subclades-076/>

LAYOUT OF THE TREE BY MAJOR SUBCLADES WITH TIMELINE AND GROUPING LABELS FOR THE PROJECTS SERVED (For Group demarcations see website referenced in the 9th block)







