

R-L21
(FTDNA R1b1a2a1a1b4)
R-DF13

STRs Haplogroup R1b1* Super Western Atlantic Modal Haplotype (SWAMH) Modal Alleles (as Ysearch ID 55G9J for pos. 1-67)

FTDNA Panel	FTDNA Panel	FTDNA Panel	FTDNA Panel (where applicable)
1 393 390 19/29 4 391 385a 385b 426 388 439 389-1 392 389-2 13 24 14 11 11 14 12 12 12 13 13 29	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	3 460 GATA H4 YCA 456 607 576 570 CDYa CDYb 442 438 11 11 19 23 16 15 18 17 36 38 12 12	4 531 578 395S 395S 1a 1b 590 537 641 472 406S 511 425 413a 413b 557 594 436 490 534 450 11 9 15 16 8 10 10 8 10 10 12 23 23 16 10 12 12 15 8
FTDNA Panel (where applicable)	FTDNA Panel (where applicable)		
4 (cont.) 444 481 520 446 617 568 487 572 640 492 565 12 22 20 13 12 11 13 11 11 12 12	5 710 495 632 495 540 714 716 717 505 556 549 569 522 494 533 636 575 638 462 452 445 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 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		

LEGEND

- DF21 and P314.2 +ve; L362 -ve
- P314.2 +ve and L362 -ve
- P314.2 +ve
- P314.2 and L362 +ve
- L362 +ve (P314.2 not tested)
- L362 -ve (P314.2 not tested)

The "-" symbol in connection with a DYS / DYF No. denotes a STR mutation. It otherwise indicates "after" in connection with a year.

POSSIBLE PHYLOGENETIC TREE FOR HAPLOTYPES ASSOCIATED WITH SNPs R-P314.2 AND R-L362

(To be read in conjunction with analysis under "HAPLOGROUP R - GROUP B: McCARTHY AND SNPs R-P314.2 AND R-L362" at <http://www.familytreedna.com/public/McCarthySurnameStudy/default.aspx?action=results>)

N McCarthy
05 March 2013

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- NOTES:**
- Mutations at DYS 447 and 456 have been the most difficult to postulate and are likely to be the most significant source of errors.
 - P4 indicates marker in 38th - 67th markers in FTDNA sequence. P5 indicates in 68-111 marker range.
 - Several permutations featuring a common ancestor selected from 458: 17-16, 576: 18-17 and 456: 16-15 are possible in this part of the tree. Back mutations must also be considered. Testing of key participants to 111 markers may resolve this.
 - (deleted)
 - If Driscoll (21275) and / or Crowley (N55690) prove L362 -ve, they should be shown connected in parallel with Higgins; if Crowley is L362 +ve, note some similarities with Carter (135483).
 - Precise location of P5 mutations is subject to further testing to 111 markers. Data shown identifies which are common and which pertain to nominal "Dairiadi" and "Munster" branches.
 - Cannot assign the following without further STR testing:
Mahoney (84534) and O'Shea (140951) (P314.2 +ve), O'Mahoney (164296), O'Shea (98369), Reynolds (74905), Wallen (140541), Ward (114678), Wilson (119554)
 - There could be multiple independent mutations at this point, with subsequent branches having earlier common ancestry than indicated here.
 - The order in which the SNP 314.2 and the nine STR mutations occurred is unknown
 - Only STR mutations which might be significant in alternative structures for the early sub-branching of the DF21 tree are indicated for SNPs Z246, L20 and S424.

