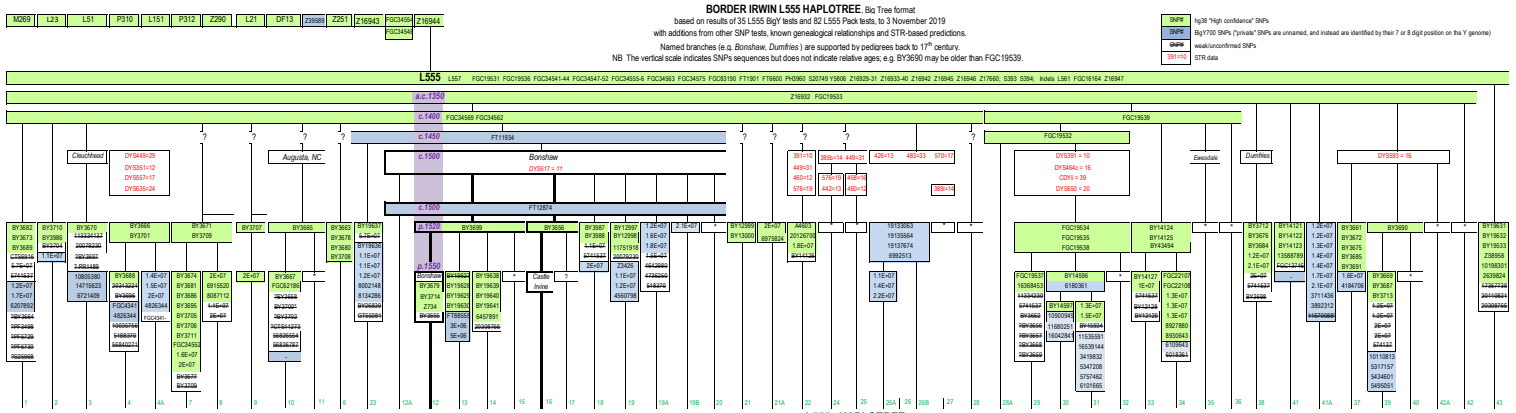
BORDER IRWIN L555 HAPLOTREE Big Tree format

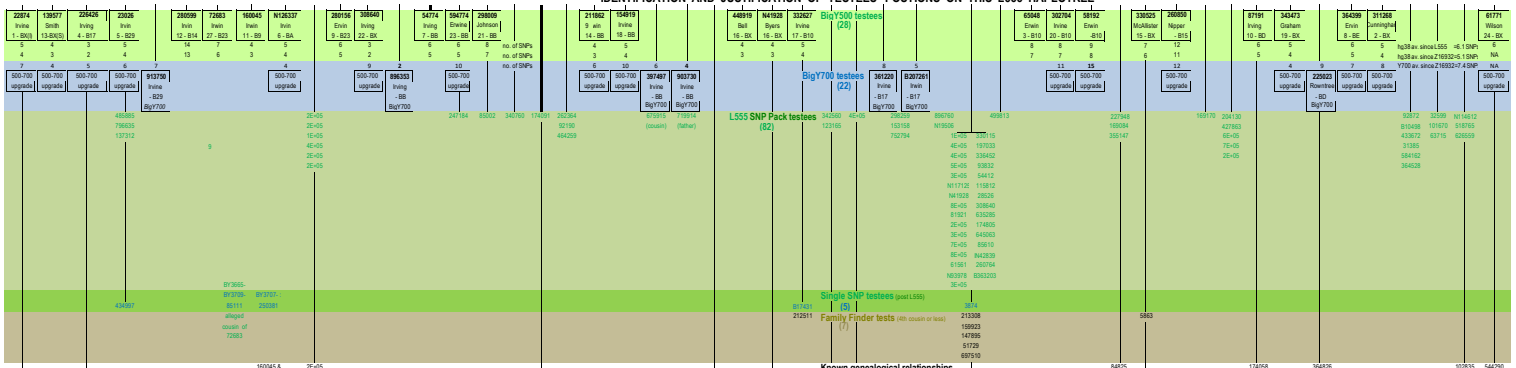
based on results of 35 L555 BigY tests and 82 L555 Pack tests, to 3 November 2019
with additions from other SNP tests, known genealogical relationships and STR-based predictions.
Named branches (e.g. *Bonshaw, Dumfries*) are supported by pedigrees back to 17th century.
NB The vertical scale indicates SNPs sequences but does not indicate relative ages; e.g. BY3690 may be older than FGC19539.

SNP9 hg38 "High confidence" SNPs
SNP4 BigY700 SNPs ("private" SNPs are unnamed, and instead are identified by their 7 or 8 digit position on the Y genome)
SNP8 weak/unconfirmed SNPs
391>10 STR data



L555 HAPLOTREE

IDENTIFICATION AND JUSTIFICATION OF TESTEES' POSTIONS ON THIS L555 HAPLOTREE



Conclusions

1. Haplotree now has 53 branches below L555, with up to 6 bifurcations between L555 and private SNPs.
2. If #61771 (column "43") is not an Irwin NPE but was originally a Wilson, as seems quite plausible, then it is Z16932 who was the earliest Border Irwin, not L555.
3. Local history records suggest the earliest Border Irwin was probably born in the early/mid 14th century.
4. Reliable genealogy shows #54774 (column "12") and #174091 (column "16") are 12th cousins, both descended from a Christopher Irving of Bonshaw born c.1500. This ability to place a conventional family tree within a haplotree is perhaps the "holy grail" of genetic genealogy, and still extremely rare.
5. By extrapolation it follows that FT12874 might be dated c.1450 and FGC34569 might be dated c.1400, although mutation ingtervals are random, not uniform.
6. It also follows that #594774 and #298009 must be c.1550 or later.
7. The dates in (4) to (6) above are shown in purple in the table; all are VERY approximate.
8. Assuming Z16932 dates from c.1350, average years per SNP = 118 years for BigY500, and 80 years for BigY700.
9. On average BigY700 is giving 49% more SNPs than BigY500, but there is much variation: one BigY700 testee has only 2 SNPs since L555 (i.e. c.10 generations per SNP), one has 15 (i.e. 1 generation per SNP)!
10. FTDNA are likely to revise some SNPs: the haplotree is dynamic.

STR predictions (30) (DYS617 and DYS693 apart, my criterion for inclusion is generally patterns of 3 markers or more, with exact matches (or a more distant mutation) in 2 of these 3)

338622 6E+05 160759 115781 116077 184294 641353 404193 277705 900818 74798 81705 856038
294650 320721 78458 76137 247772 289667
321166 258169
225682 227553 211119 167511 37398 226131 193768 120138
131683