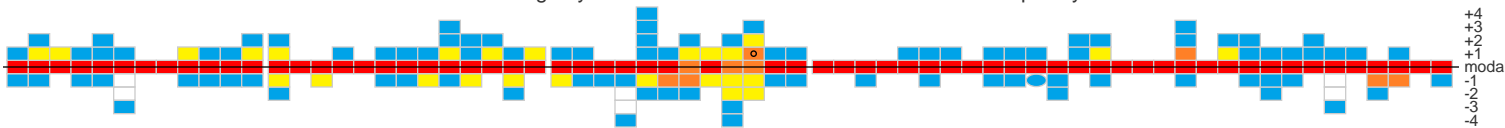


R-L513

This is the modal haplotype for the whole tree including any subtrees.

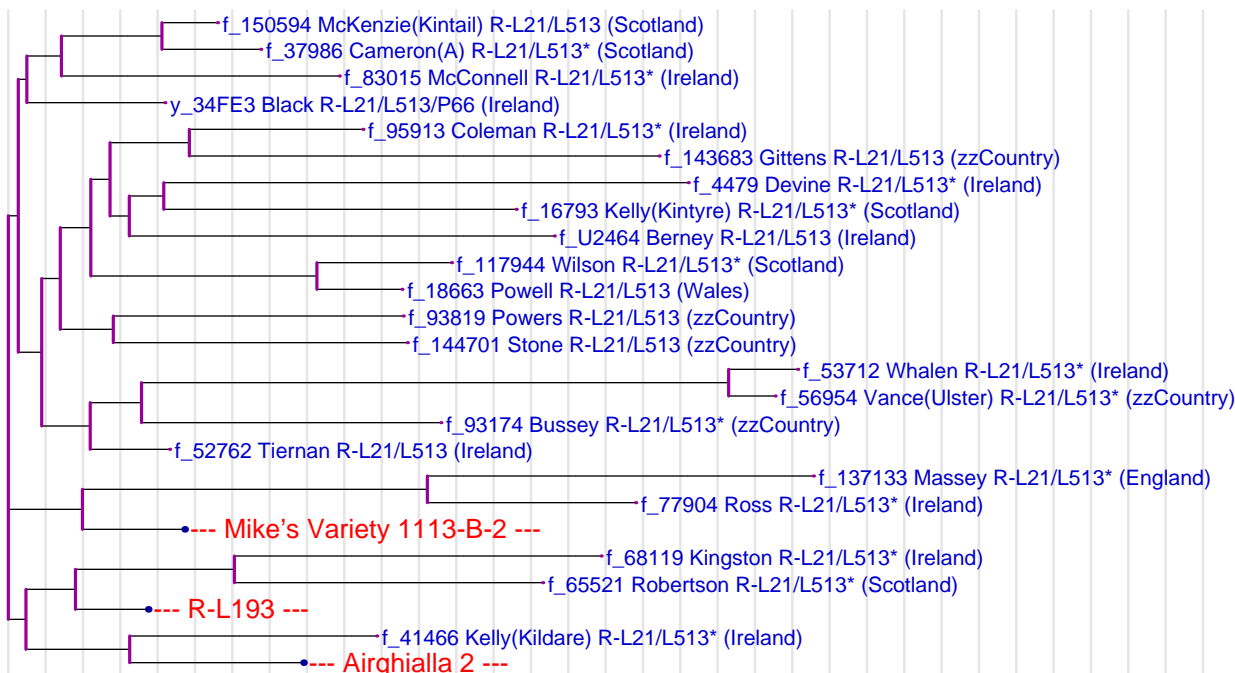
393	390	19	391	385a	385b	426	388	439	389i	392	389i-I	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	466	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	24	14	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	16	16	18	17	18	38	39	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	13	12	12	12	12

This is the marker distribution for the whole tree including any subtrees. The color indicates the relative frequency of the alleles.



Age Analysis

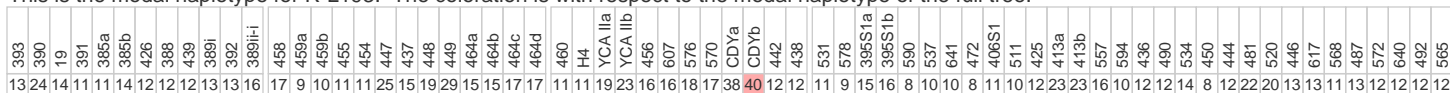
Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
73	4891	815	16.66%	90.87±9.20	2271.74±323.195



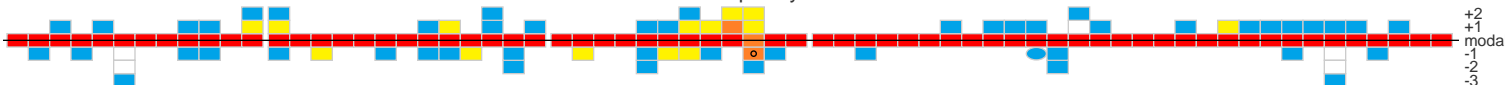
The vertical grey lines are separated 10 generations apart.

R-L193

This is the modal haplotype for R-L193. The coloration is with respect to the modal haplotype of the full tree.

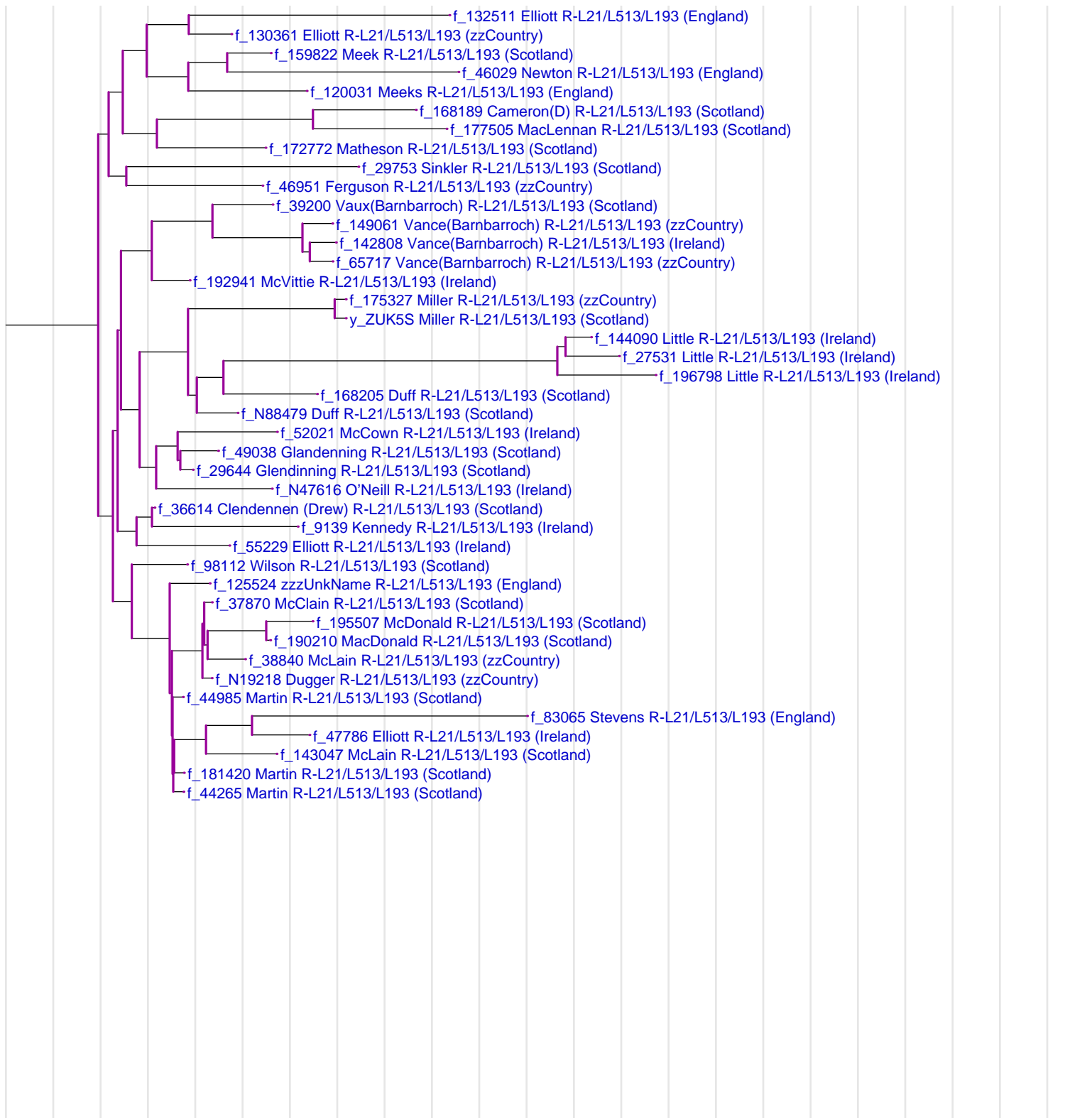


This is the marker distribution for R-L193. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
42	2814	250	8.88%	46.48±4.74	1162.11±165.932



The vertical grey lines are separated 10 generations apart.

Airghialla 2

This is the modal haplotype for Airghialla 2. The coloration is with respect to the modal haplotype of the full tree.

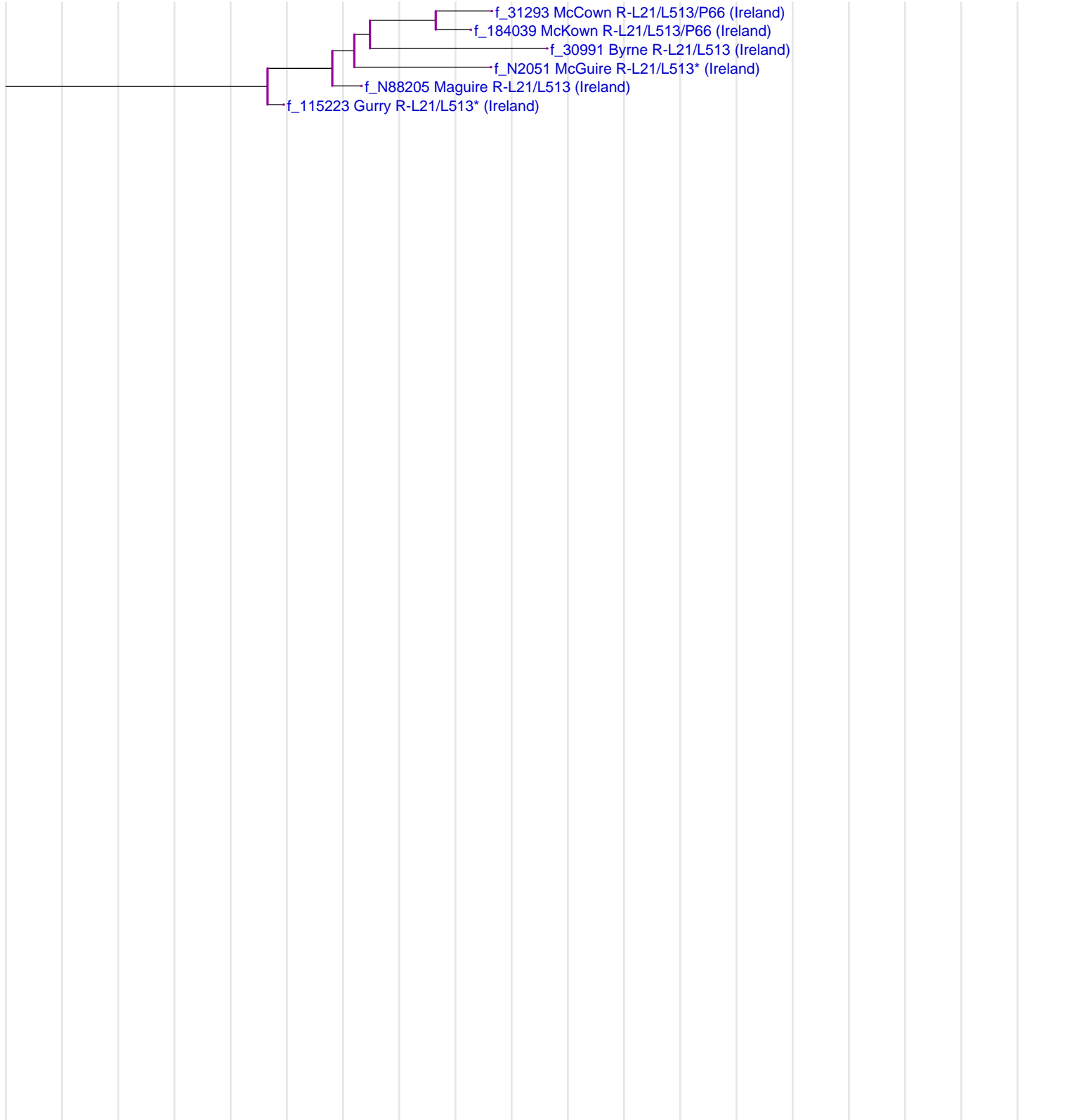
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	25	14	11	14	12	12	12	12	13	13	16	15	9	10	11	11	25	16	18	29	15	15	17	18	11	11	19	23	17	15	17	17	37	37	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	12	24	20	13	13	11	13	11	12	12	12

This is the marker distribution for Airghialla 2. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
6	402	19	4.73%	24.20±2.72	605.093±90.9785



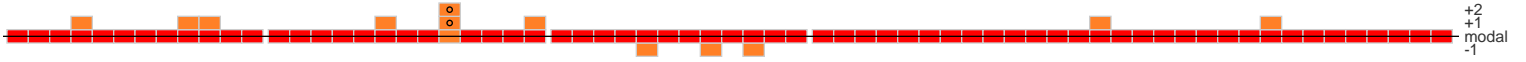
The vertical grey lines are separated 10 generations apart.

Mike's Variety 1113-B-2

This is the modal haplotype for Mike's Variety 1113-B-2. The coloration is with respect to the modal haplotype of the full tree.

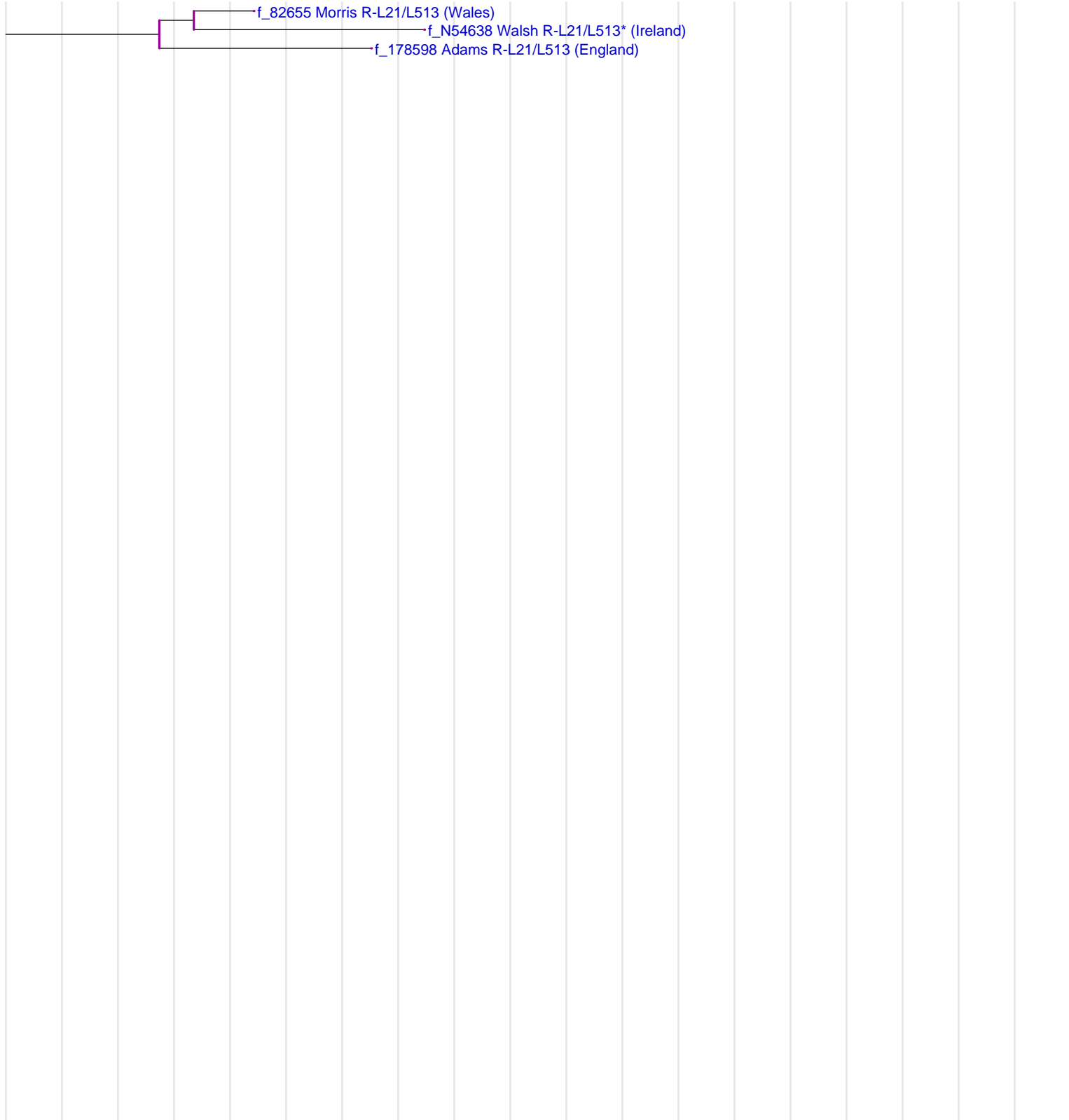
393	390	19	391	385a	385b	426	388	439	389i	392	389i-i	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	537	641	472	406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565	
13	24	15	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	18	23	16	15	18	18	37	38	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	12	15	8	13	22	20	13	13	11	13	11	11	12	12

This is the marker distribution for Mike's Variety 1113-B-2. The color indicates the relative frequency of the alleles.



Age Analysis

Total number of members	Total number of markers	Total number of mutations	Mutation fraction	Age estimate (in generations)	Age estimate (in years)
3	201	13	6.47%	33.42±4.13	835.466±132.895



The vertical grey lines are separated 10 generations apart.

Cluster Modals

Full Tree (R-L513)

Age: 2271.74±323.195 years

393	390	19	391	385a	385b	426	388	439	389i	392	389iH	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438	531	578	395S1a	395S1b	590	597	641	472	406S1	511	425	413a	413b	567	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
13	24	14	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	16	16	18	17	38	40	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	11	13	12	12	12	12

R-L193

Age: 1162.11±165.932 years

13	24	14	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	16	16	18	17	38	40	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	14	8	12	22	20	13	13	11	13	12	12	12	12
----	----	----	----	----	----	----	----	----	----	----	----	----	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	---	----	----	---	----	----	---	----	----	----	----	----	----	----	----	----	----	---	----	----	----	----	----	----	----	----	----	----	----

Airghialla 2

Age: 605.093±90.9785 years

13	25	14	11	11	14	12	12	12	13	13	16	15	9	10	11	11	25	16	18	29	15	15	17	18	11	11	19	23	17	15	17	17	37	37	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	12	24	20	13	13	11	13	11	12	12	12
----	----	----	----	----	----	----	----	----	----	----	----	----	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	---	----	----	---	----	----	---	----	----	----	----	----	----	----	----	----	----	---	----	----	----	----	----	----	----	----	----	----	----

Mike's Variety 1113-B-2

Age: 835.466±132.895 years

13	24	15	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	18	23	16	15	18	18	37	38	12	12	11	9	15	16	8	10	10	8	11	10	12	23	23	16	10	12	12	15	8	13	22	20	13	13	11	13	11	11	12	12
----	----	----	----	----	----	----	----	----	----	----	----	----	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	---	----	----	---	----	----	---	----	----	----	----	----	----	----	----	----	----	---	----	----	----	----	----	----	----	----	----	----	----

Notes

The Tree

The tree was generated using the neighbor-joining algorithm provided by the PHYLIP phylogeny package. This algorithm requires a distance matrix, for which the data came from the 2011-05-31 version of Mike Walsh's Excel spreadsheet. Only members with at least the 67 FTDNA markers, and who tested positive for L513, For now, only the markers in FTDNA's standard set of 67 were used to calculate the matrix, but I will use markers beyond these in the future.

Modal Values and Age Estimates

For each cluster on the tree, I provide both its modal haplotype determined from its descendant members on the tree, as well as an age analysis. The age analysis was completed in the style of what Anatole Klyosov describes in his Journal of Genetic Genealogy article, 5(2):186-216, 2009. I have not taken into consideration the up/down mutation asymmetry, but may do so in the future. I used a 67-marker average mutation rate of 0.002 and assumed 25 years per generation. I included a 10% uncertainty for the average mutation rate, and a 10% uncertainty for the average number of years in a generation.

For the calculation of the modal haplotypes, in the event of a tie for a particular marker, with two or more different allele values having the same count of haplotypes, the allele closest to the R-L513 modal haplotype was chosen. This was done so that the modal haplotype would more closely resemble what might be the ancestral haplotype for the cluster.

Allele Distribution Diagram

The allele distribution plot attempts to display relative frequency information of the various allele values for each marker. For each possible allele value of each marker, a different coloured box is used to represent the fraction of haplotypes, with that particular allele value. A red box indicates that more than 50% of the haplotypes have that particular value, an orange box indicates more than 33% have that particular value, yellow for more than 25%, and blue indicates that the fraction is simply greater than 0.

If the fraction for an allele is within 5% of what it is for the modal value, I have indicated that allele with a small circle. The idea here, is that if the other allele value is so close, then if you were to use different sample data, you could potentially end up with a different modal value.

- - greater than 0% of haplotypes
- - greater than 25% of haplotypes
- - greater than 33% of haplotypes
- - greater than 50% of haplotypes

Consider the following example of DYS 464c for the whole of R-L21. We look at what fraction of the 1483 people in this cluster have a particular allele value. The modal value is clearly 17, but 16 is not far behind. As 16 is within 5% of the modal value, I have indicated that close relationship with a small circle.

Allele	Count	Fraction	Colour
19	0	0.00%	
18	14	0.94%	■
17	694	46.80%	■
16	626	42.21%	■
15	145	9.78%	■
14	2	0.13%	■
13	2	0.13%	■
12	0	0.00%	

