A Preliminary Genetic Investigation of the Corca Laidhe

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This is an analysis of the Corca Laidhe and Eoghanacht tribes relative to a Munster control group using the same methods and a similar presentation as researchers at Trinity College in a study of the Dal Cais and the Eoghanacht tribes, McEvoy et al (2008). The genealogy of the Corca Laidhe is summarized and shown that it should be split into two branches as they might differ in paternal ancestry. An analysis of haplotype variance partitioned by tribe and surname is presented using 17 marker data from the Trinity study and 32 marker haplotypes from online public data. In both cases similar results were obtained showing the Corca Laidhe differ from Eoghanacht and the difference is attributed to a significant presence of haplogroup I2a in the Corca Laidhe ensemble of names. The 32 marker data is then further analyzed using via network and phylogenetic diagrams. Lastly the O'Driscoll genealogy and DNA are examined separately.

Genealogy

The genealogy of the Corca Laidhe is described by John O'Donovan in his treatise published in 1849 by the Celtic Society in the book Miscellany of the Celtic Society. He described his treatise as "various readings" from the Book of Ballymote as compared with the Book of Lecan, two books complied about 1400 from various manuscripts. Another important source is the Book of Glendalough, known as Genealogies from Rawlinson B 502, which dates from 1130; therein one finds the *Genelach Sil Lugdach Meic Itha*. Transcribed copies of the aforementioned books are available via a project at the University College Cork known as CELT, the Corpus of Electronic Texts (CELT, 2012). An O'Leary pedigree can be found in The O'Clery Book of Genealogies written in the 1600s and is available online (Cumann Clann Lochlan, 2012).

The pedigree of the Corca Laidhe is illustrated in Figure 1. The death of founder Lughaid Maccon is recorded in the Annals of the Four Masters in the year 225M as follows (O'Donovan, 1848, p.111): "Lughaidh i.e. Maccon, son of Macniadh, had been thirty years in the sovereignty of Ireland, he fell by the hand of Feircis, son of Coman Eces, after he had been expelled from Teamhair Tara by Cormac, the grandson of Conn". The genealogy varies from source to source in part because Maccon is sometimes confused with his son Maicniadh and references to "son of Maicniadh" in the Irish manuscripts are not always interpreted as "grandson of Niadh". These variations cause uncertainty in the number of generations from Maccon to present but they do not affect current surnames listed as patrilineal descendants.





In the case of Fotadh Cannan there is yet another Maicniadh, this one being son of son of Gnathal. Confusion here can effect conclusions as to patrilineal descent. O'Donovan's section on the Saltair Chaisil document (1849, p. 25) indicates that Fothadh Cannan is a son of Fuinnche whose sister Teite is a daughter of Maicniadh, son of Lughaidh as depicted in

Figure 2. This is a major problem the solution to which demands that the Corca Laidhe be treated as two branches based on the descendants of (1) Fothadh Cannan and (2) of Duach and Aenghus sons of Maicniadh.



Figure 2 – An Alternative Pedigree for Fothadh Cannan from the Saltair Chaisil

AMOVA Analysis, Trinity Data

The assignment of some names to tribes is equivocal because they are mentioned in the genealogies of multiple tribes. The O'Driscoll are unequivocally Corca Laidhe, at least so far as recorded history is concerned, in that no other genealogies exist for the name. An O'Connor on the other hand could originate from any of six different septs (MacLysaght, 1985, p.55). The pedigree in Figure 1 shows six names for which more than mere mention is found in the ancient manuscripts. The Calraidhe share a common paternal ancestor with the Corca Laidhe, as such the Clancy and Travers families of Leitrim can be grouped as Corca Laidhe for a genetic study. There are some 70 other names mentioned in lists such as *The Hereditary Proprietors of Corca-Laidhe* (O'Donovan, 1848, p.49). A hereditary proprietor could originate as a cadet line, a son-in-law or reward for loyalty or service rendered. The listing of proprietors may simply be a record of land owners (Ó Corráin, 1992) and are thus these names are the most equivocal as being Corca Laidhe.

The name Kelly could be Corca Laidhe but it is said to be the second most common surname in Ireland with septs in Galway, Derry, Wicklow, Laois and Cork. The effect of internal migration over the past one to two thousand years is unknown. Here it is assumed a contemporary sampling of a Kelly is more likely to represent a group of individuals not related to one another and similarly with the name Connor.

The name Flynn was treated as Eoganacht in the Trinity study. According to de Bhulbh (2008, p. 235) there were two septs of Flynn in Cork. The Corca Laidhe and Calraidhe Flynn are paternally related, with two families to consider the Flynn were grouped as Corca Laidhe. According to the Clan O'Leary website (2012) there are also two different families of O'Leary in Cork, one in Sligo and probably others now extinct. The Clan tradition is that the O'Leary of Cork are Corca Laidhe.

Corca Laidhe	Ν	Eoganacht	Ν	Munster Control	Ν
Coffey	9	Doran	6	Cahill	10
Cronin	8	Kirby	8	Carroll	5
Kennedy	7	McCarthy	7	Healy	6
O'Donovan	2	McGillycuddy	7	Kelly	7
O'Driscoll	8	Moriarty	8	Maher	12
O'Flynn	6	O'Callaghan	10	O'Connor	11
O'Leary	6	O'Donoghue	7	O'Loughlin	5
	46	O'Keeffe	8	O'Shea	6
		O'Mahony	3	Whelan	4
		Quill	8		66
		Sullivan	7		
			79		

Table 1 - Surnames By Tribe Used In AMOVA Analysis

AMOVA (Analysis of Molecular Variance) computations were done using the Trinity data grouped by surname as shown in Table 1. There is not enough data available to split the Corca Laidhe in two branches rendering the analysis here preliminary.

The computations were done using the Arlequin software. The data is input as a set of tribes with haplotypes grouped by surname. The output is the percentage of variation, fraction of the total variance, in the data attributed to the tribes, to the set of surnames in the tribe and finally to the surnames themselves. The results in Table 2 are similar to what was obtained by McEvoy et al (2008) in that the percentage of variation is mostly within surnames and partly among surnames within tribes. Consistent with the McEvoy et al there is no significant difference among tribes when the Eoganacht are compared with the control group.

Trinity 17 Markers	Corca Laide/control		Eoganacht/control		Corca Laide/Eoganacht			Eoganacht/Corca Laide/control		
	Percentage		Percentage		Percentage			Percentage		
	of	P-value	of	P-value	of	P-value		of	P-value	
	Variation		Variation		Variation			Variation		
Among tribes	6.9	0.028	0.6	0.347	6.9	0.022		4.5	0.017	
Among surnames within tribes	29.2	0.000	21.8	0.000	20.1	0.000		24.7	0.000	
Within surnames	64.0	0.000	77.7	0.000	73.0	0.000		70.8	0.000	

Table 2 - AMOVA Statistics Based On Trinity Data

The percentage of variation among surnames within tribes is a measure of patrilineal signature that survives since the adoption of surnames on the order of 1,000 years ago. At that time the number would have been high and falling ever since due to non-paternal events. It never would have been 100% because even when surnames were adopted there were people of different surnames with the same genetic origin. An idealization of one way this could occur is if a patrynomic surname system was suddenly frozen and surnames then adopted, at the point you would have sons of brothers taking patrynomic versions of their respective father's given name. Thus you end up with sibling sons adopting different surnames reducing the percentage of variation among surnames. If at some later time descendants of one of those sons changed tribes this would reduce percentage of variation among tribes.

The Corca Laidhe show a percentage of variation among tribes on the order of 5% with respect to both the Munster Control and the Eoganacht. No significant difference is found between the Eoganacht and the control group as evidenced by the small percentage of variation, the associated P-value exceeds 0.055 and meaning the 0.6% is not a statistically significant number.

To understand the difference between the Corca Laidhe and the Eoghanacht the distribution by subclade within the data was examined. The subclades in haplogroup I were determined from rules on the Y-Haplogroup I2a Project pages (FTDNA, 2012). The majority of the data is in haplogroup R1b. There are several subclades of interest but only a few that have enough off modal markers that coincide with the 17 used here (or 19 when DYS385 is included).

Ref	Clade	GD	390	391	385a	385b	388	439	392	389ii-i
XQJ7H	R1b		24	11	11	14	12	12	13	16
Z9HCX	South Irish	3	24	10	11	15	12	11	13	16
M5UKQ	M222	3	25	11	11	13	12	12	14	16
MP	L362	3	23	11	11	14	13	12	13	15
QJJNX	Irish IV	3	24	10	12	15	12	12	13	16
NT4BZ	L226	1	24	11	11	14	12	11	13	16
TG7S3	Ely Carroll	1	25	11	11	14	12	12	13	16
B9NW4	L159.2	0	24	11	11	14	12	12	13	16
779RQ	Hy Maine	0	24	11	11	14	12	12	13	16

Table 3 - R1b Subclade Off Modal Markers

Table 3 shows subclades of interest. Three letter codes in the reference column refer to a ySearch ID (2012) and the two letter code MP refers to the Munster DNA Project (FTDNA, 2012). Since there are no off modal markers for L159.2 and Hy Maine the analysis does not differentiate between them and R1b. The four having three off modal markers are used as the basis of partitioning the data into subclades, a haplotype is said to fall into one of the four subclades if it matches all three of the off modal markers. The resultant distribution is in Figure 3.

There are a significant number of Corca Laidhe surnames of haplogroup I whereas that is not the case with the Eoganacht or the control group. All the I2a-Isles-A haplotypes are O'Driscoll and all the I2a-Isles-C haplotypes are O'Flynn. With respect to the R1b modal, the I modals differ at 10 to 13 of the markers and some by multi-steps. The data is dominated by R1b haplotypes such that the addition of one more R1b haplotype would have a little influence on the average variance of the set. The addition of an I haplotype being significantly different than the average haplotype of the set would have a larger influence on the variance of the set. As a result the difference between the Corca Laidhe and the Eoganacht due to haplogroup I2a manifests itself as percentage of variation between tribes and the difference due to R1b-South Irish between the Eoganacht and the Munster control does not.



Figure 3 – STR Based Subclade Assignments Within The Trinity Data Set

AMOVA Analysis, Public Data

Surname data was compiled from the genetic genealogy databases at FTDNA, ySearch, SMGF and Ancestry. Such an approach was necessary because most Driscoll data is found at FTDNA but most Leary data is at Ancestry. This limits the number of markers to the 32 in common between the 37 marker FTDNA set and the 43 makers used by SMGF and Ancestry (if one used 67 marker results from FTDNA an additional two markers can be picked up but the number of haplotypes available is then significantly reduced). Haplotypes were limited to those whose earliest known ancestor was said to originate in Munster. This is assumed to mimic samples collected in Munster thereby increasing chances that the data represents an ancient ancestor from Munster. This reduces dramatically the amount of data available such that some names are under represented. No doubt more data exists but it is inadvertently hidden because many surname projects do not display ancestral data and in many of those that do the data is too often blank, incomplete or otherwise ambiguous.

Corca Laidhe	Ν	N_{10}	Eoganacht	Ν	N ₁₀	Munster Control	Ν	N ₁₀
Barry	7	7	Donoghue	9	9	Carroll	7	7
Coffey	8	8	Egan	14	11	Connor	9	9
Collins	6	6	Mahony	28	11	Crowley	15	10
Donovan	3	3	McCarthy	17	9	Kelly	7	7
Driscoll	23	11	Neil	3	3	Murphy	12	11
Flynn	4	4	Sullivan	14	11	Ryan	4	4
Hayes	5	5		85	54	Shea	36	11
Kennedy	3	3				Whelan	10	10
Leary	9	9					100	67
Lynch	5	5						
	73	61						

Table 4 - Haplotypes Found In Public Databases

Table 4 shows the resulting set of names grouped by tribe used in the analysis. Some names have been added because enough data was found and some dropped for lack of data. There is still not enough data available to split the Corca Laidhe in two branches. Data was selected in such a way that the no two haplotypes of the same name were closer than a

genetic distance of 2 to avoid sampling too many haplotypes known to be related. Other names were considered but only names with instances of 3 or more were included. The column N represents the total number of haplotypes after removal by pairwise GD. The column N_{10} denotes a subset where a random number generator was used to select names such that each name had no more than a nominal 10 haplotypes yet the subclade distribution for that name remained the same. This was done to minimize effects of over representation of any one name.

The names added include Collins with Cullen lumped in as a variant. The hereditary proprietors of the Corca Laidhe includes the O'Cuilin now Cullen, O'Donovan (1849, p. 49). MacLysaght (1985, p.51) speaks in general of O'Coileain anglicized as Cullane but when spelled O'Cuileain it refers to the Corca Laidhe and is anglicized as Collins which is also a well known English name.

McEvoy et al (2008) excluded DYS385 from their analysis because it is a multi-copy marker and genetic distance as a measure of difference can be ambiguous. There is a trade off with removal of multi-copy markers from the analysis. The pairwise genetic distances are better defined but available information is not used. The prediction of the subclades of R1b to which a haplotype belongs can often be identified by examination off modal markers and in some cases multi-copy markers must be considered. So even though those markers cannot be modeled unequivocally they can correlate data when treated as sets of single copy markers. Analysis was done both with and without the multi-copy markers. The only practical difference noted was better organization in phylograms and for this reason the results presented use all 32 markers.

With 32 markers it becomes possible to develop some exclusion rules and thereby begin to deal with names that have multiple origins. The Corca Laidhe Kennedy are said to descend from the Coffey. According to de Bhulbh (2008, p. 291) the name Kennedy is a leading sept of the Dal Cais. The studies by Wright (2009) indicate the Dal Cais Kennedy should be R-L226 and carry a set of distinctive STR markers which can be used to differentiate them from other Kennedy. No haplotypes predicted to be L-226 were included for the Kennedy nor any other name for if you accept that the Corca Laidhe Kennedy are not L-226 then neither are the Corca Laidhe to whom they are supposed to be related.

The haplogroup and subclade of the Hy Maine Kelly has been established (ySearch ID 779RQ). One participant in the Kelly project is Count Walter Lionel O'Kelly who has a documented pedigree going back 29 generations to Murchadh O'Ceallaigh, the first in Hy-Many to use the name. Hence no haplotypes of this type are included in the analysis since the Hy Maine are not associated with Munster.

The results are similar to the 17 marker results in the difference among tribes. Among surnames within tribes the percentage of variation has dropped from numbers like 25% to less than 10%. The implication is that the patrilineal signature that survives since the adoption of surnames is less with the public data. It may be a difference between the descendants still in Ireland and those of emigrants.

N10 - 32 Markers	Corca Laide/control		Eoganacht/control		Corca Laide/Foganacht			Eoganacht and Corca Laide/control	
	Percentage		Percentage]	Percentage		Percentage	
	of	P-value	of	P-value		of	P-value	of	P-value
	Variation		Variation			Variation		Variation	
Among tribes	5.0	0.012	-1.8	0.978		5.4	0.022	3.5	0.017
Among surnames within tribes	6.2	0.014	8.9	0.000		7.1	0.034	7.4	0.002
Within surnames	88.8	0.001	92.9	0.000		87.5	0.001	89.1	0.000

Table 5 - AMOVA Results Using Public Data

As before the subclades in haplogroup I were determined from rules on the Y-Haplogroup I2a Project pages (FTDNA, 2012). In the case of R1b a haplotype was assigned to a subclade if it matched more than 75% of the subclade's off R1b modal markers and more than 75% of the subclade's modal markers. As with the Trinity data the results in Figure 4 show the data is mostly R1b, that all tribes have South Irish haplotypes and that the Corca Laidhe have more haplogroup I than the other tribes. Differences appear, R-L159.2, R-L362 and R-M222 are present in larger proportions than in the Trinity data. These differences are due a larger fraction of Mahony in the Eoganacht group and the addition of Egan and Murphy to the control group.



Figure 4 – STR Based Subclade Assignments In The N₁₀ Public Data

Network and Phylogenetic Analysis

A network diagram was constructed to see if any additional structure could be detected not revealed by the previous analysis. For this the FLUXUS software was used with individual markers weighted in proportion to the inverse of the square root of the mutation rate. The network was created by two successive computations: reduced median and median joining. The resultant network is shown in Figure 5. The taxa are colored by tribe on the right and in the left haplogroup R1b is shown separately colored coded by subclade.



Figure 5 - Network Diagrams for R1b and for all Haplogroups

Within the haplogroup I2a are three clusters defined by Nordtvedt as Isles-A, B and C (Y-Haplogroup I2a Project, FTDNA 2012). The Isles-A group herein is dominated by the Driscoll and there are single instances of Cohig (Coffey), Collins, and O'Leary. The largest clustering in haplogroup R1b is the South Irish and it is composed nearly equally of haplotypes from each of the tribal and control groups. Subclade M222 is evident in the diagram and therein are minority instances of Coffey, Murphy and Kennedy.

Network diagrams become noisy as the number of markers is increased because the number of identical haplotypes is reduced. The node sizes are proportional to the number of haplotypes therein and with more markers these shrink and the number of smaller nodes increases. This noise coupled with overlaid ancestral nodes and their surrounding descendants makes it difficult to see structure. Hence a phylogenetic diagram was constructed to provide an alternative view.

The phylogenetic diagram is based on the hybrid mutation model in McGee's utility which uses the stepwise mutation model for all alleles used here except YCA and DYS464 which use the infinite allele model. The output table from McGee's utility for hybrid genetic distances is corrected for back mutations and then used as an input matrix in the Phylip utility kitsch.exe. A best fit tree to the input matrix is computed subject to the constraint that all haplotypes represent the present generation. The best fit tree typically fits the input matrix with a standard deviation of 25% and is a measure of the uncertainty in the result. The equation of Nordtvedt (2007) is used to correct for the effect of back mutations which when applied to the total genetic distance between two contemporary haplotypes is:

$$GD_{C} = GD_{O}^{*}[1 + A^{*}GD_{O}/N/4]$$

where GD_C is the corrected genetic distance, GD_O is the observed genetic distance, N is the number of markers and A depends on the relative variance in marker specific mutation rates. For the 32 marker set the variable A is equal to 1.7 based on the mutation rates of Heinila (2012).



Figure 6 - Hybrid Mutation Model Phylogram for R1b Subclades.

The phylogram is shown in Figure 6 and is scaled as node age in mutations coincident with the rho statistic computed by the FLUXUS network software. The GD between two haplotypes is twice the age of the node corresponding to their most recent ancestor. The diagram served it purpose for it reveals structure that is easily overlooked in the network diagrams. The purple cluster within M222 is a group of Egan with a four step off M222 modal marker unique to their name. The L362 haplogroup is dominated by McCarthy and includes minority instances of Mahony and Sullivan.

The Murphy of Munster are said to be a branch of the Wexford *Mac Murchadha* (de Bhulbh 2008, p.380). This is consistent with them being mostly R-L159.2 as it is associated with Leinster. Within L159.2 are minority instances of Barry, Connor, Shea, Sullivan and Whalen.

The 2515 cluster is is dominated by Mahony and includes instances of Carroll, Flynn, Ryan and Leary. It is off R1b modal with DYS390=25 and DYS456=15 coincident with the Ely Carroll modal haplotype. However, only one of the haplotypes was Ely Carroll *a priori*. According to the Ely Carroll DNA project (FTDNA, 2012) the most significant marker that

characterizes a Ely Carroll haplotype is DYS492 = 11 which is not in the set of 32 markers. That marker is tested in the 67 FTDNA set. Inspection of those haplotypes which tested 67 markers shows some but not all have a value of 11.

Any of the haplotypes that fell within the South Irish group in the phylogram that were not classified as South Irish based on the STR criteria are reassigned to that clade. Such *a posteriori* subclade corrections are sometimes necessary because STR based assignments are probabilistic. The probability of error increases as genetic distance from the modal haplotype increases. Six of the 43 or about 15% of the haplotypes in the subclade were not predicted to be South Irish *a priori* and one was predicted to be South Irish that did not fall within the subclade.

Using just South Irish haplotypes from the phylogram a network diagram was constructed. TMRCA estimates and the associated standard deviations were then calculated from network using the rho statistic as implemented in FLUXUS. The R-P312 haplotype was used a reference and FLUXUS determines a root proxy node as the haplotype closest the reference. Note that descendants defined this way do not depend on the *a priori* subclade assignment. The resulting diagram, Figure 7, has some reticulation which is highlighted in gray; this where the network calculation was unable to determine between alternative paths and thus displays both. The median vectors fill in for what the network software perceives as missing data. A Steiner tree was constructed using the FLUXUS software. This is a tree which gets around reticulation by use of the shortest of the alternative paths from root to terminus haplotypes.

The age of the set of the descendants of Proxy Root is according to the rho statistics 4.7 mutations and the standard deviation is 1.2 mutations. This is consistent with the phylogram where rho for the MRCA of the South Irish cluster is seen to be 4.5 mutations. The TMRCA in terms of rho and the average mutation rate mu is computed in FLUXUS as:

TMRCA = rho/mu

Using an average mutation rate of 0.0024 based on the marker rates reported by Heinila (2012), the TMRCA is then 63 ± 36 generations. The ancestral haplotype for the South Irish tree is that of the proxy root, it is off R-P312 modal with DYS391=10, DYS385=11-15 and DYS456=15. Node B is coincident with the South Irish modal haplotype and Node A differs with DYS442=12.



Figure 7 - South Irish Steiner Tree

Node A is the MRCA of the Corca Laidhe with a TMRCA = 39 ± 16 generations. Given that the progenitor of the Corca Laidhe died in the year 225M the TMRCA of his descendants should be about 60 ± 15 and if he is said to be R1b-South Irish the order of magnitude of the network computed TMRCA does not contradict such an assertion. Figure 7 also shows no pattern which correlates descendants of either of the two largest nodes with any of the tribes. The origin of the earliest known ancestor for nodes A and B and their descendants is dominated by county Cork.

The O'Driscoll

The O'Driscoll are unique in that the origin of the name is associated with no other genealogy. Within the 1901 census of Ireland (National Archives of Ireland, 2012) if one queries the database for male Driscoll and O'Driscoll heads of house the results will show that 97% are born in Cork. The average for all the Corca Laidhe names in table 4 is 56%. Since it is almost certain anyone named Driscoll has an ancestor from Cork, the Driscoll data need not be limited to those haplotypes where the earliest known ancestor was born in Munster.

According to the genealogy of the O'Driscoll as discussed in O'Donovan (1849, p.16) the progenitor of the modern Driscoll, Eiderscel, was alive in the year 942 AD. The Driscoll pedigree has 18 generations between Eiderscel and a Cornelius O'Driscoll living in 1615, see Figure 8. Another 10 to 16 generations would correspond to the present so in total the genealogically determined TMRCA is about 31 ± 3 .



Figure 8 – O'Driscoll Pedigree

Data for I2a-Isles-A haplotypes for persons by and name and any origin was extracted from the public databases. The data is still 32 markers in order to use data from Ancestry.com. This was used to construct the Phylogram in Figure 9 and a network. The node labeled B on the phylogenetic diagram is the most recent common ancestor of all the Driscoll and several other names in the diagram. The age of node B is estimated to be 3.1 mutations or 40 generations. With the Network diagram and a proxy root based the age is 34 generations. The I2a-Isles-B modal haplotype was used as the reference to define the proxy root since the Haplogroup I tree of Nordtvedt (2012) shows Isles-A branching off Isles B.

It is curious that of the haplotypes that listed an Old World place of origin, at 42% less than half were Irish and the sum of England, Scotland and United Kingdom was 54%. One can only speculate at how this came to be. Nordtvedt (2011) estimates the TMRCA of the subclade I2a-Isles-A to be 1500 years. That is plenty of time for persons of the subclade to have ended up in Ireland, Scotland and England resulting in names said to originate in those countries. It could also be

that the Driscoll's founder Eiderscel was R1b and a subsequent non-paternal event introduced I2a-Isles-A into the mix of the O'Driscoll haplotypes. About half the haplotypes in the Driscoll DNA Project (FTDNA, 2012) are I2a-Isles-A.



Figure 9 – I2a-Isles-A Phylogram of Persons By Any Name And Origin

In the case of R1b-South Irish a database of was constructed of R1b haplotypes of Corca Laidhe names where the earliest ancestor was said to have been born in Ireland. The purpose of the database was to provide a mix of haplotypes so that the Driscoll haplotypes could be categorized South Irish *a posteriori* via a phylogram. The cluster that contained all the Driscoll within to the *a posteriori* South Irish had a TMRCA of 57 generations. The Driscoll therein differ from that of the R1b-South Irish modal at two key markers: DYS385=11-16 and DYS456=16. A network diagram of the same data and use of a proxy root yielded 50 generations. The proxy root differed from the South Irish modal haplotype at DYS442=12 and is the same haplotype as Node A in Figure 7 which was the MRCA of the Corca Laidhe in that tree.

In table 6 the TMRCA computed by the various methods are compared to those obtained using the variance method of Nordtvedt (2012) applied to the same set of 32 markers. The R1b-South Irish Driscoll appear to be older than the I2a-Isles-A Driscoll by about 15 generations. I2a-Isles-A Driscoll emerge as a better candidate haplotype for the Driscoll MRCA based on the genealogically determined TMRCA of 31 ± 3 generations. However, with confidence intervals on the order of 20 generations, systematic errors in modeling and small sample sizes the uncertainties stack up such that neither haplogroup can be ruled out as that of the O'Driscoll with confidence.

	TMRCA ± 2*Sigma (gen)							
mu=0.0024	Phylogram	Fluxus	Variance					
l2a-Isles-A	40 ± 20	34 ± 13	29 ± 16					
R1b-South Irish	57 ± 28	50 ± 22	56 ± 18					

Table 6 – Various TMRCA Computations Compared.

It is easy to focus on I2a-Isles-A and R1b-South Irish because these are the largest groupings but that is a form on tunnel vision. There are a few O'Driscoll in other subclades such as I1, R1b-Irish IV and R-M222 that could be the line of Eiderscel. A thousand years ago the O'Driscoll would have been at least as heterogeneous as they are today. That coupled with the evolutionary process of genetic drift would be the underlying reason why there are now majority and minority subclades (Evolution 101, 2012). Lankford (2005) writes ""a central and tantalizing mystery for present day O Driscolls is who should be considered 'The O Driscoll', the hereditary chieftain of the clan". It is ironic that one of the initial goals of the Driscoll DNA Project was to answer that question. Now it is back to square one, that question needs to be answered before the haplotype of "The O'Driscoll" can be established.

To that end, the O'Driscoll pedigree in figure 8 has been worked forward from Cornelius O'Driscoll, living 1615. The heritable line is generally assumed to be extinct in Ireland. Murchada (1996, p. 185) quotes Rickard O Donovan:

writing at the time of the Famine, referred to many members of the clan then striving to keep alive in the workhouses of Skibbereen and Schull. He mentioned one William O Driscoll then 84 and living in England who claimed the title of 'O Driscoll' as a descendant of Col. Cornelius. Since his only son was unmarried, however, this branch appeared likely to become extinct, and the title would then devolve on cousins in Charleston, U.S.A

Two of gg-grandsons of said Cornelius end up in South Carolina. Matthias (Mathew) O'Driscoll came to America in 1794 and his only son Dennis at age 22 was killed in a duel on August 17 1817 in Savannah, GA. Cornelius O'Driscoll of South Carolina was appointed a Lieutenant in the US Navy by President John Adams in 1800 (Executive Journal, 1828, p 334). Captain Cornelius O'Driscoll married Maria R. Talvande in 1807 (Salley, 1919 p. 53). Their son William Cornelius O'Driscoll of Charleston, SC is described as "having legitimate issue male" (O'Donovan, 1849, p. 398).

William Cornelius O'Driscoll died 15 Jun 1878 in Savannah, GA and his will is indexed in the England and Wales, National Probate Calendar (Ancestry, 2012). The US census records for Savannah, GA indicate William was born between 1808 and 1815 in Charleston, SC and had a son Francis died without male issue. His grandson Frank O'Driscoll Hunter 1894-1982 was a World War I flying ace and a General in World War II (Georgia Aviation Hall of Fame, 2012).

Conclusions

The AMOVA results herein for both datasets show a significant difference exists between the Corca Laidhe and the Eoghanacht. That difference is attributed to a high incidence of haplogroup I2a-Isles-A within the O'Driscoll which is not found in the Eoghanacht. Consistent with the Trinity findings, no statistical difference was found between the Eoghanacht and the control group using an analysis of haplotype marker variance. When the Eoghanacht and the Munster control are examined by their haplogroup and subclade composition differences are evident.

The majority of the data within R1b takes the form of singletons not part of any recognized subclade. If systematic differences exist amongst these singletons they could not be detected with the data set examined here. Both branches of the Corca Laidhe and the Eoganacht have substantial numbers of R1b-South Irish and construction of a Steiner tree revealed no tribe specific branch within the South Irish subclade. Within R1b differences do exist, the Eoganacht have significant numbers of L162 and M222 whereas the Corca Laidhe do not in either branch. The Eoganacht differ from the Munster Control having L162 and lacking in L159.2 haplotypes.

There is not enough data to split the Corca Laidhe into two branches for analysis as demanded by conflicts in the genealogy. There are too many such caveats to draw any definitive conclusions regarding the Corca Laidhe. Direct sampling of documented descendants is needed to deal with those caveats.

The O'Driscoll are one family that epitomize the Corca Laidhe. They have a pedigree that goes back to the progenitor of the Corca Laidhe, their most recent common ancestor is identified and there is no other known origin of the name. The O'Driscoll pedigree has been worked forward to discover if living males of the line exist and none have been found. There are loose ends and a living male may yet be found as more historical documents are put online.

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