

# Oriel and Thomond McMahon DNA

## An Analysis of DNA material pertaining to Project McMahon Testers



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## Preface

It has been assumed for the purposes of this analysis that DNA testing by FTDNA<sup>1</sup> was a fairly random process and would approximate to the distribution of different McMahan lineages among today's descendants. The historical perception is that McMahons are descended from one of two Septs which are briefly defined as follows (Ref 1):

### Oriel

The MacMahons of Oriel originated in the province of Ulster, in County Monaghan. The McMahons rose to power in 1250 AD, in the Kingdom of Oriel, which roughly evolved into the present day County Monaghan. They were chieftains of the territory for nearly 400 years.

### Thomond

The MacMahon's of Thomond originated in the province of Munster, in County Clare and allegedly descend from the founder of the O'Brien Dynasty, Brian Boru, through his son Teige, d. 1023, his son Turlough, d. 1086, his son Murtagh More, d. 1119, and his son Mahone 'a quo MacMahons of Corcabaskin' d. 1129. They became lords of the Corca Bhaschind or Corcavaskin area of south-west Clare which comprised the baronies of Moyarta and Clonderlaw, displacing the local O'Donnells and O'Baiscinn.

### Glossary

A Glossary of terms used is given in Appendix 3.

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<sup>1</sup> Family Tree DNA.

# INTRODUCTION

As Edward Gibbon famously said, “*we wish to discover our ancestors, but we wish to discover them possessed of ample fortunes, adorned with honorable titles and holding an eminent rank in the class of hereditary nobles*”.

In a nod to Gibbon, there is indeed good evidence that some might be descended from royalty, that is, if you accept that "royals" were simply the most vicious warlords to survive battle and conquer territory. This could apply to Colla descendants in Oriel and the O'Brien descendants in Thomond.

Early Irish genealogy describes the appearance in Ulster in about AD 330 of the three Colla brothers, known as Colla da Crioch, Colla Uais and Colla Meann. Their arrival was allegedly at the behest of the High King of Tara. Their descendants have been kings, lords, chiefs, and saints. Their history survived through oral tradition and eventually written histories as evidenced below (Ref 2).

## **The Three Collas**

The three sons of Eochaidh, great their fame,  
The three Collas we have heard of;  
Colla Meann, Colla fo Chri,  
And Colla Uais the high king.

The names of the three I know,  
And they slew the high king  
On yon wide bright plain,  
Aodh Muireadhach and Cairioll.

Cairioll, Colla Uais the king,  
Muireadhach, Colla fo Chri,  
Aodh, Colla Meann, great his fame;  
These three were mighty beyond all strength.

There is a long held belief that the earliest inhabitants of Ireland were Milesians thought to have come from the Iberian Peninsula. However, this is thought to be largely mythical and to quote Katherine Simms<sup>2</sup> :

*“The myth of the invasion of Ireland by the sons of Míl or Milesius is only relevant to the researcher of medieval history because it provides the framework within which the later genealogies were arranged. Every later surname was ordered under its earlier dynastic group, its wider population group, and its presumed descent from a son of Míl. For example, the Mac Mathgamna or MacMahon (surname) chiefs of Monaghan, together with their collateral Ó Cerbaill or O’Carroll (surname) kinsmen, belong to the Uí Nadslúaig dynasty within the Airgialla (population group), a federation of mid-Ulster kingdoms who claimed descent from the Three Collas and ultimately from Eremón son of Míl”* (Ref 3).

This can be regarded as the authentic genealogy for Monaghan McMahons - there are other references saying much the same thing as well. However, the difficulty is that not all McMahons (from Monaghan and elsewhere) carry the DNA that is thought to be representative of Colla (i.e. having similar DNA profiles to other known Colla surnames); it has to be accepted that there were multiple origins for McMahons as indeed for many other surnames as well. From a previous study (Ref 4), it was concluded that Colla DNA was present in Oriel (Airgialla) Clans such as Carrolls, McKennas, McMahons, McGuires and many others. In addition, there were strong contingents representative of Wales such as Calkin and Roderick and of Scottish names such as McDonald, McDaniel, Paden etc. This, in conjunction with the occurrence of the null mutation (a key indicator of Colla DNA) at the beginning of the first millennium, is strongly suggestive that the Colla tribe was well established and had branched in NW Britain before coming to Ireland. It is well documented that the three Colla brothers arrived in Ireland about AD 330, allegedly as mercenaries to the High King. As

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<sup>2</sup> Senior Lecturer in Medieval History and Fellow, Trinity College Dublin.

such it has to be assumed they were trained soldiers (presumably Roman) and would have been accompanied by a band of warriors (otherwise they would never have established themselves in a hostile environment). A further assumption might be that the band of warriors was composed of their null-bearing kinsmen, kinsmen without the null and co-opted non-kinsmen. In fact, in order to conquer Oriel (which they did), it must have been a mercenary army.

In Munster, the O'Briens emerged as chiefs of the Dalcassian race from the south-west of Ireland — a cohesive set of septs, related by blood, all claiming descent in tradition from a common ancestor of Cormac Cas. Academic histories generally accept the Dalcassians as being the Déisi Tuisceart, after adopting a new name. The Déisi, a people whose name means literally *vassals*, originally occupied the Southern counties of Munster and are ethnically Erainn. During the 8th century the Déisi Tuisceart, who would become the Dalcassians, annexed the area known today as Clare and made it their home.

Having first examined wider Colla inheritance (Refs 5 & 6), this analysis is concerned with a detailed analysis of McMahan data, both of Colla and non-Colla descent. The present study is an update of Reference 5 but having a wider scope in that it includes the Southern McMahan Septs and those whose origin predates the R\_L21 McMahons.

## **Aim**

The aim of this analysis was to try and deduce, given the limitations of some of the data, the relationships between those testers having the McMahan name, derivatives of the name, phonetic versions of the name, Colla and non-Colla origins and particularly to explain the wide diversity in genetic differences (GDs) and clustering.

# THE DNA TRAIL

It is believed that our most distant ancestors migrated from the Rift Valley into the Fertile Crescent and eventually onto the European mainland. This migratory passage would have taken many millennia and countless generations. Throughout this pre-historic era, humans evolved into many different races and acquired different mutations thus making them distinguishable from each other. DNA studies have permitted us to categorise all humans on Earth into genealogical groups sharing one common ancestor at one given point in prehistory. These groups are called [haplogroups](#). The haplogroups we are concerned with are the paternally inherited [Y-chromosome DNA](#) (Y-DNA) haplogroups which indicate patrilineal ancestry.

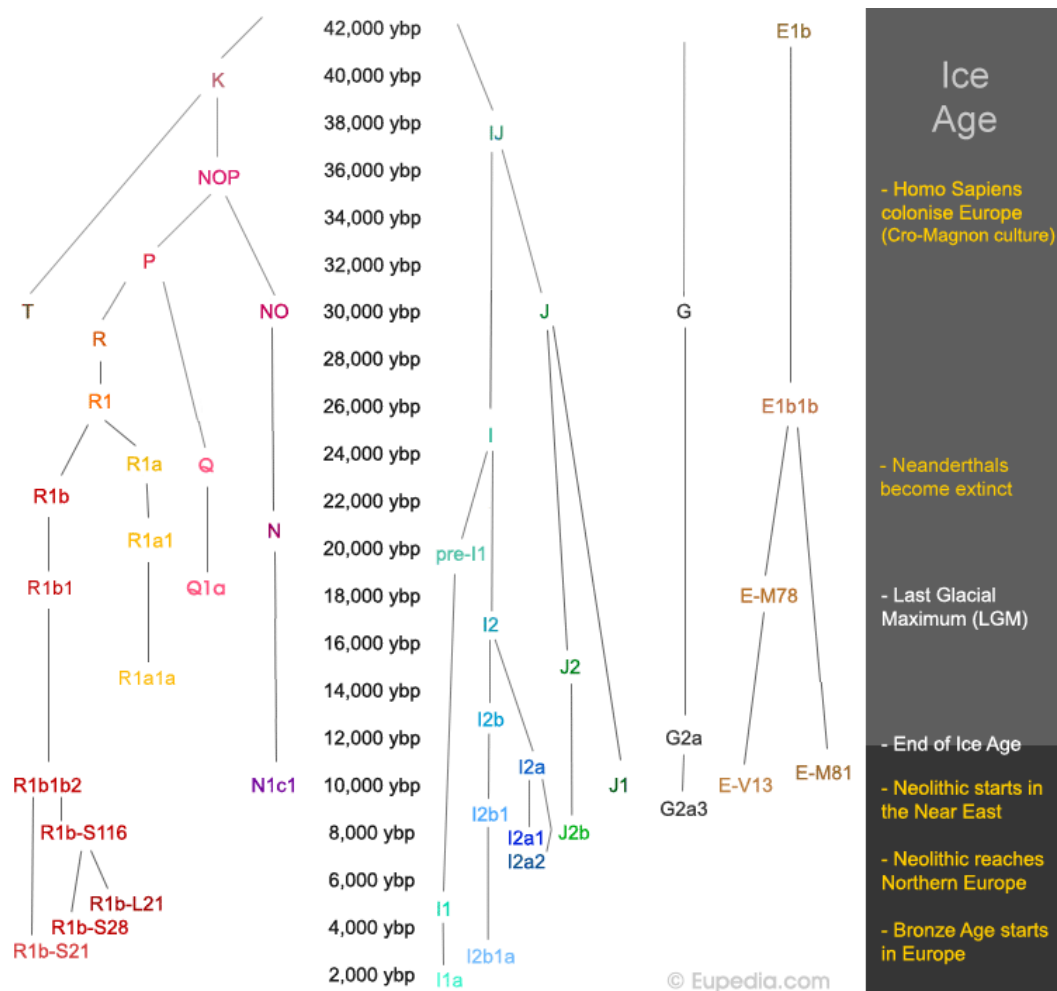
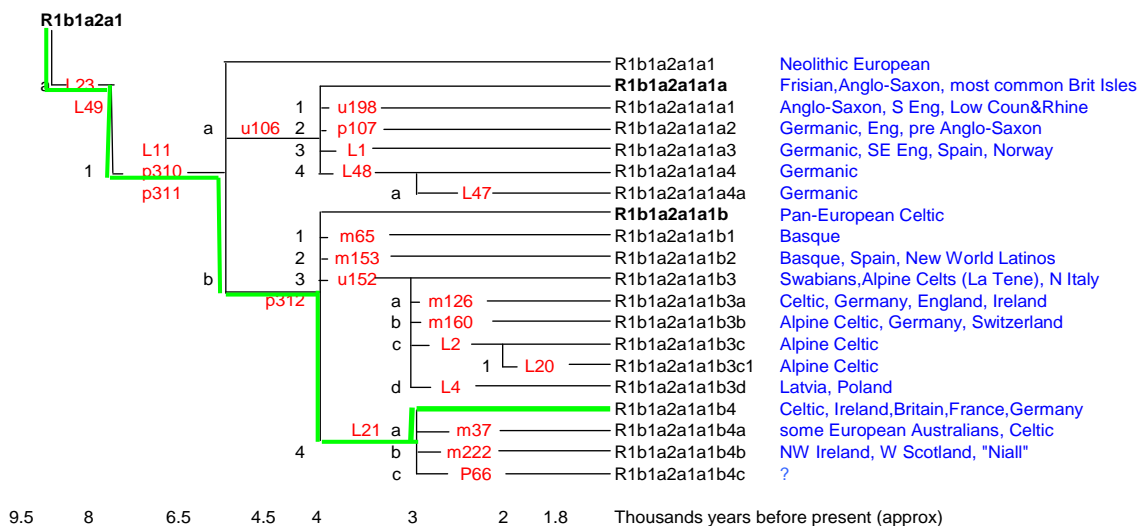


Figure 1: Chronological development of Y-DNA haplogroups

Figure 1 (from Ref 7) shows the Y-DNA haplogroups set against the timeline (ybp = years before present, AD 1950). Upper case letters indicate the major divisions while numbers and lowercase letters indicate the subdivisions of each haplogroup. These sub-divisions are the result of very specific mutations whose times of occurrence have been calculated. Thus R1b-S116<sup>3</sup> branched into R1b-L21 by acquiring the additional mutation, L21, and into R1b-S28, by acquiring the alternative mutation, S28. A phylogenetic tree showing the evolution of R1b haplogroups in Europe over the last 10,000 years is shown in Figure 2. Further explanation of the R1b haplogroups can be found in Reference 7.

<sup>3</sup> S116 is now P312, S28 is now U152, S21 is now U106.



**Figure 2: Mutations (in red) within the R1b1a21 Haplogroup over the last 10,000 years defining European haplogroups. Most common descent for McMahons in this phylogenetic tree is shown in green.**

## Migrations

It is thought that a population of R-L21 people arose (by acquiring the L21+ mutation) north of the Alps about 4,100 years ago. R-L21 descendants spread through France, the Low Countries, Britain and Ireland (Figure 3 from Ref 8). It is estimated they could have started to populate Ireland shortly after this. By the time the Romans came to Britain, these Celtic people would have subsumed earlier cultures and diverged from one another over the 50 or so generations. They developed into tribal groups as they did in Ireland and the Romans gave them names such as the Brigantes, Trinovantes, Cornovii, Silures etc. The L21+ mutation is most concentrated in Ireland (60-70% according to the Co-administrator of the "Ireland yDNA" Project) and to lesser extents in parts of Britain and north-western Europe. This supports the findings in Figure 3 showing a north-western migration from continental Europe over time. It is thought that these British Celtic tribes were mainly R-L21.

Ancestral populations migrated in waves over longish periods, with the latest wave replacing (but probably never completely) the previous one by force or evolutionary advantage. The best understanding that we have is that Ireland began to be first occupied about 9,000 years ago by stone-age people who were quite different to the later bronze-age people from whom most McMahons are descended. We can be fairly certain of this because the R Haplogroup had only evolved to R1b1a2a1 by this time and these peoples were only to be found east of the Black Sea. Maps in Eupedia suggest only partial occupation of Britain and Ireland 6,000 years ago by Megalithic Cultures (Haplogroups I, I2, I2b). It is thought that the Bell-Beaker folk initially brought the Copper Age to these shores around 2450 BC, homing in on the copper belts of Ireland and Wales<sup>4</sup>.

<sup>4</sup> In Ireland, they left their characteristic bell shaped pottery beakers at a copper mine on Ross Island, in Lough Leane, Co. Kerry. Judging from its chemical composition, copper from Ireland was traded into Britain, along with gold from the Mourne Mountains. These incomers boosted what had been likely a dwindling population of farmers and created a thriving society. By 2200 BC, Beaker interest in Britain intensified, as Cornwall was discovered to be rich in tin, essential to the manufacture of bronze.

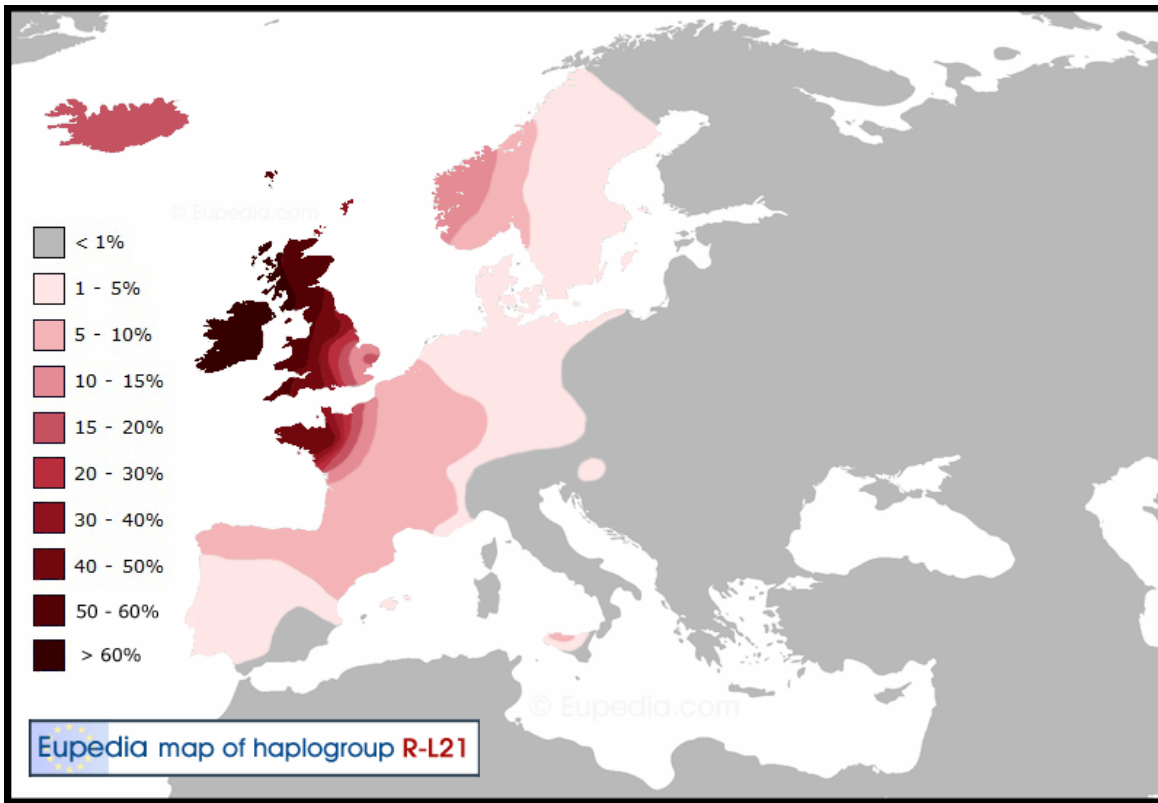


Figure 3. Distribution of R-L21 in Europe.

## Diversity

Among McMahons, apart from R-L21, there are E1b1b2, I1, R1a, I2a haplotypes and among other Colla names such as McDaniels, there are also I2a, R1a1, E1b1a, I2b1, and J2 as well. No doubt this type of diversity will also be found among other surnames. The Eupedia document (Ref 7) would suggest that these are remnants of early Bronze Age Bell-Beaker and Megalithic culture people who inhabited the British Isles and NW Europe about 5,000 years ago. After a further 2,000 years, the R-L21 folk have settled throughout Europe and as Insular Celts in the British Bronze Age. It is reasonable to assume that these E1b, I2a etc haplogroups (having McMahon and other Colla names) are descendants of much earlier Bronze Age Bell-Beaker occupiers of Ireland who were subsequently retained by L21 invaders (possibly as slaves, vassals etc). Ultimately, when surnames were being adopted (600 years later), these non R-L21 descendants had become integrated into the clans and acquired the Chieftain's surname as well (it is doubtful if anyone would have been aware of original blood relationship by this late stage).

## The Collas

Recent work established that the precursors of the Colla profiles examined had diverged prior to the allocation of surnames. Early branching suggested the approximate date of birth of the Colla Progenitor to be c. AD 280 (Ref 4). The Colla Progenitor gave rise to a population of Collas, possibly in NW Britain, who expanded into Dalriada and Ulster. Most but not necessarily all of the 'Irish' Collas are allegedly descended from three Colla brothers who came to Ireland in about AD 330.

Taking the above into account and given the wide variety of names, many of which are 'non Irish'<sup>5</sup>, it is hard to escape the conclusion that the origin of the Colla clan was among the British Celts. If as alleged (Ref 5), the Colla Brothers' arrival as Roman trained mercenaries was at the behest of the High King of Tara, then this would support that view. Genetically, the closeness of Calkin to McMahon, Carrolls and many others is strong supportive evidence. Similar arguments can be extended to Rodericks, McDonalds, and Paden. The simplest explanation is that however many sons Papa Colla had, they or their progeny spread over North West Britain, Dalriada and Ulster, their descendants all showing relatedness to this day.

Early divergence is the most likely explanation as to why genetically diverse lines finished up with the same surnames. Examples of this are some McMahons, two McGuire Groups and three McDonald Groups as well as several singletons. Equally, it goes some way to explaining mixed origins where 2/3 to 3/4 of many of the major Colla names did not have Colla DNA. The precursors of these non-Colla DNA McMahons, McGuires, Carrrolls etc must have been already associated<sup>6</sup> with the Colla tribes prior to the allocation of surnames (Ref 5).

The Collas are part of a broader genetic grouping identified as R-L21. A new subset was discovered recently within this L21 grouping; this subset has been termed Haplogroup R-DF21, having acquired the extra DF21 mutation about 3000 years ago. The Colla population is defined (so far) by being R-DF21 and having two further specific mutations<sup>7</sup>. In other words, these marker values are particular to the descendants of the Collas who are believed to be the progenitors of many (but not all) families in the ancient kingdom of Oriel. The evidence appears to indicate that the Colla line arose about 2000 years ago. The key events in the evolution of the Collas and their kinsmen are depicted diagrammatically in Figure 4.

### Colla Origins

The DNA evidence does not support the historical contention that Collas are descended from the son of Eochaid Doimlen, younger son of Cairbre Lifechair, High King of Ireland in the 3rd century AD (as described in the Glossary). That is to say, the Collas did not arise indigenously in Ireland as they have a large genetic footprint in Britain. Further, the DNA evidence does not support the Annals of the Four Masters which specifically states that the father of the three Collas was a brother of Fiachra Srabhteine (ancestor of Niall of the Nine Hostages). Niall's descendants have an additional mutation (to L21+), M222+, which arose more recently making them R1b1a2a1a1b4b Haplogroup (Fig 2). This mutation could have occurred in Fiachra Srabhteine or in his later descendants as the DNA evidence precludes this close a blood tie. Another possibility is that Eochaidh Dubhlen and Fiachra Srabhteine were merely "foster brothers", which was a common practice among the Gaelic nobility. In any event, the DNA evidence would appear to indicate that the ancestors of the Colla brothers were part of a gradual westward migration through Britain to Ireland in either pre-Roman or Roman times.

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<sup>5</sup> Names such as Calkin, Roderick, Paden, McClain, McDougall, Walden, Dever, McDonald, Rattray, Rice, Godwin, Kern, Judd.

<sup>6</sup> Some tribesmen who lived with or near the Colla clan could have taken on the names McMahon, McGuire, Carroll etc. Even with a strong oral history tradition and over a period of 20 generations, it must have been difficult to keep track of who were pure male Colla descendants especially as the Brehon Laws encouraged concubinage.

<sup>7</sup> These are termed Single Tandem Repeats (STR) having a null value for one (DYS 425) and nine repeats at the other marker (DYS 511). A further defining mutation (for those tested to 111 markers) was nine repeats for marker 505.



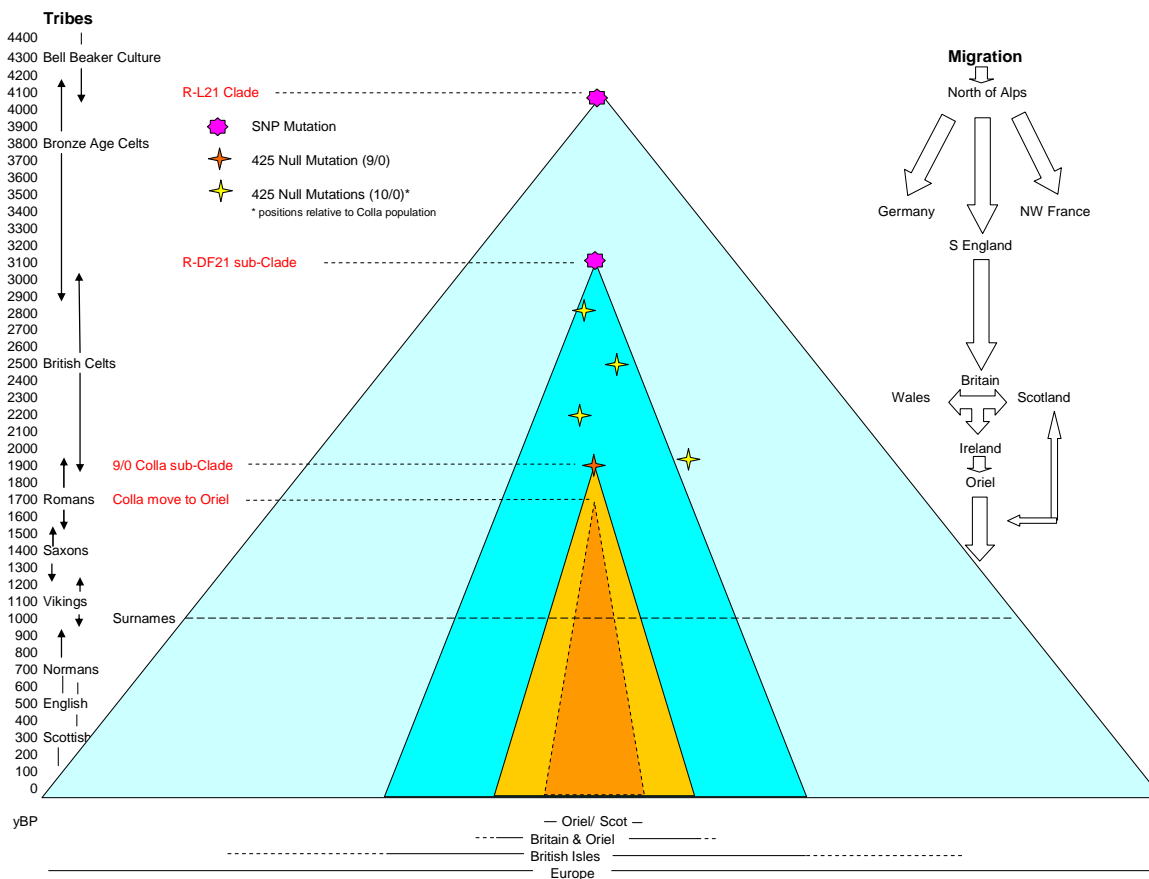


Figure 4. Pictogram relating key events in the evolution of the Celtic R-L21 Clade.

## Collas in Ireland

The most colourful explanation of Colla origins has been put forward by Don Schlegel in the Clogher Record (Ref 10). He states that the Collas are perhaps the only instance in prehistoric or early historical Ireland of three brothers having each a personal name, a name in common, and an epithet. The implication is that such a naming convention must have been imported, and the obvious source is the Roman Empire. He suggests they were not descended from Irish Kings but instead were Romanized Britons, originating in the Celtic tribe named Trinovantes (Ref 11) from Colchester, originally a Celtic settlement and the oldest recorded Roman town in England. They received military training from the Romans and eventually went to Ireland as mercenaries in the service of the King of Ireland. The most supportive evidence for this idea can be seen in Figure 3 which shows a hotspot in the Essex region for R-L21 although no specific Colla clustering has been found (mainly because most testers don't know where their ancestors originated).

Whatever their origins, the Romanized ancestors of the Collas may simply have been hired as mercenaries by the Irish High-King as described above and elsewhere, possibly due to their having acquired valuable military skills in the service of Rome. Indeed, could it be that they were retired centurions, which would place them in their forties (Roman soldiers usually retired after 20-25 years service) at the time of their arrival in Ireland?

The Book of Ballymote, written in 1390AD, claims Cairpri Daim Airtit, King of Orgiall (Kingdom of Oriel) died in 513AD. This King of Oriel is five generations down from Colla da Chroich. The King had seven sons, Cormac from whom the Maguires descend; Nadsluaigh from whom the McMahons and Carrolls descend; and Daimine from whom the Boylans and Kellys descend.

Colla da Crioch was one of The Three Collas who sought to restore the monarchy to their line. At one point, the Three Collas were exiled from Ireland to Scotland. However, through the influence of the King of Alba and the intervention of the Druids, the Collas were pardoned by the Irish King and were invited back to Ireland. Colla da Chroich was the first King of Ulster after its conquest by the Three Collas in the 4th century. He was the founder of the Kingdom of Orgiall. The Clan Colla ruled over that Kingdom, and they were styled "Kings of Orgiall," down to the twelfth century. Colla da Crioch died about the year 357 AD.

## Collas Elsewhere

From a recent analysis, the heaviest concentrations of Collas outside of Oriel are to be found in Scotland, followed by England and Wales (Table 1). This is in broad agreement with the migratory movements of R-L21 through Europe which would have included the Collas (Fig 3). Colla Lineages<sup>8</sup> are a more reliable indicator of early branching as they avoid distortion from large family groups (13 of the 16 Welsh testers were from one family).

<b>Surname Root</b>	<b>Scottish</b>	<b>English</b>	<b>Welsh</b>	<b>Irish</b>	<b>Totals</b>
<b>Lineages</b>	10	8	3	47	68
<b>Total Testers</b>	24	22	16	115	177

*Table 1. Distribution of Colla Origins*

These results support the scenario proposed by Schlegel (Ref 10) outlined above or an alternative one, in which the Collas were pushed north into Scotland from whence they invaded and conquered Oriel.

There will always be controversy over whether the roots of Collas with a Scottish, Welsh or English presence (today) were indigenous to mainland Britain or migrated from Ulster to mainland Britain<sup>9</sup>. The latter would be counter to the population drift of the Celtic tribes in general, and it would have been difficult to establish so many lineages over such a wide area. Previous results (Ref 6) suggested that Collas were well established in Britain before conquering Oriel. The converse (excluding much later 18/19<sup>th</sup> c. migrants), although not impossible, would have been more difficult to achieve as it would imply being able to integrate into a rigid feudal system and propagate over several generations. The exception would have been Alba/DalRiada (which was a unified Kingdom on both sides of the Irish Sea) and from which a large proportion of Collas seem to have originated; indeed, the evidence is suggestive that the Collas might well have originated in Alba.

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<sup>8</sup> A lineage is defined as a descent group that can demonstrate their common descent from an apical ancestor or a direct line of descent from an ancestor. Can often be a single representative of a cluster which arose from recent branching of (usually) family members.

<sup>9</sup> The spread of Collas seems to have been more widespread on Mainland Britain than in Ulster, where they are largely limited to the Oriel territory.

## Method

The genetic identities (particular to the male Y-chromosome) of McMahon Project members were established through laboratory analysis of DNA (obtained through a mouth swab). Various levels of analysis and deductions were performed (by FTDNA) on these samples to determine haplogroups and further marker values. The final defining mutation for Haplogroup R1b1a2a1a1b4, L21, occurred about 4,000 years ago. The vast majority of samples belong to Haplogroup R1b1a2a1a1b4 (shorthand name: R-L21) although there were some exceptions.

This analysis is based on differences between profiles (of testers) of their Single Tandem Repeat (STR) mutations. The source for this data was FTDNA as compiled into the 'McMahon Project'<sup>10</sup> (Ref 12). Joining the 'McMahon Project' was optional for testers and over time some testers with inappropriate names &/or DNA had joined; these were removed prior to analysis. Exceptions were made for those with matching DNA but non-matching names, some of whom were known to be adopted. Four other testers from different projects and five reference testers were added to the database making a total of 110 testers examined.

Project data<sup>11</sup> was downloaded into an Excel spreadsheet which was used to tabulate the data and organise it<sup>12</sup> for inputting into the McGee Utility Tool (Ref 13). The 'Genetic Distance' (GD) matrix output from McGee, where a GD value for every pair-wise combination was calculated, and the deduced 'time to Most Recent Common Ancestor' (tMRCA) values, were used to demonstrate relationships. The latter values were used to generate an infile for the 'Phylogeny Inference Package' (PHYLIP) program.

## Assumptions

The Colla administrators are agreed that all Colla descendants are R-L21+ in so far as all of those who deep clade tested proved to be R-L21+ and none proved to be R-L21-. It is therefore a reasonable assumption that Collas are a sub-set of R-L21+ and that genetic relatives will be found among R-L21+ people.

A new subset was discovered recently within this L21 grouping; this subset has been termed Haplogroup R-DF21, having acquired the extra DF21 mutation about 3000 years ago. Among Collas who tested, all are DF21+.

Collas are defined as per Glossary (Appendix 3). Those not meeting the Colla criteria are defined as non-Colla.

It is assumed that the Kitsch programme (one of many in the PHYLIP collection) using the Fitch & Margoliash methodology was able to differentiate the relative branching events in the dataset from the aggregated marker values. To achieve the best resolution, 99 iterations were performed in the Kitsch Programme.

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<sup>10</sup> As at 8 November 2012.

<sup>11</sup> For consistency with previous studies and statistical credibility, only 67 marker data was used.

<sup>12</sup> Labels were compiled using the first three digits of the FTDNA ID and a truncated name up to a limit of 10 characters.

## Results

The basic Project data can be viewed at Reference 12. The Project output shows the distribution of testers among the different categories and is summarised in Table 2.

Septs	Category	Defined			Tested to 67 markers	Potential		
		McMahon (incl. derivatives)	Other names	Total		Subject to Upgrading	Grand Totals	
Northern	Colla (aka Airgialla 1)	18	3	21	21	11	32	
	Airgialla 2	7	4	11	10		11	
	Z 246 Mahon	6		6	4		6	
	R-P312	1		1	1		1	
	R-SYR2627		1	1	1		1	
	<b>totals</b>	<b>32</b>	<b>8</b>	<b>40</b>	<b>37</b>	<b>11</b>	<b>51</b>	
Southern	Clare 1 - L226 Dal Cais	6	1	7	5		7	
	R-M222	1	1	2	2		2	
	McMahan Cluster	3	1	4	3		4	
	Clare 2 (Z255?)	7		7	5		7	
	R-M269 (WAMH)	2	1	3			3	
	<b>totals</b>	<b>19</b>	<b>4</b>	<b>23</b>	<b>15</b>		<b>23</b>	
	PHYLIP Testing				<b>52</b>			
	Haplogroups other than R1b1a2	5		5	3		5	
	Unclassified					22	22	
<b>As at 8 Nov 2012:</b>			<b>Are Defined</b>	<b>68</b>		<b>33</b>	<b>in need of upgrade</b>	<b>101 Testers</b>

**Table 2. The distribution of McMahon, McMahon derivatives and other names (having McMahon type DNA) between the Northern and Southern Septs broken down by category, in the 'McMahon Project'<sup>13</sup>.**

Using background knowledge and the very limited geographic information from the Project, the categories (and their members) are shown divided between Northern (Ulster) and Southern (Munster) septs. The most obvious deductions to be made from these results are:

- Colla (Airgialla 1) is the largest dynastic group followed by Airgialla 2.
- Twice as many testers were from Northern Septs as opposed to Southern Septs.
- There is no corresponding dominant dynastic group (to the Collas) among the Southern McMahons.

<sup>13</sup> As at 8 Nov 2012, there were 109 entries in the 'McMahon Project'. Table 2 excludes the two McKenna, one McDaniel and five duplicates reducing the entries to 101.

## Haplogroups

Haplogroup testing was very poor among Project members with only 31 % having tested. This was not critical for Colla members as it has been established (elsewhere) that all Collas are R-L21 and DF21. However, it is critical for other Septs as, excluding R-L21 and non-R1b1a2, the following haplotypes were detected:

- R1b1a2a1a1b R-P312 1 one step upstream of R-L21
- R1b1a2a1a1b4b R-M222 2 downstream of R-L21, aka NW Irish.
- R1b1a2a1a1b4c R-P66 1 downstream of R-L21
- R1b1a2a1a1b4h R-L226 2 downstream of R-L21, Dal Cais
- R1b1a2a1a1b5a R-SRY2627 1 two steps downstream of R-L21
- The Z246 SNP was not detected and is attributed by modal matching. It is downstream of R-L21.

Clare 1, R-L226 (Dalcassian), is the alleged origin of Thomond McMahan and yet there is only one (proven) McMahan with this haplotype (the other is a Cusack); five others are associated within this group, one being a (proven) R-L21. These testers were grouped under Clare 1 on the basis of their positions in the evolutionary tree (Figure 5). However, the group doesn't show clustering in McGee as most of the branching is too far back in time. The closest pair was 204McMahon/110McMahon at a GD of 13; the one Dalcassian (185McMahon) has a common ancestor with this pair at AD 150 and is in effect a singleton lineage from that date onward. The remaining two are only tentatively associated with this group.

R-M222 is normally associated with Northwest Irish but there are emerging doubts about it being constrained to this part of Ireland. The fact that there are four O'Briens and 229McMahon (from Limerick) who are confirmed R-M222 would support this view. On the present evidence, the most numerous groups are the Clare 1 (above) and the Clare 2 grouping which doesn't have any affinity with known modals and one member has tested positive for Z255 (the 'Irish Sea' haplotype).

## McGee Output

In order to generate a Genetic Distance matrix for this sub-set of the R-L21 population, the 52 defined McMahon Project testers (who had tested to 67 markers, Table 2) together with the two McKenna and one McDaniel Project members were used. To these were added two McGuires and two McCowns from other projects and five reference testers (a total of 64). These 64 defined profiles plus six modals (to which matches were found) were examined in the McGee Utility tool @ 95% p. The output is shown in Appendix 1 in two parts (because of matrix size). The first half covers testers up to and including Airgialla 2; the second half, covers the remainder.

### Modals

Seventeen modals were used for comparative purposes but only the six shown had some affinity to the testers. The Colla, L69 and L222 modals were unrelated but South Irish Type II, L226 and Z246 showed significant cross relationship, particularly the last two.

### Clusters

The largest cluster was Colla (Airgialla 1) which was termed the 'Monaghan McMahon' Cluster. This included known derivatives (McArdle, Matthews) and a fair number of non-McMahons, at least two of whom (Bogner, Woods) were known to be adopted names. The remaining Collas had ever increasing distant relationships from the 'Monaghan McMahon' Cluster, two McMahons who diverged early as Singletons, a pair of McKennas and most distant, a McDaniel.

Quite distinct from the Collas was the Airgialla 2 grouping. This was characterised by having high GDs to the Colla modal (in the 20s), close relationship to the L69 modal and good clustering of members. This cluster was also characterised by having a mixture of a few Colla names without Colla DNA. The remaining clusters were small and can be summarised as follows:

- Cluster 150Mahon-194McMahon which had no cross relationship to modals or others. Loosely associated (mid teens GD) to N11Corcoran.
  - 718Mahon showed affinity to the Z246 modal and was loosely associated with the 258McMahan-N19Mahan cluster.
  - 228Mullin and 229McMahon had a GD of 6 to the M222 modal and a GD of 10 between them.
  - Cluster 898McMahan-190McMahan had no cross relationship.
  - A loose grouping of 110McMahon-204McMahon had affinity with Type II and L226 modals.
  - 113McMahon-153McMahon formed a loose cluster without relationship to anything else.
  - The remaining five members were classed as singletons that had diverged very early.
-

## PHYLIP Output

In order to generate an evolutionary tree for this sub-set of the R-L21 population, the same 64 defined testers (as used in the McGee analysis) but without the modals, were used. The references were used to mark the earliest Colla so far detected (125Conley), a genealogical date (337McGuire), the minimum of the date range (30 years) and the maximum of the date range (128Lee) (Appendix 2).

Data prepared @ 95% and 50% probability in McGee was examined and the latter used in the present analysis. The phylogenetic tree produced from the tMRCA (@50%p) input (59 testers + 5 references) is shown in Figure 5. This is overlain with colour coded labels corresponding to the groupings in the 'McMahon Project' (Ref 12) and estimated dates for when the different McMahon common ancestors arose. Reference profiles are indicated with an '\*'.

### Interpreting PHYLIP

Other workers have indicated that the PHYLIP software overestimates early branching and underestimates later branching (Ref 14). The overestimating is largely due to the statistical method used in McGee (degrees of significance associated with small numbers) and the underestimating, partly from not knowing how much reversion might have occurred over time.

PHYLIP trees are good at showing relative branching (as they are based on DNA differences) but the times (as given by branch length) can only be a rough guide. A literal interpretation of the tree says that an ancestor gave rise to Airgialla 1 and 2 lineages about 700 and 800 years ago. It is known that Colla went further back than this and it is probable that Airgialla 2 did as well. The problems with the PHYLIP trees is that they are not intended to estimate when branching occurred but simply the relative positioning of branching within the tested sample and the degree of relatedness of the profiles. Because it is essentially a reverse engineering process it can only predict the most recent of branching for a particular profile that is being examined. The hundreds of thousands of earlier branches that never made it to the 20th c. or whose descendants didn't have their DNA tested, cannot be estimated.

The method used to estimate dates from PHYLIP branch lengths, shown in Figure 5, is described in Appendix 2. By way of validation, Appendix 2 and Figure 5 show the most distant Colla yet discovered, 125Conley, to have a branch length of 663 which extrapolates to 1700 yBP, a value similar to that derived in earlier studies.

### Output

The output shown in Figure 5 breaks down into three distinct groupings. Within the L21 population, Airgialla 2 evolved about 1,000 BC followed about 400 years later by those lineages that developed into the Thomond McMahon Septs. The Colla population became established sometime before AD 250 from which the majority of McMahon descend.

### Airgialla 1 (Colla)

The Colla McMahons are by far and away the most numerous among Project members. This is indicative of the large putative McMahon clan that established itself in Oriel from the 4<sup>th</sup> c. onward. The composition of the clan was not limited to Colla members but included those designated Airgialla 2 who carried the McMahon surname. Colla DNA was not found in the Southern Septs. Apart from the two early evolved lineages, all the remaining Colla McMahons were tightly related as shown by their significant clustering in Appendix 1 and their close branching relationship in Figure 5. The most recent common ancestor for Airgialla 1 represented in the data set was AD 250.

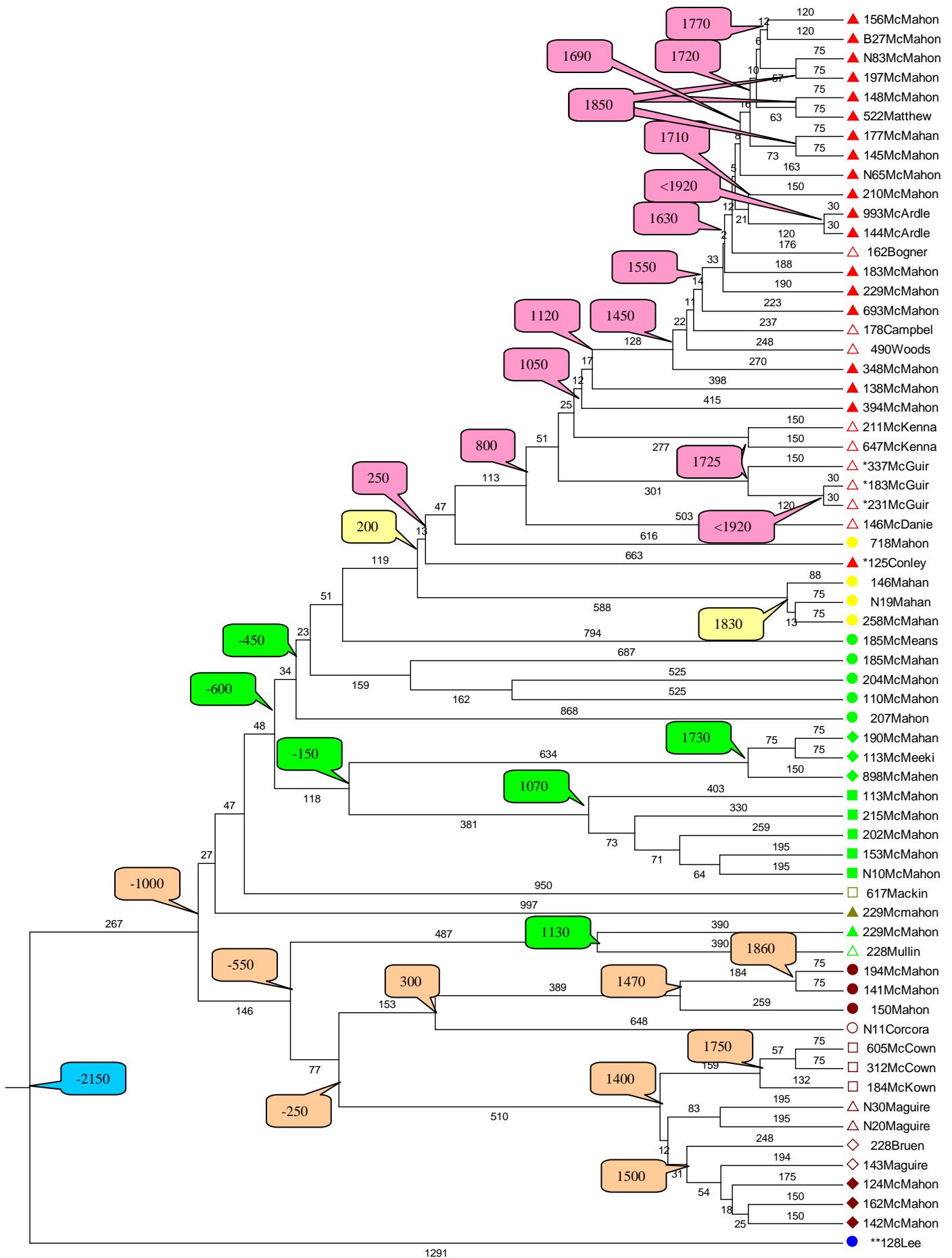


Figure 5. PHYLIP Output for 'McMahon Project' together with five reference testers, two McGuire and two McCown (from other projects).



▲ = Colla McMahons (Airgialla 1)

△ = other Collas (Airgialla 1)

□ = B1 - non-Colla R-P66 (Airgialla 2)

△ = McGuire non-Collas (Airgialla 2)

◆ = B2 - non-Colla R-L21 (Airgialla 2)

● = B3 - non-Colla Mahon (Airgialla 2)

□ = B4 - non-Colla R-SRY2627

● = B5 - non-Colla Z246

▲ = B6 - non-Colla R-P312

● = C1 – non-Colla Clare 1 - L226

▲ = C2 – non-Colla R-M222

◆ = C3 - non-Colla McMahan

■ = C4 – non-Colla Clare 2

● = L21 (root)

Symbols with no filled colour = names other than McMahan

\* indicate reference haplotypes.

\*\* indicates earliest branching R-L21 tester.

Balloons show the estimated dates for common ancestors, colour coded for the different groupings. The generated branch lengths were extrapolated into yBP using the method described in Appendix 2. These values were subtracted from AD 1950 (the ‘Present’ in yBP) to arrive at the estimates.

### Legend for Figure 5.

## Airgialla 2 (Non-Colla)

The non-Collas show a clear separation from Collas about AD 200, with the earliest common ancestry for the Southern Septs at 600 BC. These in turn separated from Airgialla 2 about 1,000 BC. Those thought to be Airgialla 2 were grouped into 3 categories (B1-B3) and those thought not to be, into B4-B6 (Ref 12). All those classed as Airgialla 2 showed close affinity to the L69 modal for Airgialla 2. Other studies have shown a wide variety of Oriel names, often those associated with Colla, in the Airgialla 2 sub-clade. The most distant common ancestor for Airgialla 2 represented in the data set was 250 BC.

## Non-Airgialla 2

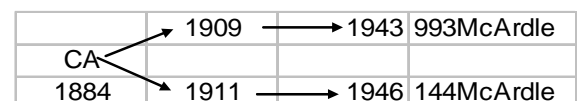
There were three groups which were difficult to place geographically, B4 was R-SRY2627, B6 was R-P312 and B5 was a Z246 Mahon cluster centred (from the limited geographic information) around Galway. It is arguable as to whether these should be placed under Northern septs as shown in Table 2. B4 and B6 could be from any part of the country, show no affinity to any of the modals or other testers and branch extremely early as singletons in the evolutionary tree (Figure 5). B5 on the other hand, shows some affinity to the Z246 modal (one member) and it branches at about the same place as Colla in the evolutionary tree (Figure 5).

## Thomond

Those thought to be of Thomond origin were grouped into four categories (C1-C4). C1 was thought to be Dalcaisian although only two members were proven R-L226 and only one of these was McMahan<sup>14</sup>. Two Project members (only one of whom was McMahan) were proven R-M222 and constituted C2. C3 was a McMahan cluster and C4 was the Clare 2 grouping, one member of which was positive for the Z255 SNP (‘Irish Sea’ haplotype). The most recent common ancestor for Thomond septs represented in the data set was 600 BC.

## Close Relatives

There were three instances of close relatives among the testers. The first was for two McArdle first cousins who had a GD =0 (@67 markers). This was straight forward showing no mutations over an elapsed time of c. 60 years in both branches.



<sup>14</sup> This is the only McMahan/McMahon out of 122 testers in the R-L226 Project.

The other two instances were more complex. A GD of 1 was recorded between 145McMahon (the author) and 177McMahan. This closeness suggests a common ancestor about 1860. However, the genealogy suggests both lines were separate from mid 18<sup>th</sup> c. (“Robert McMahan and his wife Catherine left Dublin, Ireland in 1746, bound for Virginia”). This could be an example where a second mutation occurred in one line followed by its reversion (net GD=1 instead of 3) thus accounting for the elapsed time of c. 200–300 yr.

A similar observation was made for two McGuire reference testers (231McGuire/183McGuire) who had a GD = 0. Again, the genealogy suggests a separation of several hundred years but there were no (expected) mutations. Although it is possible to have such an elapsed time without mutations, it is unlikely. It is possible that this is another example of a forward mutation being cancelled out by a later reversion (net GD=0 instead of 2).

## **Common Ancestors (CA)**

Table 3 summarises the data for the major ancestors depicted in Figure 5.

<i>CA Date</i>	<i>Descriptor</i>	<i>Comment</i>
2,150 BC	L21 Root - earliest branch detected in the L21 Project	There may be an even earlier profile as yet undetected.
1,000 BC	Separation of Airgialla 2 from Southern Septs	
250 BC	Most recent common ancestor (CA) for Airgialla 2	Origin of four Airgialla 2 lineages
600 BC	Earliest CA for Southern Septs	
450 BC	CA for non-Colla Clare 1	Project C1 – L226
150 BC	CA for non-Colla McMahan and Clare 2 McMahons	Project C3 and C4
AD 1070	Most recent CA for Clare 2 McMahan	Project C4
AD 1730	Most recent CA for McMahan	Project C3
AD 200	Separation of Colla from non-Colla	Project B5
AD 250	Origin of earliest Colla (reference profile)	125Conley
AD 800	Most recent CA for remaining Collas	Inclusive of McKennas and McGuires
AD 1050	Separation of early Colla McMahan lineage	394McMahon
AD 1120	Separation of early Colla McMahan lineage	138McMahon
AD 1450	Beginning of Colla McMahan Monaghan cluster	Continued evolving until AD 1850.

*Table 3. Major McMahan Common Ancestors (to be read in conjunction with Figure 5)*

## Multiple Origins

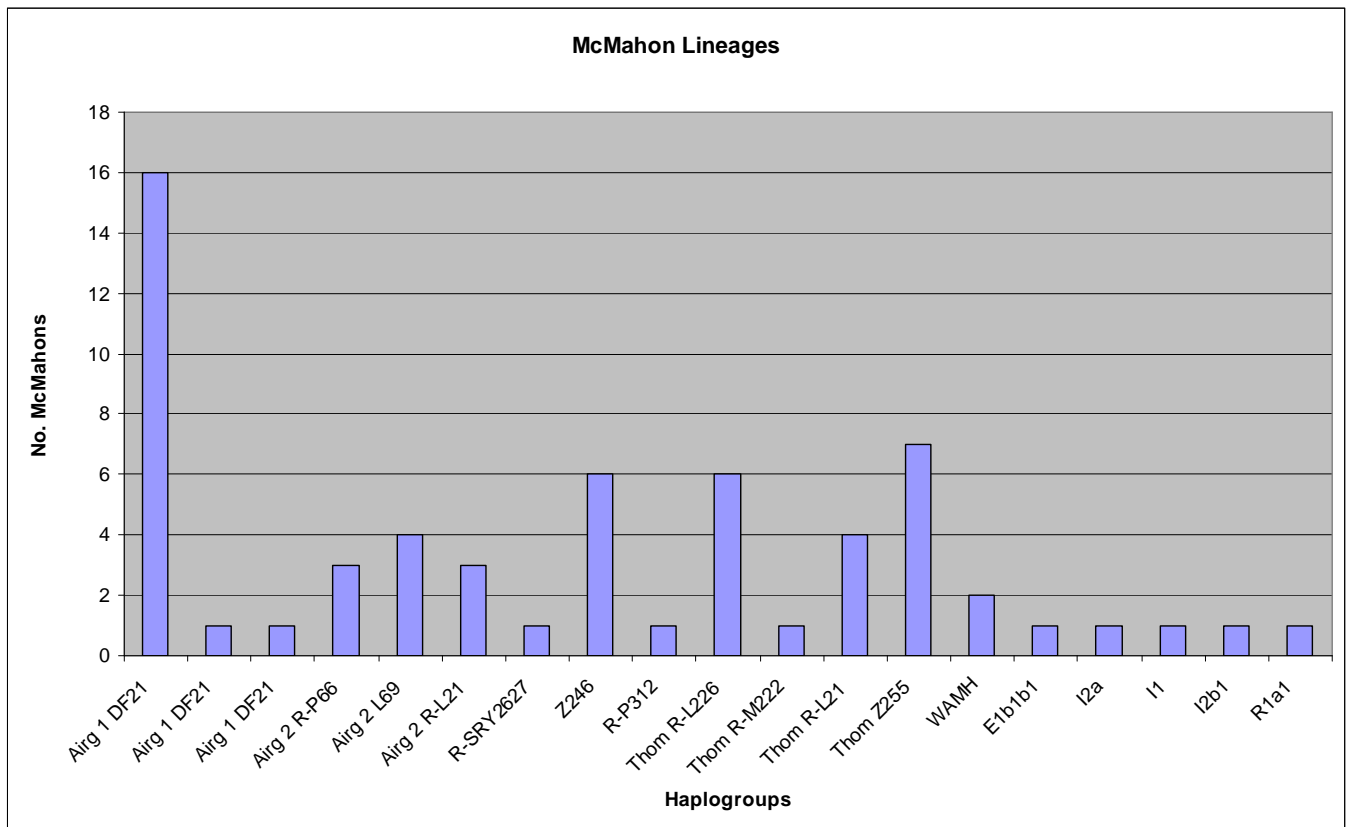
These results underpin the observations made in other studies that the McMahan surname arose in many different DNA backgrounds. This is obvious from the analysed Project data and supported by the PHYLIP results shown in Figure 5. The distinctions between the different lineages are summarised in Table 4 and shown graphically in Figure 6.

There is a general understanding that a population sample reflects to a certain degree, its ‘starting’ population status. If this holds true, then the Colla population was very successful in procreative terms, in amplifying its population size. Within the Colla population was the McMahan subset which paralleled this amplification as judged by the abundance of Colla McMahons among today’s McMahan testers. However, there were significant other sources of McMahan in the Northern McMahons, namely Airgialla 2, a branch of Airgialla 2 and a grouping of Mahan/Mahon.

The Southern McMahons are not dominated by any one dynastic group unlike the Northern McMahons. The two most numerous groups are the Dalcassians (from whom all Thomond McMahan are supposed to have been descended) and a group, one of whom has the Z255 SNP classifying him as having the ‘Irish Sea’ haplotype. Two further haplogroups are represented, R-M222 and a grouping of McMahan.

<i>Lineage</i>	<i>Population Group</i>	<i>Project Group</i>	<i>SNP</i>	<i>Haplogroup</i>	<i>No. of McMahons</i>	<i>No. of Non-McMahons</i>
1	Colla (Airgialla 1)	A1	L21, DF21, Monaghan Gp	R-L21	16	3
2	“	A2	L21, DF21, Singleton	R-L21	1	0
3	“	A2	L21, DF21, Singleton	R-L21	1	0
4	Airgialla 2	B1**	L21, L69, P66	R-P66	3*	0
5	“	B2	L21, L69	R-L21	4	2
6	“	B3	L21	R-L21	3	1
7	?	B4	SRY2627	R-SRY2627	1*	0
8	?	B5	DF21, Z246	R-L21	6*	0
9	?	B6	P312	R-P312	1	0
10	Thomond	C1	L21, L226	R-L226	6	1
11	“	C2	L21, M222	R-M222	1	1
12	“	C3	L21	R-L21	4*	0
13	“	C4	L21, Z255	R-L21	7	0
14	Western Atlantic	D1	M269	R-M269	2	1
15	Non-R1b1a2	F1	L336, M243, M35.1	E1b1b1	1	0
16	“	F2	P37.2	I2a	1	0
17	“	F2	M253	I1	1*	0
18	“	F2	P223	I2b1	1	0
19	“	F3	SRY10831.2	R1a1	1	0
<b>Totals</b>					<b>61</b>	<b>9</b>

**Table 4. Breakdown of Project/PHYLIP Results less 2 McKenna & 1 McDaniel. \* Mahon, Mahan, McKown, Mackin, McMeekin & McHugh were counted as McMahan. Non-R1b1a2 sources are included (Lineages 15-19). \*\* Inclusive of 2 non-project McCown.**



**Figure 6. Number of McMahaons descended from 19 Lineages.**

## Naming

How naming came about from AD 950 onward will always be debatable but what is clear from these results is that the groups who took what was presumably their chieftain's name<sup>15</sup> (in different parts of the country) were heterogeneous with respect to their DNA. There doesn't seem to be any other obvious explanation as to how such diverse lineages could finish up with the same surname. These L21 lineages had been evolving and migrating for about 3,000 years before naming so it is possible to see how they could have become mixed.

More difficult to explain are the four non-L21 (E and I) haplotypes who evolved away from the R haplotypes about 50,000 years ago (Figure 1). As they carry the McMahon (or a derivative) name, they were part of the genetic mix at the naming time (E1b1b1 is Southern Sept and R1a1 is Northern Sept). A creditable explanation (as outlined in the section on Diversity) is that E1b, I1, I2a, I2b haplotypes are descendants of much earlier Megalithic Culture/Bronze Age Bell-Beaker people, who pre-dated the R-L21 people and were subsumed by the later migrants. The R1a1 haplotype is thought to be of Norse origin.

<sup>15</sup> Many surnames were initially derived from 'son of' Mahon, Hugh, Ardle and other commonly used first names. This could account for the occurrence of the same surname in different septs.

## Discussion

This study reveals the complex nature of the DNA underlying the inheritance of the McMahon surname. Those from the Northern Sept dominate the Project by two to one and among them, the (defined) Colla McMahons (Airgialla 1) are shown to be the dominant dynastic group at 53% of Northern Sept McMahons (with the potential to reach to 63%). The next most numerous were Airgialla 2 at 28%. The size of the Airgialla 1 & 2 samples was dictated by the McMahon Project membership; there are in fact many more Airgialla 1 & 2 outside the Project.

The Colla McMahons (as represented in the Project) seem to evolve from the mid 11<sup>th</sup> c. with two separate unbranching lineages followed 400 years later by one or more lineages that became the 'Monaghan' cluster. This cluster expanded rapidly which is consistent with the evolution of parallel family lines and the McMahon genealogy of the period.

The earliest detected Colla (so far), 125Conley, branches at AD 250 supporting the view that Colla was in existence before the Ulster invasion by the 'Three Collas' in AD 330. It is not possible to say if this is close to the Colla origin but simply that this is where this particular lineage branched and then evolved to become Conley eventually. The fact that this lineage terminated in Conley and not a non-Irish name, presumably meant that the ancestor of the lineage travelled to Ulster with the Colla invading force. A similar argument can be applied to the branch points for the Colla McMahons.

Airgialla 2 has low representation in the Project which is why it was augmented by two McCown and two McGuire from outside the Project. The resulting tree shows divergence at 250 BC into a lineage which becomes Corcoran at AD 300 and a McMahon/Mahon cluster (B3) at AD 1470; the second branch from AD1400 evolves into McCown, McGuire and McMahon/McGuire clusters. This latter cluster probably represents what Livingston referred to as "McMahon of McGuire"

Among the Southern Septs, Clare 1 (at 30%) and Clare 2 (at 30%) are the most numerous. Clare 1 is assumed to be Dalcaisian although only one McMahon has the appropriate SNP classification; as a group, their branching is distant or very distant making it a very tenuous grouping. Clare 2 branches early giving rise to the McMahan (C3) grouping. As a member of Clare 2 has tested positive for Z255, indicating an 'Irish Sea' haplotype, could mean that this is a much more widespread grouping encompassing the Eastern seaboard and points westward in Ireland. The evidence does not support the perception that Thomond or Clare McMahons are descended from the O'Brien line.

The McGee Utility Tool was used to evaluate the data in the first instance and then generate tMRCA data in the correct format for use in the PHYLIP software. What the program in PHYLIP does is assume that somewhere in the past (however far back) there was a profile which could mutate into both candidates. What it doesn't know is the proportions of mutations in each branch and so it proposes splits (proportionately) which it refines by a process of averaging, substitution and taking into account nearest neighbours, over 99 iterations. The evolutionary trees produced have a common root and therefore every haplotype within the tested sample has got to be 'branched'. Where the branching occurs is dependent on the deduced ancestor distance and the sample size. It doesn't necessarily follow that a given common ancestor literally gave rise to a specific branch at that point but simply that this is the place in the tree where that branch could have arisen. It is highly probable that these lineages would have developed in parallel (with thousands of other lineages) over a much longer time frame.

A new approach was adopted to convert branch lengths into times in order to overcome the known deficiency of PHYLIP in overestimating recent common ancestors and underestimating distant ones. A power-law relationship was established between branch length and years before present (yBP), admittedly from very few datum points. By extrapolating from this relationship, it was possible to estimate yBP values and hence dates, for common ancestors. This appears to have worked well particularly for the more distant estimates.

The observed results that the McMahon name is found in such diverse genetic haplotypes as L69, L226, M222, Colla (DF21), I1,I2 and E1 can best be explained as follows. There was about 3,000 years from the

L21+ mutation to the adoption of surnames which allowed a huge amount of concurrent genetic diversity and population drift (generally in a NW direction from mainland Europe) in the L21 population before becoming 'locked down' in specific names and locations. Thus L69, M222, L226 and Colla people had become intermingled and some located in Oriel by the time the McMahan name was adopted. Others such as McGuire, McCown, McAuley probably located to other chieftain territories in Oriel before adopting the appropriate chief's name.

## Conclusions

The conclusions drawn from this study were:

- The McMahon Project membership was analysed using two different methodologies. Results obtained showed that the two methods were in support of each other, the PHYLIP method supporting the McGee clustering, producing finer detail and the order of branching.
- Clear separation was obtained between the Collas and non-Collas. The Colla McMahons were derived from at least three lineages that evolved from the mid 11<sup>th</sup> c.
- Collas were detected as early as the mid 3<sup>rd</sup> c. supporting the view that the Colla tribe was not indigenous to Ulster.
- Colla (Airgialla 1) is the largest dynastic group followed by Airgialla 2.
- Twice as many testers were from Northern Septs as opposed to Southern Septs.
- There is no corresponding dominant dynastic group (to the Collas) among the Southern McMahons. The majority fell into two groups, Clare1 and Clare 2. The former has two Dalcaisian members (but only one McMahon) while the latter has no known associations with the exception of one member being 'Irish Sea' haplotype.
- The DNA evidence does not support the historical contention that Collas are descended from the son of Eochaid Doimlen, younger son of Cairbre Lifechair, High King of Ireland in the 3<sup>rd</sup> century AD nor that Thomond McMahons are descended from the founder of the O'Brien Dynasty, Brian Boru.
- A method was developed to extrapolate PHYLIP branch lengths into dates thus providing approximate time estimates for common ancestors.
- The Project membership is divided into 67% defined and 33% unclassified. The defined members break down into Colla (31%), non-Colla (62%) and non-R1b1 (7%). The Collas can be further divided into 86% McMahon and 14% non-McMahon; the non-Collas into 79% McMahon and 21% non-McMahons.
- Four of the five non-R1b1 haplotypes were thought to descend from the much earlier Megalithic Culture/Bronze Age Bell-Beaker people. The fourth non-R1b1 haplotype has Norse DNA.
- The McMahon name is found in such diverse genetic haplotypes as L69, L226, M222, Colla (DF21), I1, I2 and E1.
- At least 19 lineages can account for the 68 defined Project members.



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[e](#)

# Appendix 1

ID	Genetic Distance																																									
	C	L	T	L	Z	3	1	B	2	1	1	9	1	4	N	1	1	5	1	6	2	1	N	1	3	6	2	1	1	3	6	1	1	2	1	N	N					
Colla Modal	6	2	2	2	4	4	4	2	1	9	4	9	6	9	8	7	8	6	4	9	2	8	6	3	9	4	1	4	8	1	3	6	1	4	2	4	2	6	2	0	0	
L69 Modal	9	2	2	4	8	5	7	0	7	4	3	2	0	3	7	8	6	2	8	3	9	3	5	8	4	7	1	6	4	2	5	4	2	4	3	8	2	0	0			
L222 Modal	2	1	6	6	M	M	M	M	M	M	M	M	B	W	M	C	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M			
Type II Modal	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
L226 Modal	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
Z246 Modal	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
348McMahon	5	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
145McMahon	4	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
B27McMahon	3	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
210McMahon	4	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
197McMahon	3	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
144McArdle	4	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
993McArdle	4	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
162Bogner	4	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
490Woods	4	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
N83McMahon	4	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
177McMahan	3	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
178Campbell	6	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
156McMahon	5	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
522Matthew	4	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
148McMahon	3	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
693McMahon	6	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
229McMahon	5	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
183McMahon	3	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
N65McMahon	4	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
138McMahon	8	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
394McMahon	7	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
647McKenna	6	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
211McKenna	9	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
146McDanie	7	2	3	1	8	1	3	4	5	6	6	6	6	7	6	5	8	7	6	5	8	7	6	6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
184McKown	2	5	1	7	2	2	1	4	2	7	2	7	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6
312McCown	2	5	1	7	2	2	1	4	2	7	2	7	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6
605McCown	2	5	1	7	2	2	1	4	2	7	2	7	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6
124McMahon	2	5	1	7	2	2	1	4	2	7	2	7	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6	2	6
142McMahon	2	1	1	8	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
143Maguire	2	3	1	7	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
228Bruen	2	3	1	7	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
162McMahon	2	4	1	6	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
N20Maguire	2	5	1	7	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
N30Maguire	2	4	1	6	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
Related		Probably Related										Possibly Related																														
- Hybrid mutation model is used																																										

Genetic Distance																																						
ID	C	L	L	T	L	Z	1	1	1	N	7	2	1	N	2	2	2	2	8	1	1	1	1	1	1	2	N	2	1	1	2	6	*	*	*	*	*	
	o	6	2	y	2	2	5	4	9	1	1	5	4	1	2	2	2	9	1	9	1	0	8	1	0	1	1	5	8	0	1	7	7	1	3	1	1	2
	l	9	2	p	2	4	0	1	4	1	8	8	6	9	9	8	9	8	3	0	0	4	5	3	2	0	5	3	5	7	7	2	8	7	5	3	1	
	a	M	M	I	M	M	a	c	c	o	a	c	a	a	c	u	c	c	c	c	c	c	c	c	c	c	c	c	c	a	a	8	M	C	M	M		
	M	o	M	M	M	h	M	M	r	h	M	h	h	a	h	a	h	e	e	a	h	h	h	h	h	h	h	h	h	o	k	L	C	M	M			
	o	d	I	M	M	o	a	a	o	o	a	a	a	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	n	i	e	G	C	M	M			
	d	a	M	a	a	n	o	o	r	a	n	n	n	o	o	o	o	o	o	o	o	o	o	o	o	o	o	n	n	r	e	u	o	n	G	G		
	a	l	a	a	a	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	
Colla Modal	-	21	20	14	15	10	21	21	22	22	14	13	13	14	25	24	21	22	21	23	18	21	16	18	19	21	18	20	18	20	19	29	9	13	7	7		
L69 Modal	21	-	17	21	19	14	18	19	20	20	19	21	21	22	27	21	17	25	24	26	22	25	22	22	21	23	24	24	23	27	20	28	24	23	23	23		
L222 Modal	20	17	-	21	19	14	18	18	17	26	15	20	19	21	26	6	6	20	17	19	22	25	21	20	22	26	23	28	18	29	23	25	23	21	23	23		
Type II Modal	14	21	21	-	9	8	18	18	19	21	12	15	14	16	18	26	22	22	19	21	9	9	18	17	17	20	17	22	16	23	19	26	22	17	21	21		
L226 Modal	15	19	19	9	-	6	16	16	17	19	11	14	13	15	16	24	19	19	16	18	4	13	9	15	15	18	15	20	14	20	17	24	22	16	22	22		
Z246 Modal	10	14	14	8	6	-	14	14	15	15	8	11	10	12	16	19	14	16	13	15	10	11	11	12	15	12	17	10	16	13	24	16	12	17	17			
150Mahon	21	18	18	18	16	14	-	6	5	15	18	20	20	21	21	23	19	23	21	23	18	23	22	17	13	17	18	19	21	26	22	22	26	21	25	25		
141McMahon	21	19	18	18	16	14	6	-	1	15	18	18	18	19	21	23	17	23	21	23	18	23	21	17	17	19	18	21	21	26	20	26	26	20	25	25		
194McMahon	22	20	17	19	17	15	5	1	-	16	17	19	19	20	20	22	18	24	22	24	19	24	22	18	16	20	19	22	20	27	21	25	27	21	26	26		
N11Corcora	22	20	26	21	19	15	15	15	16	-	22	24	24	25	25	31	25	27	25	27	21	24	22	23	21	23	22	24	25	23	23	33	28	23	27	27		
718Mahon	14	19	15	12	11	8	18	18	17	22	-	14	13	15	18	20	20	24	21	23	15	17	18	20	18	23	20	25	16	23	21	30	21	16	21	21		
258McMahan	13	21	20	15	14	11	20	18	19	24	14	-	1	1	21	24	20	20	17	19	17	20	18	16	19	19	18	22	18	22	16	28	21	16	19	19		
146Mahan	13	21	19	14	13	10	20	18	19	24	13	1	-	2	21	23	19	20	16	18	17	19	17	15	18	19	18	22	17	21	16	28	20	15	19	19		
N19Mahan	14	22	21	16	15	12	21	19	20	25	15	1	2	-	22	23	21	19	18	18	18	21	19	15	20	20	19	23	17	23	17	27	20	17	18	18		
229Mcmahon	25	27	26	18	16	16	21	21	20	25	18	21	21	22	-	29	28	25	23	25	17	21	21	22	22	22	19	26	17	21	22	30	31	22	31	31		
228Mullin	24	21	6	26	24	19	23	23	22	31	20	24	23	23	29	-	10	21	21	21	28	30	26	20	25	30	27	31	22	34	27	26	25	26	26	26		
229McMahon	21	17	6	22	19	14	19	17	18	25	20	20	19	21	28	10	-	20	17	19	22	25	21	20	22	24	23	26	20	27	23	27	24	22	24	24		
898McMahan	22	25	20	22	19	16	23	23	24	27	24	20	20	19	25	21	20	-	5	3	20	25	23	17	20	21	20	22	18	32	23	30	26	23	25	25		
113McMeeki	21	24	17	19	16	13	21	21	22	25	21	17	16	18	23	21	17	5	-	2	18	22	20	17	17	19	18	21	17	27	20	31	26	20	26	26		
190McMahan	23	26	19	21	18	15	23	23	24	27	23	19	18	18	25	21	19	3	2	-	20	24	22	17	19	21	20	23	17	29	22	31	26	22	26	26		
110McMahon	18	22	22	9	4	10	18	18	19	21	15	17	17	18	17	28	22	20	18	20	-	13	12	19	19	20	17	22	15	24	20	23	26	20	24	24		
204McMahon	21	25	25	9	13	11	23	23	24	24	17	20	19	21	21	30	25	25	22	24	13	-	20	19	21	22	19	24	19	25	22	29	27	21	28	28		
185McMahan	16	22	21	18	9	11	22	21	22	22	18	18	17	19	21	26	21	23	20	22	12	20	-	17	21	22	19	22	16	19	19	27	22	15	22	22		
113McMahon	18	22	20	17	15	12	17	17	18	23	20	16	15	15	22	20	20	17	17	17	19	19	17	-	11	10	7	11	17	26	18	23	20	16	20	20		
202McMahon	19	21	22	17	15	12	13	17	16	21	18	19	18	20	22	25	22	20	17	19	19	21	21	11	-	5	9	8	19	24	23	22	25	22	25	25		
N10McMahon	21	23	26	20	18	15	17	19	20	23	23	19	19	20	22	30	24	21	19	21	20	22	22	10	5	-	6	5	23	23	25	25	28	21	26	26		
215McMahon	18	24	23	17	15	12	18	18	19	22	20	18	18	19	19	27	23	20	18	20	17	19	19	7	9	6	-	8	20	24	22	24	25	18	23	23		
153McMahon	20	24	28	22	20	17	19	21	22	24	25	22	22	23	26	31	26	22	21	23	22	24	22	11	8	5	8	-	25	23	26	24	27	23	25	25		
185McMeans	18	23	18	16	14	10	21	21	20	25	16	18	17	17	17	22	20	18	17	17	15	19	16	17	19	23	20	25	-	24	17	24	21	19	21	21		
207Mahon	20	27	29	23	20	16	26	26	27	23	23	22	21	23	21	34	27	32	27	29	24	25	19	26	24	23	24	23	24	-	23	34	27	22	27	27		
617Mackin	19	20	23	19	17	13	22	20	21	23	21	16	16	17	22	27	23	23	20	22	20	22	19	18	23	25	22	26	17	23	-	29	24	23	24	24		
**128Lee	29	28	25	26	24	24	22	26	25	33	30	28	28	27	30	26	27	30	31	31	23	29	27	23	22	25	24	24	24	34	29	-	31	34	30	30		
*337McGuire	9	24	23	22	22	16	26	26	27	28	21	21	20	20	31	25	24	26	26	26	26	27	22	20	25	28	25	27	21	27	24	31	-	20	3	3		
*125Conley	13	23	21	17	16	12	21	20	21	23	16	16	15	17	22	26	22	23	20	22	20	21	15	16	22	21	18	23	19	22	23	34	20	-	19	19		
*183McGuire	7	23	23	21	22	17	25	25	26	27	21	19	19	18	31	26	24	25	26	26	24	28	22	20	25	26	23	25	21	27	24	30	3	19	-	0		
*231McGuire	7	23	23	21	22	17	25	25	26	27	21	19	19	18	31	26	24	25	26	26	24	28	22	20	25	26	23	25	21	27	24	30	3	19	0	-		

Related      Probably Related      Possibly Related

- Hybrid mutation model is used

## Appendix 2

### Scaling

A new approach in estimating dates was adopted using the following rationale. McGee can only count the number of mutational steps between two divergent profiles. What it can't do is estimate the number of reversions that could have occurred during this time span. In fact if a marker mutated and later reverted back, this would be 'invisible' to McGee (a GD net sum = 0). Effectively, this would be a loss of a GD of 2 or 200-300 years in the time span. The solution proposed was to extrapolate yBP values proportional to the generated branch lengths. This might be a means to compensate for 'lost' time in estimating early branching.

### Calibration

Often biological processes such as population growth can be represented exponentially. In order to establish the validity of such an approach, it was necessary to plot datum points to establish if such a relationship exists. The datum points used were:

Shortest branch length of 30 equates to smallest time interval of one generation i.e. 30 yBP.

McGuire 1 pedigree (represented by 337McGuire) branch length of 150 equates to 225 yBP

Most distant L21 branch (128Lee) of 1291 (as given in Figure 5) equates to 4,135 yBP<sup>16</sup>.

The trendline in Figure A2.1 shows a linear relationship supporting the view that there is a valid relationship between branch length and 'years before present' (yBP). Projecting the line intersects the Y-axis at 2.4. A trendline is most reliable when its R-squared value (coefficient of determination) is at or near 1 which is the case for these datum points. This in effect is modelling the evolutionary tree as a 'Random Walk'<sup>17</sup>, where the spread from the origin is proportional to a power of the number of steps. The best estimate of the parameters is made from the three data points.

Despite the good statistical fit, care must be exercised in using these extrapolated values as they are based on only three datum points<sup>18</sup>. However, logic dictates that all dates in the L21 population must fall between the shortest detected interval (one generation) and the earliest possible date for the occurrence of the L21 mutation, currently set at 4135 yBP. It would therefore seem rational to use this relationship to estimate yBP values from PHYLIP generated branch lengths. Obviously, adjustments would need to be made should there be a revised estimate for the L21 mutation date or should an even earlier (than 128Lee) L21 branch be discovered.

### Random Walk Evolution

This can be visualised as a start genotype of DYS markers mutating over time, each mutation establishing an evolutionary branch. The mutation rates of individual markers will dictate which mutate most frequently and which infrequently or hardly at all. These events will in general be independent, although there are a few exceptions, and will be in forward and, in some cases, reverse directions. Evolutionary branches acquiring rare (stable) mutations will be defining for that lineage and those, such as Colla, having an exceptionally stable combination (the null, which is irreversible, accompanied by two markers having stable values) will pass all the way down the tree unaltered. Branches will evolve in parallel, some showing more relatedness to each other (low GD) and some less relatedness (high GD), as dictated by the stochastic

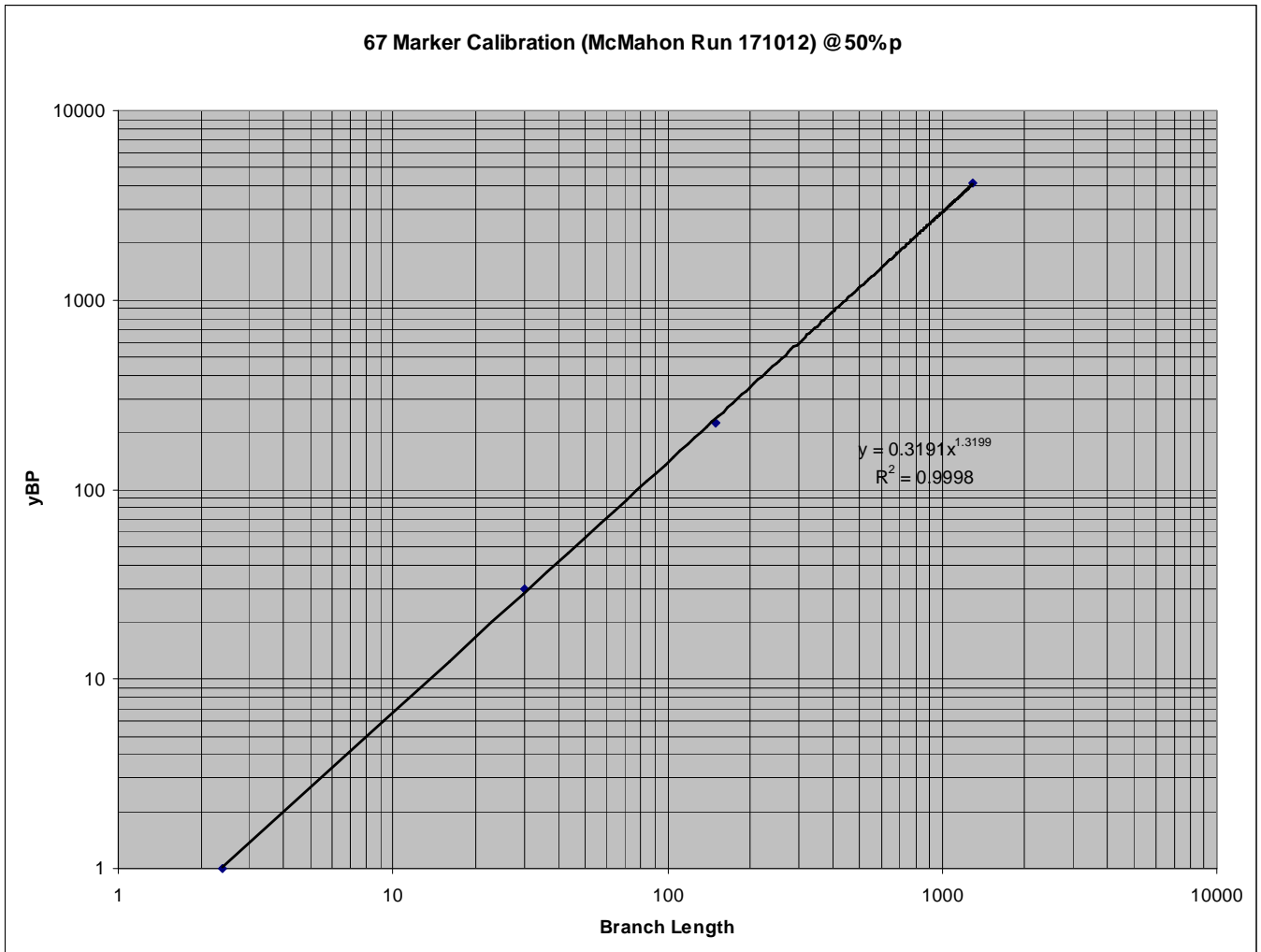
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<sup>16</sup> It was established by other workers that the L21 mutation occurred 4,135 years ago.

<sup>17</sup> The stochastic process formed by successive summation of independent, identically distributed random variables. Evolution (of these non selective DYS mutations) is a process that follows a random path, mutating forward and sometimes reverting, without any influence from past events.

<sup>18</sup> It is improbable that further data points will be discovered, especially for the mid region.

process. This evolution will be independent of geography and name and can explain why some lineages show close relationship even though they evolved in different locations and had acquired different surnames.



*Figure A2.1. Log-Log plot of the tree datum points and intersect.*

## Appendix 3

### Glossary

<b>Allele</b>	An allele is an alternative form of a gene (one member of a pair) that is located at a specific position on a specific <a href="#">chromosome</a> .
<b>Britain</b>	For the purposes of this analysis, Britain refers to mainland Britain comprising England, Scotland and Wales. The British Isles comprise mainland Britain and Ireland.
<b>Celts</b>	A sub group of the Indo-European people, originally of central Europe and spreading to Western Europe, the British Isles, and southeast to Galatia during pre-Roman times, especially to Britain and Gaul.
<b>Clades</b>	The clade is a hypothetical construct based on experimental data. Clades are found using multiple (sometimes hundreds) of traits from a number of species (or specimens) and analysing them statistically to find the most likely phylogenetic tree for the group.
<b>Clan Colla</b>	As described in various Annals ..... In the beginning of the 4th century, three warlike princes, called the <a href="#">Three Collas</a> , sons of Eochy Doimhleoin, son of <a href="#">Cairbre Lifeachar</a> , legendary High King of Ireland, of the race of <a href="#">Eremon</a> , made a conquest of a great part of Ulster, which they wrested from the old possessors, princes of the race of Ir, called the Clanna Rory, or Rudericians. The names of the three chiefs were <a href="#">Colla Uais</a> , or Colla the noble, <a href="#">Colla Meann</a> , or Colla the famous, and <a href="#">Colla da Chroich</a> , or Colla of the two territories. <a href="#">Colla Uais</a> became monarch of Ireland 327, and died in 332. The territory conquered by the three Collas comprised the present counties of <a href="#">Louth</a> , <a href="#">Monaghan</a> , and <a href="#">Armagh</a> .
<b>Colla Definition</b>	A sub-clade of R-L21 defined by a null value for DYS 425 together with a value of 9 for DYS 511 (except MacDougall). Where testing has been extended to 111 markers, a value of 9 for DYS 505 in addition, is definitive.
<b>Cluster</b>	A group of testers whose DYS markers are sufficiently similar to indicate significant relationship to each other.
<b>Dal Riada</b>	<b>Dál Riata</b> (also <b>Dalriada</b> or <b>Dalriata</b> ) was a <a href="#">Gaelic</a> over-kingdom on the western coast of <a href="#">Scotland</a> with some territory on the northeast coast of <a href="#">Ireland</a> . In the late 6th and early 7th century it encompassed roughly what is now <a href="#">Argyll and Bute</a> and <a href="#">Lochaber</a> in Scotland and also <a href="#">County Antrim</a> in Ireland.
<b>DNA</b>	Deoxyribonucleic acid is a <a href="#">nucleic acid</a> containing the <a href="#">genetic</a> instructions used in the development and functioning of all known living <a href="#">organisms</a> (with the exception of <a href="#">RNA viruses</a> ).
<b>DURRQ</b>	The ID of the Colla modal. This is a 67 marker profile consisting of the most usual marker values for the 67 markers derived from a large group of Colla testers.
<b>DYS</b>	<b>DYS</b> is jargon and thought to be short for <b>DNA-Y</b> chromosome <b>STR</b> .
<b>DYS 425</b>	A specific marker whose value is the main determinant in distinguishing Colla from non-Colla DNA.
<b>Evolutionary Tree</b>	An evolutionary tree or phylogenetic tree is a branching diagram showing the inferred evolutionary relationships among various biological species or other entities based upon similarities and differences in their physical and/or genetic characteristics. The taxa joined together in the tree are implied to have descended from a common ancestor. In a rooted phylogenetic tree, each node with descendants represents the inferred most

recent common ancestor of the descendants, and the edge lengths in some trees may be interpreted as time estimates.

<b>Excel</b>	Microsoft Excel spreadsheet.
<b>FTDNA</b>	Family Tree DNA – the testing company used by most testers.
<b>GD</b>	<b>Genetic distance</b> is a measurement of the total difference in allele values of different genetic markers between two individuals.
<b>Haplogroup</b>	In <a href="#">molecular evolution</a> , a <b>haplogroup</b> is a group of similar <a href="#">haplotypes</a> that share a <a href="#">common ancestor</a> having the same <a href="#">single nucleotide polymorphism</a> (SNP) mutation in both haplotypes.
<b>Haplotype</b>	A <b>haplotype</b> in <a href="#">genetics</a> is a combination of <a href="#">alleles</a> (DNA sequences) at adjacent locations ( <a href="#">loci</a> ) on the <a href="#">chromosome</a> that are transmitted together.
<b>Kitsch Program</b>	The Kitsch program of PHYLIP was used to calculate phylogram tree files.
<b>ID</b>	The numerical or alphanumeric identity assigned by the testing company to a DNA sample.
<b>Lineage</b>	Lineage (anthropology) or <a href="#">kinship</a> , descent group that can demonstrate their common descent from an apical ancestor or a direct line of descent from an ancestor.
<b>Marker</b>	A <b>genetic marker</b> is a gene or <a href="#">DNA sequence</a> with a known location on a <a href="#">chromosome</a> that can be used to identify individuals or <a href="#">species</a> . It can be described as a variation (which may arise due to mutation or alteration in the genomic loci) that can be observed. A genetic marker may be a short DNA sequence, such as a sequence surrounding a single base-pair change ( <a href="#">single nucleotide polymorphism</a> , SNP), or a long one, like <a href="#">minisatellites</a> .
<b>McGee Utility</b>	Y-DNA Comparison Utility.
<b>Modal</b>	The mode is the number which appears most often in a dataset.
<b>Mutation</b>	A Mutation occurs when a DNA gene is damaged or changed in such a way as to alter the genetic message carried by that gene.
<b>Null mutation</b>	A null allele is a mutant <a href="#">copy of a gene</a> that completely lacks that gene's normal function. At the <a href="#">phenotypic</a> level, a null allele is indistinguishable from a deletion of the entire <a href="#">locus</a> .
<b>Oriel</b>	Oriel territory takes in the modern Counties Monaghan, Armagh and part of Louth.
<b>PHYLIP</b>	Phylogeny Inference Package.
<b>Phylogenetic tree</b>	See <b>Evolutionary Tree</b> .
<b>Phylogram</b>	A phylogram is a phylogenetic tree that has branch lengths proportional to the amount of character change.
<b>Profile</b>	The values (number of repeats) for STR markers for a given individual (67 markers in the current study).
<b>R-L21+</b>	Shorthand for haplogroup R1b1a2a1a1b4; the '4' indicates the fourth SNP downstream from P312 (in FTDNA nomenclature). This is a major European Clade thought to have occurred north of the Alps about 4,135 yBP.
<b>R-DF21+</b>	R-DF21 is a subclade under R-L21--two different SNPs. R-DF21 is comparatively quite old, with a tMRCA of 3112 yBP versus 4135 yBP for all of R-L21.
<b>Sept</b>	A division of a family, especially a division of a clan.

<b>Singleton</b>	A profile without any close matching to other profiles.
<b>SNP</b>	<a href="#">Single Nucleotide Polymorphism</a> , (SNP) is a single base-pair change.
<b>STR</b>	A <b>Y-STR</b> is a <a href="#">short tandem repeat</a> (STR) on the <a href="#">Y-chromosome</a> . Y-STRs are often used in <a href="#">forensics</a> , paternity, and <a href="#">genealogical DNA testing</a> .
<b>Taxon</b>	A taxonomic category or group, such as a phylum, order, family, genus, or species. Animal or plant group having natural relations.
<b>Testers</b>	Those who have had their DNA analysed for Y-chromosome markers.
<b>Thomond</b>	The region of Ireland associated with the name Thomond is County Clare, County Limerick and north County Tipperary; effectively most of north Munster.
<b>tMRCA</b>	<b>T</b> ime to <b>M</b> ost <b>R</b> ecent <b>C</b> ommon <b>A</b> ncesor.
<b>Y-DNA</b>	Y-DNA is passed solely along the <a href="#">patrilineal</a> line, from father to son. It does not recombine and thus Y-DNA changes only by chance mutation at each generation with no intermixture between parents' genetic material.
<b>yBP</b>	<b>Y</b> ears <b>B</b> efore <b>P</b> resent with the present being taken as AD 1950.