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Ó Maol Phádraig: the name, the people, and the clans. Part I.

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Abstract

Once upon a time, the Ó Maol Phádraig (O'Mulpatrick) was a notable clan; or, better – there were once notable clans of that name. Earlier, there were noteworthy individuals named Máel Pátraic, which is the earliest version of any name given to honour St Patrick. Among such notables were those whose given name came to transcend the individual – so, Máel Pátraic became attached to a patronym.

Our series of articles explores the name Máel Pátraic. In Part I, we discuss the origins of the name and consider the patterns apparent in early annalistic records. Connections are made to those regions of Éire where the name was commonly found. In Part II, we review authoritative Máel Pátraic genealogies, the dynasties whose members bore the name, and the emergence the Ó Maol Phádraig surname. In Part III, and we consider records that occur from the late medieval era until the nineteenth century. Finally, in Part IV, we link the living with those Ó Maol Phádraig gone before via the power of genetic genealogy.

Ó Maol Phádraig is a virtually extinct surname; today their descendants carry Fitzpatrick or other Pátraic-surname forms. Here, the name, the people, and the clans are revived.

Names, styles, edits, and historical records

This article is written in the English language, but the people and places discussed are Irish. To acknowledge the primacy of Gaeilge (Gaelic) and to allow readers to be able to find locations on modern maps, place names are provided in modern Gaeilge using the most common spelling; for example, Ard Mhacha (Armagh), unless the place name is titular, for instance, the Abbot of Ardstraw.

The rendition of personal names and by-names of people referenced in this article requires consistency because there can be variability in historical records even for the same individual, with mixtures of Gaeilge and English forms being used and sometimes with spellings imaginatively conjured up via phonetics. The approach here is to use the most obvious and correctly spelt form of the personal name, be it Gaeilge or an English form. Surnames are much less problematic, and preference is for a standard spelling, e.g., as determined and published by authorities such as Woulfe (1923)[1] and Mac Lysaght (1985)[2].

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[1] Woulfe, P. (1923). Sloinnte Gaedheal Is Gall: Irish Names and Surnames. Dublin: M. H. Gill & Son.
[2] MacLysaght, E. (1985). Irish Families: their names, arms and origins. Dublin: Irish Academic Press.

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Quotations are italicised. This article is a living work, i.e., it can, and most likely will, be edited by the authors who will retain all versions. Every effort has been made to consult all available records related to the period relevant to this article.

Introduction

Ó Maol Phádraig says Woulfe (1923), i.e., descendant of a '*servant of St Patrick*' was '*once a common surname, especially in Cavan and Cork; and while the name has disappeared, the family was too numerous to have died out*'. Woulfe's assessment provides the framework for the series, '*Ó Maol Phádraig: the name, the people, and the clans*'. When did the name arise; who were the Ó Maol Phádraig of historical note; who were the clans of Cabhán (County Cavan), and Corcaigh (County Cork); and, who and where are they today?

Woulfe also made specific mention of '*Conor O Molpatrick, chief of his name*' in 1602; what of he and his descendants? And concerning the loss of their ancient name, if the Ó Maol Phádraig '*anglicised it to Fitzpatrick*', as Woulfe asserts, for some reason by their own volition, did not die out, can they be found among Fitzpatricks today?

We demonstrate that the large-scale disappearance of Ó Maol Phádraig was later than 1602, and that is unlikely the death of the surname came by the hands of those so named. And we prove true that, as Woulfe stated, the Ó Maol Phádraig, were too numerous to have died out. Yes, their name was very largely anglicised to Fitzpatrick, but Ó Maol Phádraig descendants live and breathe today.

The origins of Máel Pátraic

It is said that Pátraic was not found in Ireland as a distinct given name until the arrival of Anglo-Normans[1]; in reverence to the saint, mere Irish considered Pátraic (Patrick) too sacred to use directly[3]. The early forms appear limited to Máel Pátraic and Gilla Pátraic (i.e., servant of and follower of, respectively, Patrick), and '*when used by the Anglo-Normans it was rendered Pádraigín by the Irish*'[1].

While Máel-type names occur in annalistic records from 611 AD, a Gilla-type name does not appear until 977 AD. Hence, it should not surprise that Annals record Máel Pátraic as a given name in 847 AD, some 136 years before Gilla Pátraic appears, in 983 AD[4]. Although the historicity of St Patrick is complicated by the fact there were '*two or possibly three Patricks*' it is clear he was revered from the mid seventh century, notably among, first, the Oirghialla and, then, the Uí Néill via their alliances. By the ninth century '*Patrick truly became Ireland's pre-eminent saint*', hence Pátraic-type names, surely, would have been expected during that era. Pátraic-type names may also have undergone a revival in the Viking era when Patrician relics began to 'come into the fore'[5].

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[3] Withycombe, E. (1978). The Oxford Dictionary of Christian Names. Oxford: Oxford University Press.

[4] Hennessy, W. (1887). Annals of Ulster: otherwise Annals of Senat; a chronicle of Irish affairs. Dublin: HMSO.

[5] Erskine, S. (2012). The relic cult of St Patrick between the seventh and the late twelfth centuries in its European contexts [thesis], University of Glasgow (Scotland). School of Humanities: pp 226.

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The use of Máel, meaning crop-headed or shorn'[6], followed by a proper name '*received its chief development after the introduction of Christianity*' to Ireland; the general form being Máel-Dei[7], i.e., it was followed by a Saint's name, indicating tonsure. Máel-type names were common throughout the seventh and eight centuries before declining from the late tenth century as Gilla-type names emerged[8]; yet, Gilla was not Norse in origin, as some have proposed[9].

The rise of Gilla-type names was due to '*a model change in Irish nomenclature*'[6], and there was a pattern of different geographic distribution of Máel Pátraic versus Gilla Pátraic. A simple survey to estimate the relative frequency of the forms used in early times can be undertaken via annalistic records, or genealogical works, and Gilla Pátraic is approximately three times more common than Máel Pátraic. Also notable is that while Giolla Phádraig is found among many clans, such as those summarised by Ó Muraíle[10], across all of Éire – a pattern matching the modern distribution of Fitzpatrick[11] – Máel Pátraic is found among few, and mostly among clans of the northern half of Éire; this is explored fully in Part II.

Annalistic use of Máel Pátraic

The basis for understanding the first uses of the name Máel Pátraic comes from various Annals of Ireland, which only record it as a given-name – never as a surname. Almost always the bearer of the name is either a religious figure or closely related to one, the first record being from 847 AD; '*Cellach son of Máel Pátraic, prior of Fera-Rois south of the river, died*'[3]. In the Annals of the Four Masters Donovan annotates, '*the Feara Rois were seated along the Boyne and at Carrickmacross, in the county of Monaghan*'[12]. Yet, Mac Iomhair's account of the history of Fir Rois, also known as Crích Rois, lays out a greater expanse of lands – most of central Lú (Louth) and extending into southern Muineachán (Monaghan) and northern Mhí (Meath); Cellach's monastery, he concludes, was in Cluain Caoin (Clonkeen), which lies south of the River Glyde[13].

This example makes it evident that, when synthesising occurrences of Máel Pátraic in the Annals and Genealogies, it is helpful to correlate the name use with population groups and geographic locations; and, as will be seen, a pattern emerges. Table 1 presents annalistic references to Máel Pátraic as a given name in isolation, which occur until 1096 AD, and Table 2 presents annalistic references to Máel Pátraic as a given name in conjunction with a surname, which do not appear until 1016 AD. The tables are annotated and run across several pages. Note, the surname Ó Máol Pádriac does not occur in Annalstic records.

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[6] Electronic Dictionary of the Irish Language. https://dil.ie: accessed 7 March 2023.

[7] Marstander, C. (1918). Altirisch Gillae. Zeitschrift für Celtische Philologie, 12, 309-322.

[8] Ó Máille, T. (1910). The language of the Annals of Ulster. Manchester: University Press.

[9] Gilla-words 'appeared in Irish literature as early as the first half of the ninth century' being derived from gildae, with probable old French or Latin roots meaning soldier, hireling (armed with a lance), recruit, etc. (Marstander, 1918). Also, Pokorny, J., (1918). Vermischtes. Zeitschrift für Celtische Philologie, 12, 298-308.

[10] Mac Fhirbhisigh, D. and Ó Muraíle, N. (2003). Leabhar mór na ngenealach. Dublin: De Burca.

[11] Fitzpatrick, E. and Fitzpatrick, M. (2020). When Everything Changes: Using Critical Family History to Deconstruct Keesing and Fitzpatrick Surnames. Genealogy, 4, 25. https://doi.org/10.3390/genealogy4010025.

[12] O'Donovan, J. (1856). Annals of the Four Masters: Annals of the Kingdom of Ireland, by the Four Masters, from the earliest period to the year 1616. Dublin, Hodges, Smith, and Co.

[13] Mac Iomhair, D. (1964). The History of Fir Rois. County Louth Archaeological Society Journal, 15, 321-348.

Table 1: Annalistic references to Máel Pátraic[14]

Reference[15]	**Date, AD**[16]	**Location**
Cellach son of Máel Pátraic, prior of Fera-Rois south of the river, died.[AU]	847	Cluain Caoin, Lú[17]
Máel Pátraic, son of Finnchu, bishop, scribe, and anchorite, and intended abbot of Ard Mhacha, died.[AFM,18]	861 (863)	Ard Mhacha, Ard Mhacha[19]
Máel Pátraic son of Cellach, abbot of Mainistir Bhuithe, died suddenly.[AU]	878	Mainistir Bhuithe, Lú[20]
Máel Pátraic son of Mael Curarda, King of the Airghialla, was killed by his associates.[AU,21]	885	Oirialla[22]
Máel Pátraic, Abbot of Cluain Mhic Nóis, of the race of the Ui-Maine … died.[AFM,23]	883 (886)	Cluain Mhic Nóis, Uíbh Fhallí[24]

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[14] Máel Pátraic is used as a standard spelling throughout.

[15] AU, Annals of Ulster; AFM, Annals of the Four Masters; AI, Annals of Inisfallen (translated by Seán Mac Airt (2008). CELT: Corpus of Electronic Texts: a project of University College Cork, College Road, Cork, Ireland. http://www.ucc.ie/celt, accessed 1 February 2023). Only the most informative among parallel records is cited.

[16] '*The chronology of the Annals of Ulster is accurate from AD 773 to AD 1023*'; dates for entries from other Annals are shown corrected, if required, in parentheses using Annals of Ulster dates (McCarthy, D., 1998. The Chronology of the Irish Annals. Proceedings of the Royal Irish Academy: Archaeology, Culture, History, Literature , 98C, 203-255).

[17] Clonkeen, County Louth.

[18] Máel Pátraic, son of Finnchu, is the first of several recorded notables of the church of Ard Mhacha who bore a name associated with the founder, St Patrick. The origin of the church is said to be in 444 AD, and was episcopal; yet, from 758 AD to 1136 AD the heir of St Patrick (Comarbai Pátraic) '*was always an abbot and the office of bishop … was subordinate*' (Moody T., Martin F., & Byrne F., 1989. A New History of Ireland. Oxford: Oxford University Press).

[19] Armagh, County Armagh.

[20] Monasterboice (i.e., the Monastery of St Buíte), County Louth.

[21] Mael Curarda (d. 853) was King of Uí Mheic Uais (i.e., among the descendants of Colla Uais, a mythical High King of Ireland; Byrne F., 1973. Irish kings and high-kings. London: BT Batsford Ltd). Two other notable sons of Mael Curarda were Mael Ruanaidh (d.871), King of Uí Mheic Uais, and Oenghus (d.881), Abbot of Ard Sratha, Tír Eoghain (Ardstraw, County Tyrone)[U]. Walsh posited the pedigree of the Uí Fhiachrach of Ard Sratha '*belonged to the ruling dynasty*' of Uí Mheic Uais of Oirialla during the ninth century (Walsh, P., 1923. Uí Maccu Uais. Ériu, 9, 55-60). The slaying of Máel Pátraic '*by his associates*' may refer to the Cenél nEógain, whose eastward expansion led them to hold the Airghialla as vassals from ca. 827 AD (Duffy S., 2005. Medieval Ireland an Encyclopaedia. New York and London: Routledge).

[22] Oriel, a medieval kingdom approximating the area of the modern dioceses of Armagh and Clogher.

[23] Graves' (1855) accounts of ancient monuments at Cluain Mhic Nóis includes '*a Latin cross, the arms combined by a circle at centre, the extremities slightly widened*' engraved with the words '*A prayer for Mael Patric*'; this, states Graves, refers to the abbot in the Annals who died in 883 AD; he was of Ui-Maine, which at the time the Annals entry was written referred to Connacht (Graves, J., 1855. A list of the ancient Irish monumental stones at present existing at Clonmacnoise. Proceedings and Transactions of the Kilkenny and South-East of Ireland Archaeological Society , 3, 293-303).

[24] Clonmacnoise, County Offaly.

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Table 1: continued

Reference	Date, AD	Location
Máel Pátraic, scribe and excellent scholar, superior of Treoid and steward of the community of Patrick for the district south of the mountain, rested.[U,25]	888	Treoid, Mhi[26]
Máel Pátraic son of Niall, superior of Shláine, fell asleep happily.[U,27]	890	Shláine, Mhi[28]
Máel Pátraic, son of Flathrai, lord of Ráth Tamhnaighe died.[AFM,29]	909 (911)	Ráth Domhnaigh, Laois[30]
Aed son of Máel Pátraic, king of Uí Fhiachrach, was killed by Niall, son of Aed.[U,31]	910	Ard Sratha, Tír Eoghain
The plundering of Leithghlin by the foreigners, where Máel Pátraic, a priest and anchorite, and Mongan, anchorite, and many others along with them, were slain.[AFM,32]	916 (917)	Leithghlin, Ceatherlach[33]

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[25] '*On the foundation of the monastery St Patrick placed an abbot in charge*' (Kelly, M., 1941. Three Monasteries of Drogheda. Journal of the County Louth Archaeological Society, 10, 25- 41).

[26] Trevet, County Meath.

[27] The Abbey at Shláine is said to be founded by Bishop Erc at the behest of St Patrick (Westropp, T., 1901. Slane in Bregia, County Meath: its friary and hermitage. The Journal of the Royal Society of Antiquaries of Ireland, 31, 404-430). In the ninth and tenth centuries, two bishops named Máel Pátraic had their seat at Shláine, and another was the son of a bishop. Hence, Westropp suggests there were '*genealogical descents*' among the bishops, including those named Máel Pátraic: from Bishop Niallan (d.867) was Máel Pátraic, son of Niall (d.886), and there followed Colman son of Máel Pátraic (d.948). Colman was '*slain by the foreigners*' (O'Donovan, 1856), during an era when Shláine was '*unfortunate enough*' to attract the attention of the Danes of Átha Cliath (Dublin) (Westropp, 1901): '*the belfry of Slaine was burned by the foreigners, with its full of relics and distinguished persons, together with Caeineachair, Lector of Slaine, and the crozier of the patron saint, and a bell [which was] the best of bells*' (O'Donovan, 1856).

[28] Slane, County Meath.

[29] One of three Lords of Rathdowney referred to in the Annals of the Four Masters, and it is possible to genealogically connect three generations, i.e., Máel Pátraic (d.909), son of Flaithri (d.874), son of Máel Dúin. A later entry in the Annals of the Four Masters records the death of '*Gillamolua Ua Bruaideadha*' Lord of Rathdowney, in 1069, providing a possible link between Máel Pátraic and clann Ua Bruaideadha, i.e., O'Brody, or similar (O'Donovan, J., 1856; MacLysaght, E., 1985).

[30] Rathdowney, County Laois.

[31] That is, Aed, son of Máel Pátraic son of Mael Curarda, King of the Airghialla (Jaski, B., 1995. The traditional rule of succession in early Ireland, [thesis], Trinity College, Dublin, Ireland. Department of History: pp 326; pp 275). This line of Uí Fhiachrach were seated at Ard Sratha, Tír Eoghain. Aed was killed by Niall Glúndub, High King of Ireland (916-919 AD) (Byrne, F., 1973).

[32] In 902 AD the Danes were expelled from Átha Cliath, where '*they left a great number of their ships, and escaped half-dead, after having been wounded and broken*'. The Danes returned with their fleets in 917 AD, led by Sitric and Ragnall, grandsons of Ímar; at that time the Danes also plundered Cill Dara (Kildare) (O'Donovan, J., 1856; Hennessy W., 1887).

[33] Leighlin, County Carlow.

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Table 1: continued

Reference	Date, AD	Location
Máel Pátraic, son of Morann, Abbot of Droim Chliabh and Ard Sratha … died.[AFM, 34]	921 (923)	Droim Chliabh, Sligeach and Ard Sratha, Tír Eoghain[35]
Máel Pátraic, son of Celen, priest and Vice-Abbot of Beannchar … died. [AFM,36]	927 (929)	Beannchar, Dún[37]
The two successors of Patrick, namely, Joseph, scribe, bishop, and anchorite, the wisest of the Irish; and Máel Pátraic, son of Máel Tuile, bishop and wise man, died. The latter was five months in the abbacy when he died.[AFM]	936	Ard Mhacha, Ard Mhacha
Repose of Aed son of Máel Pátraic, abbot of Achadh Deo.[AI,38]	939	Achadh Deo, Ciarrí[39]
Cairpre son of Máel Pátraic, King of Uí, Liatháin, and Finn son of Mután, King of Corcu Loígde, were killed by the men of Mag Féine.[AU,40]	944	Barraigh Mhóra, Corcaigh
Colmán son of Máel Pátraic, superior of Shláine, was taken prisoner by foreigners, and died on their hands.[AU,18]	948	Shláine, Mhi
Máel Pátraic son of Coscán, lector of Ard Mhacha … died.[AU]	953	Ard Mhacha, Ard Mhacha
Máel l Pátraic son of Cú Bretan, superior of Shláine … died.[AU]	956	Shláine, Mhi

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[34] The Monastery at Droim Chliabh was founded by St Columba ca. 575 AD; Máel Pátraic is the earliest abbot named in Annals. O'Donovan notes with curiosity that although Droim Chliabh was part of the territory of the descendants of Cairbre, son of Niall Naoighiallach (i.e., of the Nine Hostages) it was, in the early tenth century, '*considered to be a part of Ulster, and a tributary to the King of Aileach*', i.e., of the Cenél nEógain. (O'Donovan J., 1847. The Book of Rights. Dublin: The University Press). Hence, a connection between Droim Chliabh and Ard Sratha might be unexpected, but not inexplicable. Silke notes, '*Máel Pátraic was probably a lay comarb*'.(Silke, J. 1998. Airgialla Churches and Churches in Donegal. Clogher Record, 13, 85-89).

[35] Drumcliff, County Sligo, and Ardstraw, County Tyrone.

[36] Beannchar Abbey was founded by St Comgall ca. 558 AD. Also in 929 AD, the Annals of Ulster record '*Ceile, comarb of Comgall, and Apostolic doctor of all Ireland, went into pilgrimage*' (Hennessy W., 1887), while the Annals of the Four Masters has, '*Celedabhaill, son of Scannall, successor of Comhgall of Beannchair, throughout Ireland, bishop, scribe, preacher, and learned doctor, died on his pilgrimage at Rome, on 14 September, and in the fifty-ninth year of his age*' (O'Donovan J., 1856).

[37] Bangor, County Down.

[38] This is the first record of Achadh Deo in annalistic records, of which pre-twelfth century records are vague and limited to the Annals of Inisfallen.

[39] Aghadoe, County Kerry.

[40] Uí-Liatháin was '*the name of a territory nearly co-extensive with the present Barony of Barrymore, Co. Cork, anciently occupied by the descendants of … the Uí Fidhgeinte*'. Corcu Loígde was '*a territory anciently comprising the south-west part of Co. Cork, namely, the present baronies of Carbery, Bear, and Bantry*'. And the Mag Féin were '*a tribe anciently inhabiting the district now forming the barony of Fermoy, Co. Cork*' (Hennessey, W.,1887).

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Table 1: continued

Reference	Date, AD	Location
Máel Pátraic, Abbot of Ros Cré … died.[AFM,41]	986 (987)	Ros Cré, Tiobraid Árann[42]
Loingseach, son of Máel Pátraic, lector of Cluain Mhic Nóis … died.[AFM]	988	Cluain Mhic Nóis, Uíbh Fhallí
Conn, son of Máel Pátraic, airchinnech of Mungairit and Disert-Oenghusa, died.[AFM,43]	1034	Mungairit, Luimneach
A great mortality of the men of Ireland, so that it is impossible to enumerate all the people that died. From that pestilence died … Máel Pátraic, bishop of Ard Mhacha.[AI,44]	1096	Ard Mhacha, Ard Mhacha

Table 2: Annalistic references to Máel Pátraic in conjunction with a surname

Reference	Date, AD	Location
Máel Pátraic Ua Sluaghadhaigh, the [most] learned of Ireland, died.[AFM,45]	1015 (1016)	Lann Abhaigh, Aontroim and Beannchar, Dún
Máel Pátraic Ua Ailecain, lector of Dun-Leathghlaise … [died].[AFM,46]	1026	Dún Pádraig, Dún[47]
Máel Pátraic Ua Baoghalán, priest of Cluain Mhic Nóis …died.[AFM,48]	1028	Cluain Mhic Nóis, Uíbh Fhallí

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[41] Where '*St Cronan, the son of Odhran, erected a monastery in the latter end of the sixth century*' (O'Donovan, 1856).

[42] Roscrea, County Tipperary.

[43] Mungairit, is in Luimneach (i.e., Mungret, County Limerick) yet O'Donovan (1856) stated Disert-Oenghusa was Díseart Aonghais (Dysartenos) in Laois. The case for Disert-Oenghusa referring to '*ecclesie de Diserrengussa, Limiricensis*', i.e., Díseart (Dysert) in Lumineach, as found in the Annates of Limerick (Moloney, M. & Costello, A., 1943. Obligationes pro Annatis Diocesis Limiricensis 1421-1519. Archivium Hibernicum, 10, 104-162), is stronger.

[44] '*A plague unrelated to a famine fever*' (MacArthur, W., 1949. The Identification of Some Pestilences Recorded in the Irish Annals. Irish Historical Studies, 6, 169-188).

[45] Erenach of Lann Abhaigh (Glenavy) in Aontroim (County Antrim), and Deputy Abbot of Beannchar (Bangor); his was from Cronn Badrui of the Dál Araidhe (King of Ulster, 392-414 AD). Mac Fhirbhisigh records four other Abbots (or deputies) of Beannchar who came out of the Uí Shuanaigh (O'Slowey) – Maol Tuile, the son of Donnghal; Airmheadhach, the son of Conall; Fear Dhá Chríoch, the son of Conall; and, Congus the son of Adhamhnán (Mac Fhirbhisigh, D. and Ó Muraíle, 2003; Woulfe, 1923).

[46] Ua Ailecain, i.e., O'Halligan. (Harrison, H., 1918. Surnames of the United Kingdom. London: The Morland Press Ltd).

[47] Dun-Leathghlaise being the early medieval name for Downpatrick, County Down (Mac Cionnaith, S., 1938. Dioghluim Dána. Dublin: Office of the Taoiseach).

[48] An Abbot of Clonmacnoise, named Ua Beguláin, was deposed in 1002 AD (Hennessey, W. 1866. Chronicum Scotorum: a chronicle of Irish affairs. London: Longmans, Green, Reader, and Dyer). Kehnel considers it possible that Máel Pátraic Ua Baoghalán, '*after his deposition turned to life as a priest*' (Kehnel, A., 1997. Clonmacnois – the church and lands of St Ciarán. Münster: Lit). '*The Uí Beguláin* (also Uí Bhaoithín, i.e., Boyton or Boyne; Woulfe, 1923) *were a branch of the Uí Briúin Bréifne*' (Duigan, M., 1934. The Uí Briúin Bréifni Genealogies. The Journal of the Royal Society of Antiquaries of Ireland, 4, 90-137).

Table 2: continued

Reference	**Date, AD**	**Location**
Mael Pátraic Ua Bileóice, chief lector of Ard Mhacha, and one eminent for piety and chastity, rested at a ripe old age.[AU,49]	1046	Ard Mhacha, Ard Mhacha
Mael Pátraic Ua Drugain assumed the lectorship of Ard Macha on the feast of Ailbe and of Mo-Laisi of Daimhinis.[AU,50]	1107	Ard Mhacha, Ard Mhacha
Mael Pátraic Ua Drugain, paragon of the wisdom of the Irish, chief lector of Ard Mhacha, head of council of the west of Europe in piety and devotion, died on his pilgrimage at the Island of Loch Cre.[AFM,51]	1138	Ard Mhacha, Ard Mhacha
Máel Pátraic Ua Callada, successor of Cronáin of Ros Cré.[AFM,52]	1168	Ros Cré, Tiobraid Árann
O'Banain, Bishop of Condeiri and Dál-Araidhe, a venerable man, full of holiness and of meekness and of purity of heart, died full piously in in Hy-Columbkille, after choice old age.[AU,53]	1174	Condeiri and Dál Araidhe[54]
Máel Pátraic O’Cobthaigh died.[AU,55]	1193	Not stated
Máel Pátraic Mac Kele, Erenagh of Cill Ala, was slain.[AFM,56]	1257	Cill Ala, Maigh Eo
Máel Pátraic Ua Scannall[57]	1253-1270	Dún na nGall
A battle was fought between Donnchad, son of Domnall Ó Briain … and Lochlainn Ó hAichir … and Muirchertach, son of (Mael) Pátraic Ó hAichir, [was] captured.[AU,58]	1312	Tuamhain

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[49] Ua Bileóice apparently comes from ‘*leaf of a book*’ (Ó Murchadha, D. 1999. The Formation of Gaelic Surnames in Ireland: Choosing the Eponyms. Nomina 22, 25-44).
[50] That is, St Ailbe of Emly and St Molaise of Devenish. The Ua Drugain (Drugain) were of the Cenél nEógain (Woulfe, 1923; Pender, S. 1951. The O’ Clery Book of Genealogies: 23 D 17 (RIA). Analecta Hibernica , 1951, 18, 1-198).
[51] Loch Cre, ‘*now Moinnahinnse, near Roscrea, in the county of Tipperary*’ (O’Donovan, 1856).
[52] Ua Callada, i.e., Kelledy; ‘*extremely rare*’ (Woulfe, 1923).
[53] O’Banain , i.e., O’Bannan (Woulfe, 1923). Hy-Columbkille, i.e., Iona Abbey (O’Donovan, 1856).
[54] Condeiri and Dál-Araidhe, i.e., the modern Connor and Down (O’Donovan, 1856).
[55] O’Cobthaigh, i.e., O’Coffey (Goldman, L. 2009. Oxford Dictionary of National Biography. Oxford: Oxford University Press).
[56] Mac Kele, i.e., Mac Hale (O’Donovam 1856). Woulfe (1923) refers to them as a Mayo family who were erenaghs of Cill Ala, Maigh Eo (Killala, Mayo) and coarbs of St Caillin in Fíonach, Liatroim (Fenagh, Leitrim).
[57] Numerous annalistic entries note Máel Pátraic Ua Scannall (i.e., O’Scannell; Woulfe, 1923) and MacInerney summarised his career. He was of the Ua Scannall of Sligeach who descended from Cairbre, a son of Niall. It is possible he was born in Dún na nGall (Donegal) or an adjacent county since he became Bishop of Raphoe in 1252 before elevation to Archbishop of Armagh in 1253 (MacInerney, M., 1916. A history of the Irish Dominicans). Máel Pátraic Ua Scannall is discussed in depth later in this series.
[58] Ó hAichir, i.e., O’Hare, a branch of the Uí Fidhgheinte of Tuamhain, i.e., Thomond (Woulfe, 1923).

Fitzpatrick, I., Fitzpatrick, M. (2023). Ó Maol Phádraig: the name, the people, and the clans. Part I.
The Journal of the Fitzpatrick Clan Society 4, 1-10. doi:10.48151/fitzpatrickclansociety01223, Ver1, 17 March 2023

Other early occurrences of Máel Pátraic

A remarkable entry from the medieval Icelandic work Landnámabók (The Book of Settlements) reads:

> *Onund Bild, took possession of the area above Thver River and made his home at Bildsfell. He had a freedman called Steinrod, son of Melpatrek of Ireland, who got possession of all the Vatnslands and made his home at Steinrodarstead. Steinrod was a remarkably fine man. His son was Thormod, father of Kar, father of Thormod, father of Brand, father of Thorir who married Helga Jon's-daughter.*[59, p.145]

The arrival of Steinrod, who was once a slave, in Iceland can be dated some time from 860 to 930 AD. From ca. 795 AD a small population of Irish anchorites had occupied Iceland, driven their by Vikings. But ca. 870 AD Scandinavian settlers began to establish permanent bases, and a '*steady stream*' of immigrants arrived between 890 and 910 AD; the '*Age of Settlements*' was over by 930 AD.[58] Although nothing else is known about Máel Pátraic, father of Steinrod, it is evident that he most likely obtained his name in the ninth century.

Another occurrence of Máel Pátraic, albeit indirect, is found in a manuscript known as St Gall, Stiftsbibliothek, 904, which is dated to 850-851 AD. It is considered mostly to have been written in Éire and is well known because '*it contains the magnum opus of the Latin grammarian Priscian of Caesarea*'. In addition, the manuscript is heavily glossed, i.e., it contains extensive commentary in the form of interlineal and marginal notes. The text was written mostly by two scribes and the '*first signs himself as Calvus Patricii (a Latinisation of the Irish name Máel Pátraic)*'.[60] Calvus, meaning '*bald*' in Latin, is a literal translation of Máel and its use is observed in other manuscripts, e.g., The Book of Armagh.[61]

Discussion

A review of the annalistic occurrences of Máel Pátraic demonstrate clear patterns; although none should be considered unequivocal. Many occurrences are associated with a religious figure, and notably an individual connected with a monastic site obviously associated with St Patrick. The geography of Máel Pátraic occurrences in the Annals is, on a pro rata basis, dominated by Ard Mhacha. And an imaginary latitudinal drawn through just south of Cluain Mhic Nóis (Clonmacnoise) puts 76% of Máel Pátraic in the north of Eire (refer Figure 1). Such, an albeit crude, understanding will assist in the interpretation of genealogies, and with appearances of the surname in late medieval documents, such as the Fiants of Ireland.

Acknowledgements

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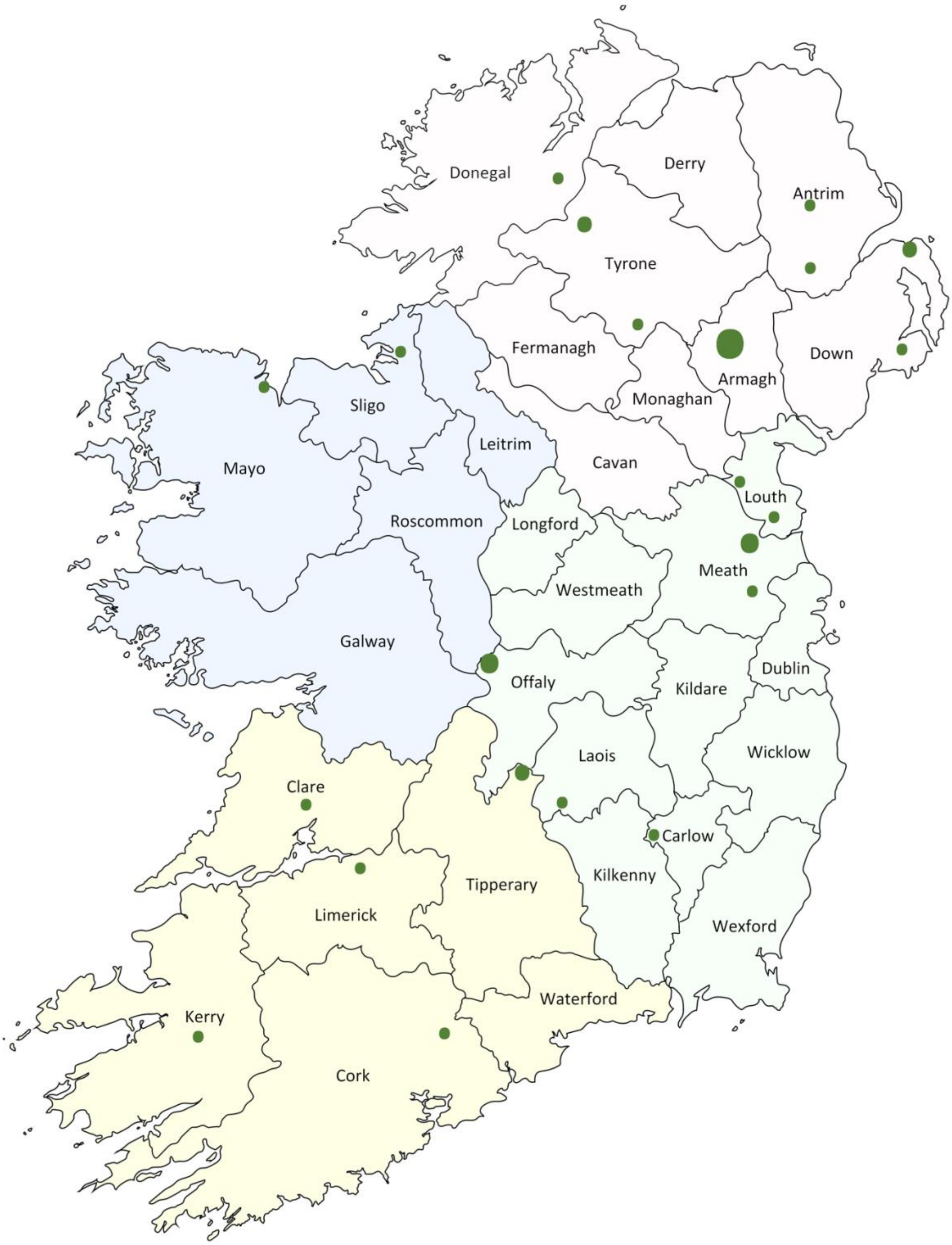
[59] Pálsson, H. and Edwards, P. (1976). The Book of Settlements: Landnámabók. Winnipeg: University of Manitoba Press.

[60] Moran, P. (2022). Latin Grammar Crossing Multilingual Zones: St Gall, Stiftsbibliothek, 904. Open Access, published by De Gruyter: https://doi.org/10.1515/9783110776492-003.

[61] Duffy, S. (2005).

Figure 1: Modern geographic locations, sometimes approximate, associated with the occurrence of Máel Pátraic in the Annals.



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A similar-sounding surnames sequel: haplogroup R-FT70038

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Abstract

Historical and Y-DNA analysis suggests that men with Branan and similar-sounding surnames of haplogroup R-BY140757 originated from the de Braham of Norman origin, who settled in Suffolk after the Norman conquest of England. Over the centuries, these de Braham took on important roles in English and Irish governance, military, and judiciaries. And in Ireland, the Norman surname took on, as was not uncommon, a Gaelic sound and written appearance, i.e., Branan and similar.

Descendants of Irish colonial settlers in Virginia with Branan-sounding surnames (Branham, Brannan, Brannon, etc.), who belong to the sub-haplogroup R-BY140757>FT70038, have been identified as the progeny of two notable eighteenth-century colonial North American settlers – Caron Brannon and Kenyon Branan.

This article identifies genealogical lines with known or hypothesized connections to Caron and Kenyon. Caron Brannon's will indicates he had four sons, three of whom have direct male descendants documented and one documented to have died without children. Additionally, there are birth records for a fifth son, the eldest, who finds no mention in Caron's will. Paper genealogy shows Kenyon Branan had one son with certainty, but three other lines are widely speculated to descend from him.

This project identified and recruited descendants from Caron's and Kenyon's lines for DNA testing. Y-DNA results for descendants of two well-documented sons of Caron Brannon form sub-haplogroups, R-FTC4333 and R-FT101136. This result is consistent with the hypothesis that Caron Brannon is the patriarch of R-FT70038. However, a striking new sub-haplogroup to R-FT70038, dubbed R-Y10443, was discovered matching two of the three lines previously thought to descend from Kenyon. The eldest son of Caron is shown as a possible father to Kenyon or as the patriarch of R-Y10443, but he cannot be both. This new insight suggests strongly that the patriarch of R-FT70038 was one to three generations prior to Caron Brannon and that Kenyon Branan plays a minor role in the lineages of the haplogroup.

The number of potential R-FT70038 haplotree options is now clearly defined. A combined analytical assessment of Y-SNP, Y-STR, and autosomal results reinforces the well-documented genealogies, debunks the speculative ones, and reveals new connections and chronologies that no single previous approach provided. Statistical modeling of the combined DNA data prefers the Haplotree with R-Y10433 descending directly from the patriarch and Kenyon Branan descending directly from Caron Brannon through his eldest son John.

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The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

Part I: Mapping Haplogroup R-FT70038

Targeted use of Y-DNA and autosomal DNA testing

R-FT70038 is a sub-haplogroup of BY140757, estimated by Family Tree DNA (FTDNA) to have originated 1,052 – 1,334 years ago (68% confidence interval)[1]. A recent publication linked R-BY140757 with the Normans in England, specifically the de Brahams of Suffolk. Eustace de Braham is the earliest recorded family member, with his name on various deeds ca. 1150 AD. The de Brahams attained some degree of prominence and are recorded as holding knighthoods and positions in administration and judiciary. It has been posited that in 1250, Richard de Braham moved from Suffolk to Ireland, where he became the position of Sheriff of Kilkenny. [2]

Y-DNA has identified North American men with Branan-like surnames as being of haplotype R-BY140757. Among them is a descendant of Richard Branham, who is recorded in a 1665 land grant in the Virginia Colony. To date, Richard is the earliest man recorded in the North American colonies with the archetype surname. Also found to be a member of R-BY140757 is a paper-tree descendant of a Caron Brannon (born ca. 1687). That member, along with two other men with similar-sounding surnames, who were hypothesized to be sons of Kenyon Branan, formed the haplogroup R-FT70038, a sub-haplogroup of R-BY140757.

A comprehensive effort was launched to expand the understanding of the R-FT70038 haplogroup using Next Generation Sequencing (NGS), in this case, Family Tree DNA's BigY-700, on candidates targeted via paper genealogies or previously reported DNA matches of R-FT70038 members.

Caron Brannon's lines

An important source laying out the Y-DNA descendants of Caron Brannon is his last will.[3]

> *In the name of God amen. I Caran Brannan being very sick and weak but of sound and perfect memory. I give devise and dispose of my Estate in the following Manner and form.*
>
> *Item: I give to my wife Margarett Brannan the use of my Plantation during her Natural Life not to be no ways Molested nor disturbed and after my wife's decease. I give my said Land and Plantation to my Son James Brannan and his heirs.*
>
> *Item: I give to my son Caran Brannan one feather Bed and furniture Now Standing in my Inner Room in the Corner after my Decease when his Mother thinks well.*

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[1] Y-DNA haplogroup R-BY140757. FamilyTreeDNA Discover. https://discover.familytreedna.com : accessed 19 September 2022.

[2] Fitzpatrick, M. and I. Fitzpatrick (2021). The Similar-Sounding Surnames of Haplogroup R-BY140757, The Journal of the Fitzpatrick Clan Society, 2 , 1-41, https://doi:10.48151/fitzpatrickclansociety00421.

[3] Virginia, US, Wills and Probate Records, 1652-1900. Ancestry.https://www.ancestry.com/discoveryui-content/view/1282048:62347: accessed 22 November 2022. Probate Place: Richmond, Virginia, USA. Caron Brannon lists his five children.

> *Item: I give to my son Joseph Brannan the Feater (sic) Bed standing in my out room in the Corner after his Mother Deceases.*
>
> *Item: I give to William Croucher and Eleanor his wife one Bed and furniture the Bed which my wife Lies upon after her Decease.*
>
> *Item: I give to my Loving wife Margarett Brannan the use of all my Personable Estate during her Natural Life after all my Debts is Satisfied and paid and after her Decease to be Equally divided between all of my Children Viz: James, Caran, Thomas, and Joseph Brannan and Elenor Croucher.*
>
> *Item: My Will and pleasure is that my estate shall not be appraised.*
>
> *Item: I hitherto nominate constitute and ordain my Loving Wife Margarett Brannan and my son James Brannan to be exectrix and Executor of this my Last Will and testament, revoking and disannulling all other Will or wills heretofore be memerd. Ratifying and confirming this and no othe to be my Last Will and Testament the 8th day of February, in the year of our Lord 1749.*

Two approaches were used to find candidates for the further mapping of R-FT70038. First, traditional genealogy was used to trace the lines for Caron's sons named in his will, viz., James, Caran, Thomas, and Joseph, to living male descendants as candidates for first-time Y-DNA testing. Second, candidates were sought among men who had already reported autosomal or Y-STR marker results and had identified Caron or his sons as direct ancestors; these candidates generally only required additional NGS testing. For Caron Brannon, meaningful results were obtained via the upgrade method.

Of the surname project participants, five were selected who had self-identified Caron Brannon (b. 1687) or one of his sons as their most distant known ancestor (MDKA).[3] In each case, the plausibility of their available paper genealogies in place supporting the claim was reviewed. Multiple descendants of Caron's sons Thomas and James Brannon provided DNA samples for the NGS testing.

To date, paper trails suggest that Caron's son Joseph Brannon (b. 1729) died at age 23 without issue[4], whereas James and Thomas Brannon had numerous offspring.[5,6] Caran Brannon Jr. is shown to have four sons, two of whom died without issue and the other two

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[3] King, George Harrison Sanford (1966). The Registers of North Farnham Parish 1663-1814 and Lunenburg Paris 1783-1800 – Richmond County Virginia. South Carolina: Southern Historical Press, Inc.

[4] Virginia, US, Wills and Probate Records, 1652-1900. Ancestry. https://www.ancestry.com/discoveryui-content/view/1282048:62347: accessed 23 November 2022. Probate Place: Richmond, Virginia, USA. Joseph leaves items to his brothers Caran, James, and Thomas – no wife or children are mentioned.

[5] *Ibid*. Thomas Dudley testified that James Brannan instructed him that all goods to go to his wife and children

[6] North Carolina, US, Wills and Probate Records, 1665-1998. Database with images, Ancestry. https://www.ancestry.com/discoveryui-content/view/662518:9061: accessed 23 November 2022. Probate Place: Johnston, North Carolina. Will – Thomas Brannon, 1804, Thomas leaves estate to his living children Anne Youngblood, Thomas Brannan, Caron Brannan, William Brannon, Tabitha Duck, Leroy Brannan.

with no documentation yet found.[7] Another child, John, was born to Caron and Margaret Brannon in 1718, but no subsequent records for him are found and he is not mentioned in Caron's will.[3] John could have pre-deceased his father or moved away and lost contact with the family, etc.

The results of the NGS of Caron Brannon lines were consistent with the reported paper genealogies. Importantly, while all testers were confirmed to belong to Haplogroup R-FT70038, as expected, two new sub-haplogroups were uncovered, which align with Thomas and James, respectively (Figure 1). The members of the James Brannon line are part of the sub-haplogroup R-FT101136 and share four unique Y-SNPs. The paper genealogy shows the participants' most recent common ancestor (MRCA) was James's only son, William Brannon (b. 1745).[4] Figure 1 depicts for convenience all four of the Y-SNP mutations for R-FT101136 as having occurred in James Brannon; however, some or all of these mutations could have occurred in William Brannon.

Thomas Brannon's line (Figure 1) contains descendants that form a new sub-haplogroup R-FTC4333 and share one unique Y-SNP. The paper genealogy shows that the two FTC4333 members' MRCA was Leroy J. Brannan (b. 1754). A third participant, BRAN20, who descends from Thomas through Leroy's brother Caren Brannon (b. 1752) is, as expected, a member of R-FT70038. However, this participant does not have the SNP FTC4333. Therefore, we know definitively that Leroy C. Brannan (b. 1754) was the patriarch of R-FTC4333. Further, the other sons of Thomas Brannon, (James, Thomas Jr, Caron, and William)[4,7] are not a part of R-FTC4333 and are therefore candidate ancestors for para-haplogroup members of R-FT70038.

The discovery of two sub-haplogroups descending from Caron Brannon's sons preserves the narrative that he was the patriarch of R-FT70038. If, for example, any of the three unique Y-SNPs discovered in this testing had been shared between Thomas and James' descendants, that Y-SNP, by definition, would have originated in Caron, not Thomas or James. While a 'Caron Brannon haplotype' is absent, defining Y-SNPs are found among Caron's sons, Thomas and James. The 'Patriarch Caron Brannon' hypothesis is revisited in subsequent sections.

The six participants were also compared via autosomal DNA analysis. The R-FTC4333 members, BRAN1 and BRAN2, are fourth cousins with a 69% theoretical chance of showing a match defined as sharing > 7 centimorgans of DNA across the autosomes[8]. For BRAN1 and BRAN2 there was no such autosomal match. Neither BRAN1 nor BRAN2 exhibited an autosomal match for BRAN20, their fifth cousin, once removed. Similarly, among the R-FT101136 members who are fourth cousins, once removed, there is a 48% chance of an autosomal match > 7 centimorgans[9] but no match was detected. The implications of these autosomal results and those of the entire R-FT70038 haplotree will be discussed later.

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[7] King, The Registers of North Farnham Parish 1663-1814 and Lunenburg Paris 1783-1800 – Richmond County Virginia, p. 20. _Birth dates and names for the nine children of Caran and his wife Susanna.

[8] Cousin Statistics. International Society of Genetic. https://isogg.org/wiki/Cousin_statistics: accessed 7 August 2022.

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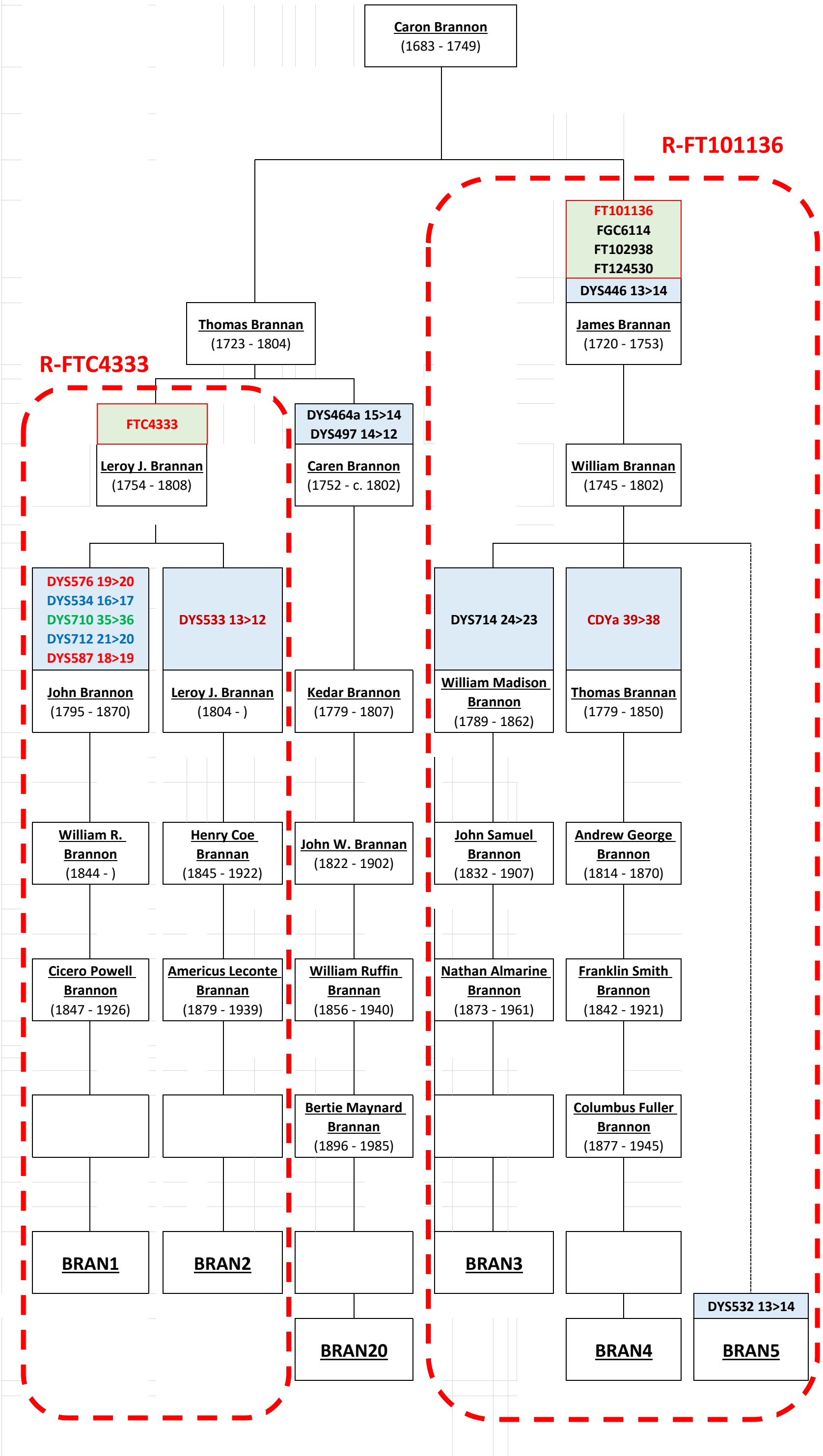
Figure 1: Haplogroup R-FT70038 – direct descendants of Caron Brannon



Notes: Matching Y-SNPs are shaded green, and matching Y-STRs are shaded blue. The font is colored for those Y-STRs that are convergent elsewhere in the R-FT70038 haplotree.

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Y-STR testing within R-FT70038 has also identified a single shared mutation in the R-FT101136 branch versus the ancestral value for the R-FT70038 kits tested to date. That mutation, DYS446 13>14, occurred in the James Brannon line in or before the MRCA, William Brannan. Figure 1 shows that the Y-STR mutation occurred within the same timeframe as the Y-SNP mutations for R-FT101136. Each of the participants' Y-STR mutations from the ancestral values are shown in Figure 1; 'private' Y-SNPs, those with no reported match in the databases, are not shown. In this analysis, the Y-STR and autosomal DNA test results do not provide any more information for defining the family tree branches than is found via Y-SNP data. Later it will be shown that combining these three types of DNA data can help establish timelines and generational steps between the various haplotree branches.

Kenyon Branan Lines

Kenyon Branan is another documented Virginian from the eighteenth century whose descendants are of haplogroup R-FT70038. The strongest documentation for Kenyon is in a family Bible for James Branan[9]. This James Branan is shown in the 1850 United States Census as being born in North Carolina in 1766[10]. James' gravestone in Wilkinson County, Georgia shows a birth date of 1770[11].

From the Cooper-Ethridge-Branan Bible:

James Branan, son of Kenyon Branan of Va., m. 1795, Sarah Tommy. Their children:

Harris	8-25-1796
Polly	1-11-1798
Adam	12-19-1799
Winnie	7-7-1801
Vashti	4-1-1803
Joseph	1-18-1805
Caswell	8-10-1807
Paschal	3-3-1809
James	12-29-1810
Alfred	7-21-1812
Sarah	12-4-1813
Frances	3-1-1815
John Tommy	2-21-1817
Littleton	12-18-1818
Almeta	4-28-1821
Elizabeth	1-18-1822

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[9] https://georgiagenealogy.org/wilkinson/brananbible.html: accessed November 22, 2022. Eileen B. McAdams. Cooper-Ethridge-(or Etheredge)-Branan Bible.

[10] 1850 US Federal Census, Ancestry. https://www.ancestry.com/discoveryui-content/view/19013389:8054: accessed 24 December 2022. Georgia > Wilkinson > Division 93, James Branan age 84.

[11] James Branan. Find a Grave. https://www.findagrave.com/memorial/15681287/james-branan: accessed November 22, 2022. Death date on gravestone 1851.

James Branan and Sarah Tommey were married in Warren County in 1795[12] and moved to Wilkinson County thereafter. They had nine sons and seven daughters.[13] Direct male descendants of Harris Branan (b. 1796), James K. Branan (b. 1810), and Littleton Branan (b.1818) were recruited for DNA analysis. Figure 2 depicts the part of the James Branan Y-DNA tree focused on the eight participants whose relationships are in the nephew/uncle to fifth cousin range.

The immediate finding from this testing is that there is no 'James Branan or Kenyon Branan haplogroup', i.e., no Y-SNP is shared across the descendants of three of the sons of James Branan (Harris, James K. and Littleton). This result is significant and makes Y-DNA-based conclusions about any potential brothers for James Branan difficult. Likewise, there can be no Kenyon Branan haplogroup for definitive Y-DNA confirmation of his sons and their descendants.

There were six project participants, BRAN8, BRAN9, BRAN10, BRAN11, BRAN12, and BRAN21 who, according to traditional genealogy, descend from Harris Branan, James and Sarah's eldest son. As shown in Figure 2, Harris Branan had two sons, James Wilson Branan (b. 1820) and Caswell Harris Branan (b. 1823), with descendants who participated in this project. The participant descending from James Wilson, BRAN12, has no named or private variant Y-SNPs, meaning that his Y-SNP profile is indistinguishable from Kenyon Branan's, i.e., there are no intervening generational mutations. The participants descending from Caswell Harris Branan all share the SNPs R-FTB27810 and R-FTB32101; FTDNA used the former as the new sub-haplogroup label. Caswell Harris Branan is the unambiguous patriarch of R-FTB27810. Also observed within R-FTB27810 is the Y-STR mutation DYS534 16>17 in BRAN8, BRAN9, BRAN10, and BRAN21, but not BRAN11; this indicates definitively that the mutation occurred in Roger Augustus Branan (1872 - 1956). The DYS534 16>17 mutation is also shared with two R-FT70038 members, who are not R-FTB27810, viz., BRAN1 and BRAN19 and are clearly convergent rather than IBD (identical by descent) as they span distinct haplogroups.

Y-DNA data is silent regarding any relationship outside of R-FTB27810 (BRAN8-11, BRAN21) beyond the mutual membership in R-FT70038. Specifically, from a Y-SNP standpoint, BRAN12-14 only sit in the R-FT70038 para-haplogroup; however, autosomal DNA links all of them to BRAN8-11 and 21. This linkage is consistent with documented paper genealogy. The autosomal match matrix for the descendants of James Branan (1770 - 1851) is shown in Figure 3. The shared segment size is shown for all possible pairs. The matrix indicates that three para-haplogroup members in question, BRAN12, BRAN13, and BRAN14, are autosomal matches with each other and with members of sub-Haplogroup R-FTB27810. BRAN12, for example, shares autosomal segments with all test participants reported as descending from James Branan (and none of the other R-FT70038 project participants, as is discussed in a later section). The autosomal evidence supports that BRAN8-14 and BRAN21 share a common ancestor, and paper genealogy indicates that the common ancestor is James Branan (1770 - 1851).

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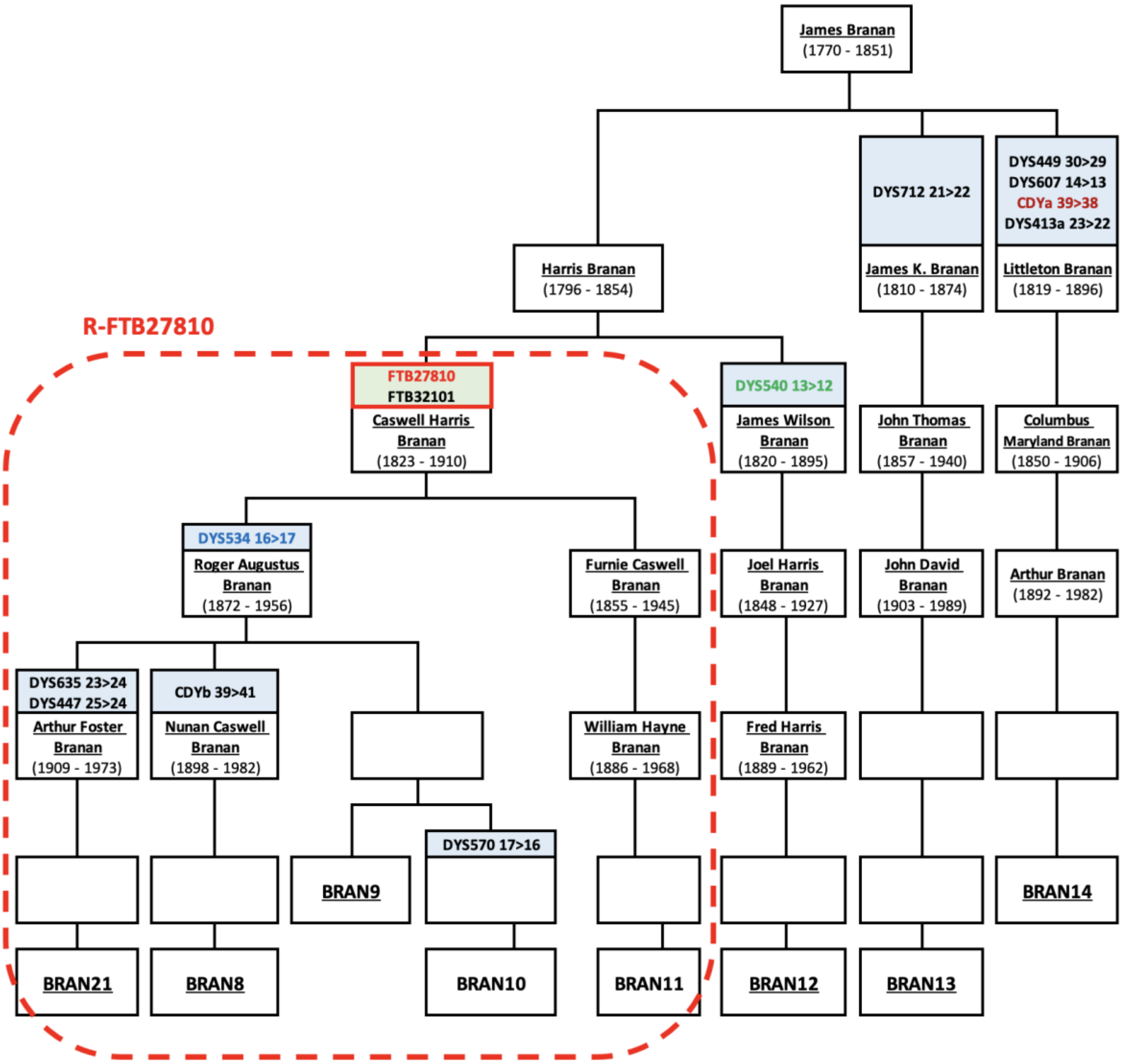
[12] Georgia, US, Marriage Records from Select Counties, 1828-1978. Ancestry. https://www.ancestry.com/discoveryui-content/view/438676:4766: accessed 23 November 2022. James Branham to Sally Tommey June 18, 1797.

Figure 2: Haplogroup R-FT70038 – descendants of James, son of Kenyon Branan



Notes: Matching Y-SNPs are shaded green, and matching Y-STRs are shaded blue. The font is colored for those Y-STRs that are convergent elsewhere in the R-FT70038 haplotree.

Three other men are asserted to be sons of Kenyon Branan in various family trees: Joseph Branan (b. 1762), Jonathan Branan (b. 1777), and Wiley Bridges Brannan (b. 1799). While there are no records of their linkage, there is some circumstantial evidence to be discussed, and their descendant lines are well-documented and easily traced. We identified direct male descendants of each through conventional paper genealogy methods and recruited them to participate in the project. The willing submitted samples for DNA testing.

Figure 3: Autosomal relationships between descendants of James, son of Kenyon Branan

	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14	BRAN21
BRAN8		393	347	0	28	0	0	167
BRAN9	393		1945	52	93	0	13	120
BRAN10	347	1945		0	17	0	0	153
BRAN11	0	52	0		50	0	57	65
BRAN12	28	93	17	50		14	121	186
BRAN13	0	0	0	0	14		11	0
BRAN14	0	13	0	57	121	11		50
BRAN21	167	120	153	65	186	0	50	

Note: shared CentiMorgans of autosomal DNA

Joseph Branan was born in North Carolina in 1762.[13] His will, dated 1857 and excerpted below, bequeathed his possessions to his five daughters and two sons.[14]

> *Georgia*
> *Putnam County*
>
> *Know all men by this so present that I Joseph Branan of the State and County aforesaid do make and ordain this my last will and testament in the manner and form as follows viz:*
>
> *I give and bequeath to my Daughter Cinthy one bed furniture, one cow and calf*
>
> *I give and bequeath to my Daughter Martha one bed and furniture, one cow and calf*
>
> *I give and bequeath to my Son Wiley Brannan, one hundred acres land, being a part of Lot No. 382 lying North of the Rushy Creek, the same being mine (f)or life? – Also I give to my Said Son Wiley one baby horse and saddle.*
>
> *I give and bequeath to my Daughter Sarah one bed and furniture, one cow and calf.*
>
> *I give and bequeath to my Daughter Nancey one bed and furniture, one cow and calf.*
> *I give and bequeath to my son Kinion Branam all the residue of my estate both real and personal in any (?) belonging to me. The land particular which I may die hopeful of , said Land known, by Law.*

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[13] 1850 US Federal Census, Ancestry. https://www.ancestry.com/discoveryui-content/view/18908421:8054: accessed 24 December 2022. Joseph Brannam age 88.

[14] Georgia, US, Wills and Probate Records, 1742-1992. Ancestry. https://www.ancestry.com/discoveryui-content/view/658587:8635: accessed 23 November 2022. Names children: Cinthy, Martha, Wiley, Sarah, Lucy, Nancy, and Kinion

> *I do hereby nominate and appoint my Said Son Kinion Branam sole executor to this my last will and testament, duly forsaking all other wills at any time heretofore made by me. In (?) whereof I have (?) to set my hand and seal this 20th day August 1857.*

Many have noted, and sometimes confused, the similarly named Kinion, son of Joseph Branam, with the Kenyon Branan of unknown birthdate but ca. 1730, the father of James and, perhaps, Joseph. Kinion Branam was born, according to census estimates, between 1812 and 1814.[15,16,17]. The 1850 Census of Kinion's household also shows his 88-year-old father, Joseph, and 85-year-old mother, Mary, living with him.[18] Kinion's descendants, and those of his brother, Wiley, are readily traced through census records.

Direct descendants of Joseph's sons Kinion Branan and Wiley Branam, BRAN6 and BRAN7, respectively, participated in the DNA testing. Joseph Branan, like James Branan, has no defining Y-SNP. BRAN6 and BRAN7 each have Y-SNPs that are not found among other R-FT70038 members (Figure 4). Likewise, there is no Y-STR mutation shared between them that could be considered Identical by Descendancy (IBD), from Joseph Branan.

The Y-DNA results neither prove nor disprove the hypothesized sibling relationship between Joseph and James Branan, i.e., both being sons of Kenyon. Autosomal results for our test participants are also neutral in providing any evidence that Kenyon Branan is a direct ancestor of Joseph Branam. Figure 5 below shows that BRAN6 and BRAN7 are autosomal matches for each other, as expected. BRAN6 matches both a Caron Brannon descendant and a Kenyon Branan descendant, while BRAN7 matches a Kenyon Branan descendant. There are currently no other autosomal matches for Joseph Branan descendants BRAN6 or BRAN7 in our test group other than those shown in Figure 5. Accordingly, the Joseph Branan line is redrawn to show no confirmed connection to Kenyon Branan or his descendants other than being members of R-FT70038. Complete haplogroup autosomal matching results are shown in the appendices.

A more definitive disruption of conventional wisdom generated by these test results is seen for the placement of the lineages descending John Brannan, Jonathan Brannan, and Wiley Bridges Brannan. Jonathan Branan (b. 1777) has been named as a speculative son of Kenyon Branan. Jonathan's son was James Kenyon Branan (b. 1818), and his grandson was Benjamin Caswell Branan (b. 1844) – the relatively uncommon names of Kenyon and Caswell appear throughout the James Branan (b. 1770) and Jonathan Branan (b. 1777) family trees. Both families resided in Georgia. Past genealogists may have considered the shared names and geographies circumstantial evidence for the presumed sibling connection.

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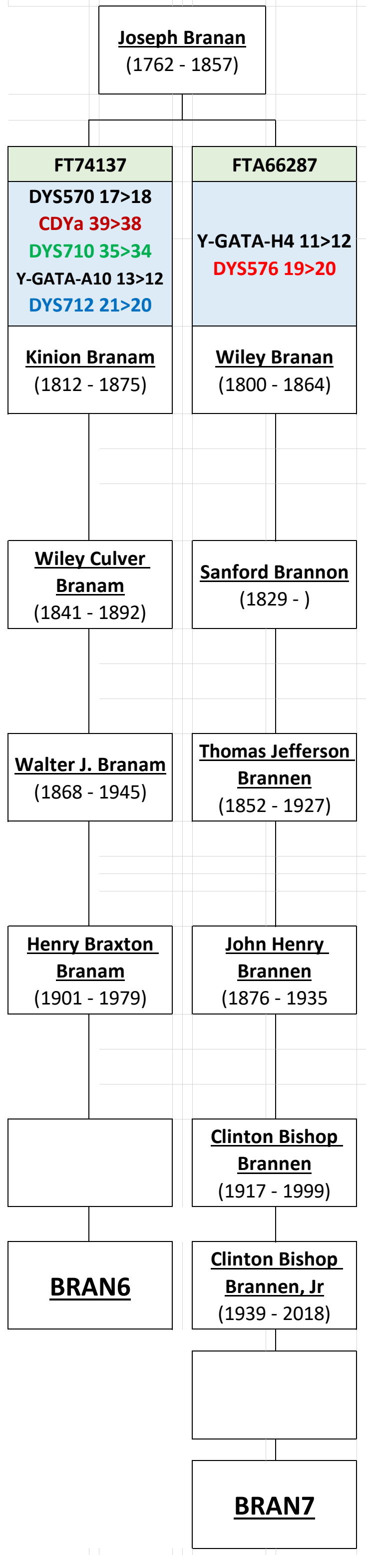
[15] 1850 US Federal Census, Ancestry. https://www.ancestry.com/discoveryui-content/view/18908412:8054: accessed 24 December 2022. Kennon Branham, age 38.

[16] 1860 US Federal Census, Ancestry. https://www.ancestry.com/discoveryui-content/view/11603850:7667: accessed 24 December 2022. Kenan Branham, age 48.

[17] 1870 US Federal Census, Ancestry https://www.ancestry.com/discoveryui-content/view/6370455:7163: accessed 24 December 2022. Kinion Brannam, age at last birthday, 56.

[18] 1850 US Federal Census, Ancestry. https://www.ancestry.com/discoveryui-content/view/18908412:8054: accessed 24 December 2022. Joseph Branham, age 88; Mary Branham, age 85.

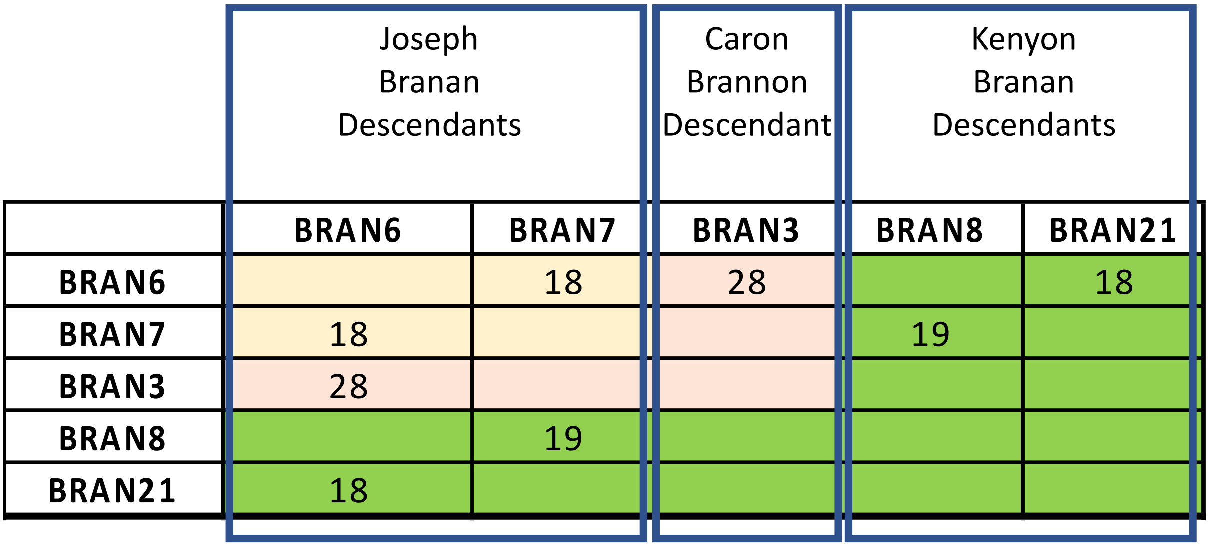
Figure 4: Descendants of Joseph, oft hypothesized son of Kenyon Branan



Notes: Matching Y-SNPs are shaded green, and matching Y-STRs are shaded blue. The font is colored for those Y-STRs that are convergent elsewhere in the R-FT70038 haplotree.

Branan, J. (2023). A similar-sounding surname sequel: haplotype R-FT70038.
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

Figure 5: Autosomal matrix between descendants of Joseph Branan and other BRANs



	Joseph Branan Descendants		Caron Brannon Descendant	Kenyon Branan Descendants	
	BRAN6	**BRAN7**	**BRAN3**	**BRAN8**	**BRAN21**
BRAN6		18	28		18
BRAN7	18			19	
BRAN3	28				
BRAN8		19			
BRAN21	18				

Note: shared CentiMorgans of autosomal DNA

Wiley Bridges Brannan (1799-1865) presents two traditional genealogy challenges. The first is that there is no record of who his father is, though, as mentioned, speculative family histories name him as a son of Kenyon Branan.[19] The second challenge is that his name and lifespan closely match Joseph Branan's son Wiley Branan (1800-1864). Many family trees link to the wrong Wiley Branan or consider them to be the same person. The traditional genealogy shows that Wiley Bridges Brannan resided with his family in Henry County, GA[20], while Wiley Branan resided with his family in Harris County, GA, some sixty miles away.[21]

The Y-DNA results, illustrated in Figure 6, tell a clear and compelling story resolving all confusion and speculation, viz.

- The descendants of Jonathan Branan and Wiley Bridges Brannan share two unique Y-SNPs and, unexpectedly, with a third project participant who descends from John Brannon (b. 1775).
- A sub-haplogroup of R-FT70038, R-Y10443, is formed based on these shared Y-SNPs.
- Within this sub-haplogroup R-Y10443, the descendants of Jonathan Branan and John Brannon share a Y-STR mutation that is not present in the descendant of Wiley Bridges Brannon. This difference suggests that one additional generation, 'Unknown Brannon 2' stands between the siblings John and Jonathan, and the Wiley Bridges Brannan line.

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[19] Wiley Bridges Brannan. Find a Grave. https://www.findagrave.com/memorial/42659438/wiley-bridges-brannan: accessed November 22 2022. Son of Kenyon and Mary Branan of Cardiff, Glamorgan, Wales.
[20] 1860 US Federal Census, Ancestry. https://www.ancestry.com/discoveryui-content/view/11283651:7667: accessed 24 December 2022. Wily Brannan, age 60
[21] 1860 US Federal Census, Ancestry. https://www.ancestry.com/discoveryui-content/view/11260178:7667: accessed 24 December 2022. Wiley Brannan, age 62.

This single Y-STR mutation, DYS533 13>12, will play a significant role in our analysis of the patriarch Caron Brannon hypothesis.

- The presence of the R-Y10443 SNPs in the descendant of Wiley Bridges Brannan, but not in the descendant of Wiley, son of Joseph Branan, disproves any notion that the two Wileys were the same person.

Concerning Figure 6, note there is a significant age difference between the presumed siblings Jonathan Branan (b. 1775) and John Brannon (b. 1777), and Wiley Bridges Brannan (b. 1799). Accordingly, another generation, 'Unknown Brannon 3', was inserted to bridge the age gap and provide a possible brother to 'Unknown Brannan 2'. The patriarch of R-Y10443, "Unknown Branan 1" at 30 years per generation, would have been born ca. 1716. It is, therefore, possible, though speculative, that 'Unknown Branan 1' is John Brannon (b. 1718), the first son of Caron Brannon Sr. Kenyon Branan's reported but undocumented birth year (1730 or 1746) suggests that he is too young to be 'Unknown Brannon 1.' Hence, the original hypothesis was revised and is illustrated in Figure 7.

It is a curious naming choice that deserves additional scrutiny for Jonathan Brannon and John Brannon to be brothers. We note that both Jonathan and John Branan, along with Jonathan's son Calvin are listed on the same page in the Newton County, Georgia census of 1830.[22] In addition to geographic proximity, they are both shown to be 50 - 60 years old, lending credence to the proposed sibling relationship and that the 'Unknown Brannon 2' named one son John and another son Jonathan.

Para-haplogroup lines from Harris Branam and Bridges Brannon

Two lines of R-FT70038 project participants, BRAN18 and BRAN19, have MDKA's Harris Branam and Bridges Brannon. Unlike other R-FT70038 lines, they are alone with no Y-DNA, autosomal or paper link to the other members. Bridges Brannon (b. 1777) was identified 25 years ago as the father of James Wallace Brannon (b. 1804, Edgefield District, SC).[23] Both died in Alabama, where most of their descendants reside today. BRAN19 descends from Bridges Brannon and exactly matches BRAN9 at 111 markers, but the implied close relationship misleads since BRAN9's membership is in sub-haplogroup R-FTB27810. Hence, the Y-STR marker mutation DYS 16>17 is convergent in BRAN9 and BRAN19 and not IBD.

BRAN18 descends through a well-documented line from Sampson Brannen[24] who plausibly descends from Harrison Brannen (b. 1774), though the link has been inferred only from their co-location in Coffee County, AL in the 1850 Census. Harrison and his wife Cynthia were the only Brannens in that county of an age to be Sampson's parents.[25]

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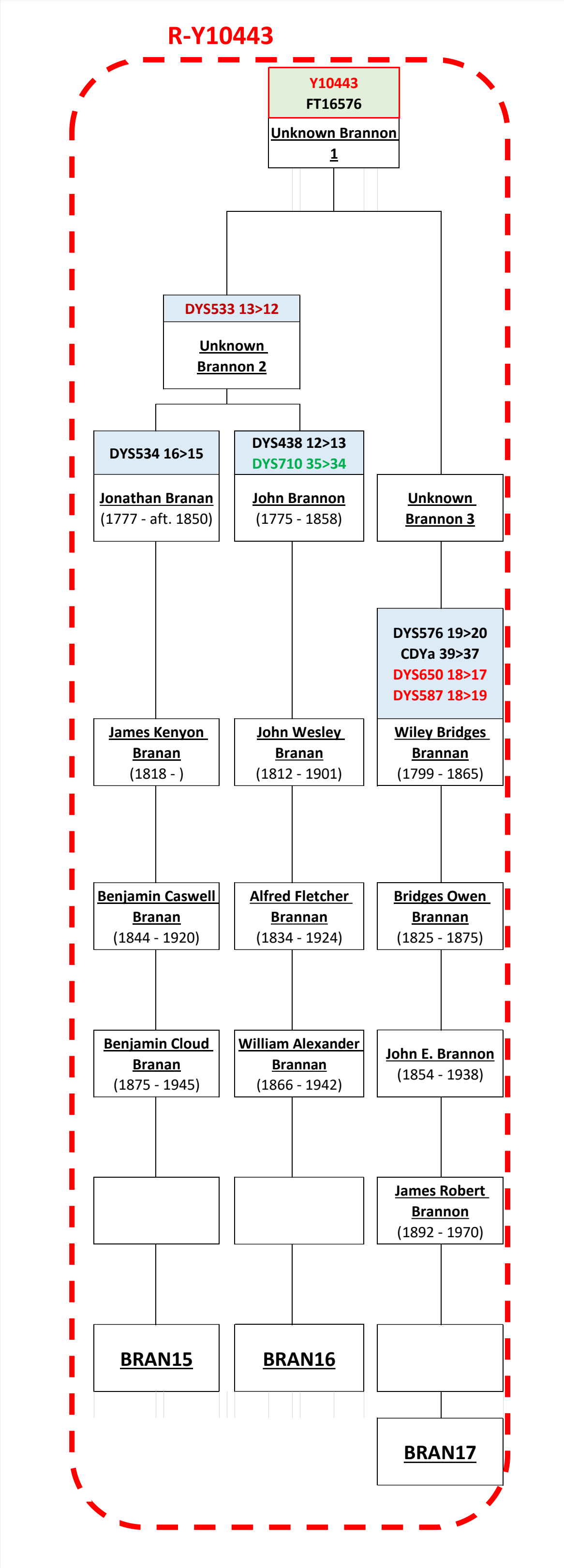
[22] 1830 US Federal Census. Ancestry.https://www.ancestry.com/discoveryui-content/view/930465:8058: accessed 24 December 2022. Jonathan Branan, male, 50-60; John Branan, male, 50-60.

[23] Bridges Brannon. Find a Grave. https://www.findagrave.com/memorial/141370423/bridges-brannon: accessed 19 December 2022. Showing Bridges Brenan first in Edgefield, SC and then in Russell County, AL.

[24] N. Quinton Brannen. Brannen History. http://jbrannen.com/Genealogy.pdf: accessed 22 December 2022.

[25] 1850 United States Census., Ancestry https://www.ancestry.com/imageviewer/collections/8054/images/4187293-00610?pId=17985618: accessed 22 December 2022. Harris and Cynthia Branam aged 74 and 84.

Figure 6: Sub-haplogroup R-Y10433 Descendants



Notes: Matching Y-SNPs are shaded green, and matching Y-STRs are shaded blue. The font is colored for those Y-STRs that are convergent elsewhere in the R-FT70038 haplotree.

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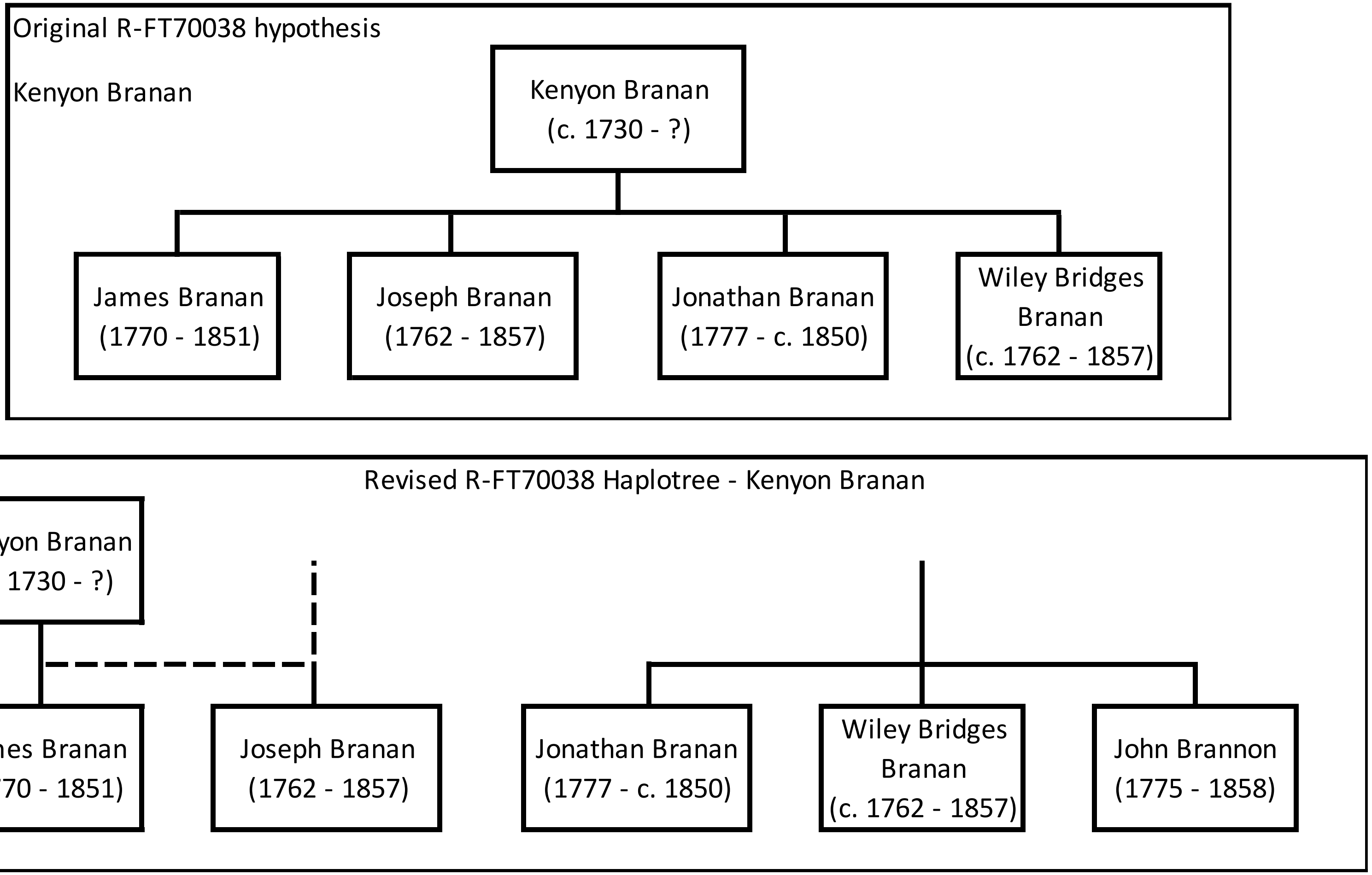
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

Figure 7: Revision of Kenyon Branan descendant Lines



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The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

Part II: Sequential use of DNA data to derive the R-FT70038 Haplotree

The time to the most recent common ancestor (TMRCA) from two or more samples is estimated from DNA testing. However, the uncertainties associated with the TMRCAs are greater than is often useful to construct traditional family trees or to validate speculative trees. The comprehensive DNA testing and documented traditional trees for the R-FT70038 project have allowed a comparison of haplotrees constructed via Y-SNP data only; Y-SNP data with adjustments from Y-STR results; and Y-SNP and Y-STR data with adjustments based on autosomal DNA matching.

The step-by-step process is described below and illustrated in the sequence of Figures 8A – 8E. The use of all the data yielded a haplotree that closely matches the chronology and number of generations suggested by the existing genealogical data and gives insight into the age of the haplogroup beyond pure genealogical information. It is highly likely that haplotree revisions will occur in the future, as further Branans undertake Y-DNA tests and 'new' archival records are uncovered.

Haplotree by Y-SNP data only

The FamilyTreeDNA Discover tool[26] was used to anchor the haplogroup and sub-haplogroup patriarchs at their most likely birth year, as shown in Table 1.

Table 1: Estimated of haplogroup origin years

Haplogroup	Most likely birth year	68% Confidence Interval	95% Confidence Interval
R-FT70038	1727	1677 - 1769	1625 - 1806
R-FTC4333	1770	1687 – 1839	1586 - 1891
R-Y10433	1777	1702 – 1840	1613 - 1889
R-FT101136	1873	1823 - 1916	1761 - 1947
R-FTB27810	1892	1843 - 1934	1789 - 1963

It was assumed the test sample contributors were born between 1920 and 2010 and the most likely birth date for the last generation in the tree was defined as 1950 +/- 15 years. For illustration purposes only, a round estimate of 30 years per generation was used. It was assumed that each tester's line branched off from different sons of the haplogroup patriarch, i.e., at the most distant relationship possible.

The resulting tree (Figure 8A) was drawn using Y-SNP results. It is similar to the FamilyTreeDNA Block tree, only more granular with generations and chronology aligned with the estimated haplogroup origin year. This haplotree fits in eight generations.

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[26] Y-DNA haplogroups R-70038, R-FTC4333, R-FT101136, R-FTB27810, R-Y10433. FamilyTreeDNA Discover. https://discover.familytreedna.com : accessed 25 November 2022.

Haplotree by Y-SNP data with adjustments from Y-STR results

Insights derived from Y-STR data alter the haplotree in the following ways (refer to Figure 8B to follow the modifications).

- For the two-member haplogroup R-FTC4333, no new information for redrawing the tree is gained from Y-STR differences. Their Y-STR mutations occurred sometime after patriarch Thomas Brannan, and they are not shared.

- For sub-haplogroup R-FT101136, Figure 1 showed that each of the three members have a unique Y-STR mutation. No additional information is gained for redrawing Figure 8B tree from the Y-STR differences.

- For sub-haplogroup R-FTB27810, BRAN8-10 share a common Y-STR mutation (DYS534 16>17) while BRAN11 has the ancestral value of the haplogroup. BRAN8-10 have a common ancestor not shared by BRAN11. Figure 8B illustrates in red the modification to the original Y-SNP only tree to add the new branch within R-FT27810.

- For sub-Haplogroup Y-10443, BRAN15 and BRAN16 exhibit DYS533 13>12 while BRAN17 has the R-FT70038 ancestral value of DYS533 = 13.

- Accordingly, a new common ancestor, indicated in Figure 8B in red, is posited for BRAN15 and BRAN16 one generation after the Y10433 patriarch. This new common ancestor is an uncle of BRAN17 but not in BRAN17's direct line.

- The STR adjustments do not change the eight-generation span of the R-FT70038 haplogroup predicted from SNP results.

Haplotree by Y-SNP and Y-STR data with adjustments from autosomal results

Insight derived from R-FT70038 members' autosomal match data alters the haplotree further in the following ways (refer to Figure 8C to follow the modifications).

- Within a sub-Haplogroup, the SNP/STR tree shown in in Figure 8B implies a specific cousin relationship between the participants to be compared now with autosomal test results.

- An exhaustive empirical study establishing actual most likely shared autosomal segment lengths for various relationships has been published by Blaine Bettinger.[27] Table 2 summarizes the relationships from that work relevant to the R-FT70038 haplotree. The SNP/STR tree was adjusted by adding or subtracting intervening generation blocks as appropriate to minimize the variation between the calculated most likely total shared segment length and the actual total matching segment length from the participants' autosomal DNA test results.

---

[27] Bettinger, Blaine T. (2020) T. The Shared cM Project Version 4.0. *https://thegeneticgenealogist.com/2020/03/27/version-4-0-march-2020-update-to-the-shared-cm-project/*: accessed 26 November 2022.

Figure 8A: Haplotree based on Y-SNP data only

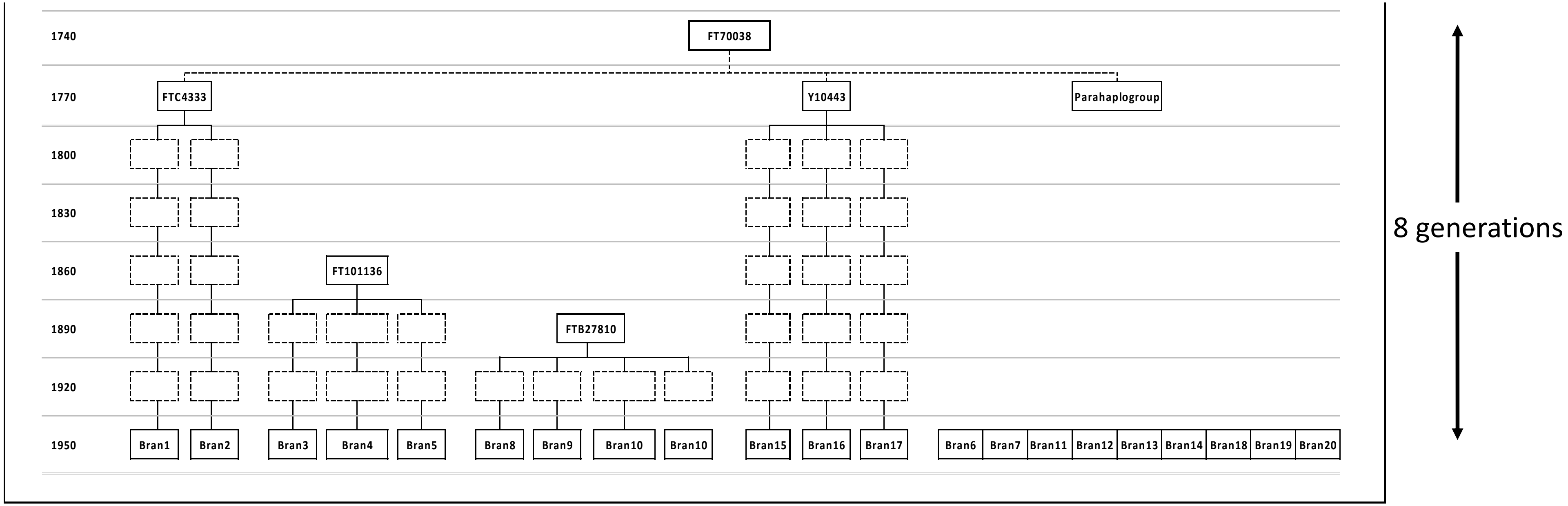
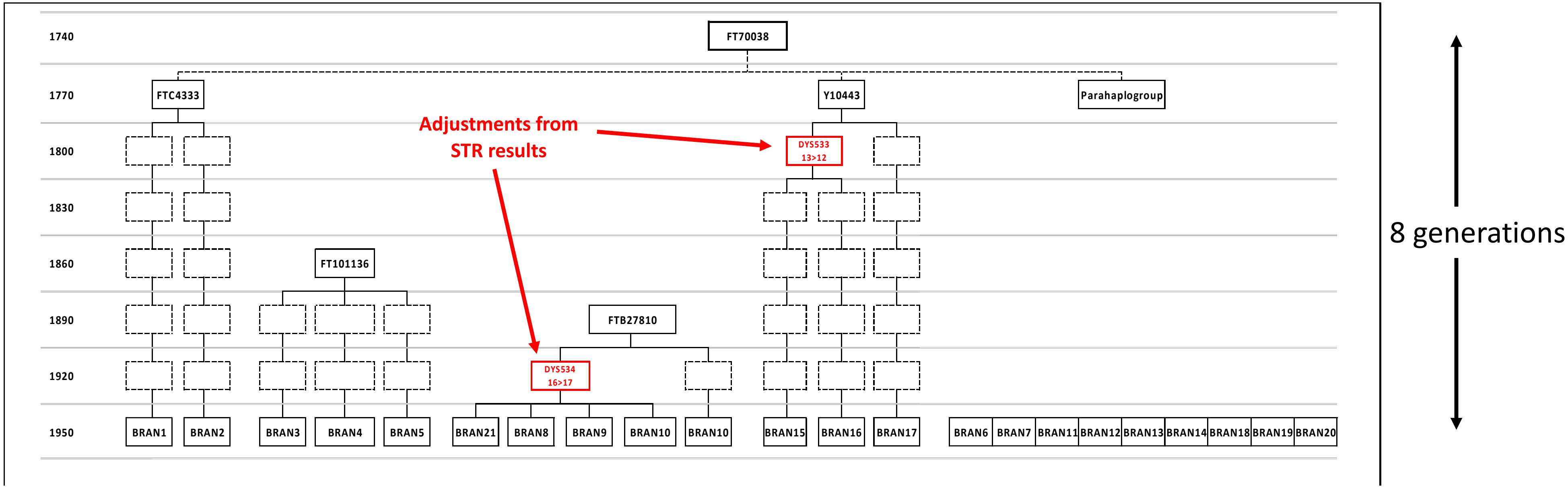


Figure 8B: Haplotree based on Y-DNA SNP and STR data



Branan, J. (2023). A similar-sounding surname sequel: haplotype R-FT70038.
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

Table 2: Autosomal DNA relationships, shared segment lengths, and match likelihood

Relationship	**Shared segment length (cM)**	**Match likelihood**
Nephew	1741	100%
1st-cousin	866	100%
1st-cousin 1R	433	100%
1st-cousin 2R	221	100%
2nd-cousin	229	100%
2nd-cousin 1R	122	100%
2nd-cousin 2R	71	98%
3rd-cousin	73	98%
3rd-cousin 1R	48	88%
3rd-cousin 2R	36	69%
4th-cousin	35	69%
4th-cousin 1R	28	48%
4th-cousin 2R	22	30%
5th-cousin	25	30%
5th-cousin 1R	21	18%
5th-cousin 2R	18	10%
6th-cousin	18	10%
6th-cousin 1R	15	6%
6th-cousin 2R	13	3%
7th-cousin	14	3%
7th-cousin 1R	12	2%

- For sub-Haplogroup R-FT101136, participants do not show any autosomal match with each other.

- From Table 2, we see that we only reach the > 50% chance of no autosomal match at the fifth cousin level implying at least five intervening generations between tester and patriarch.[28]

- Figure 8C redraws the tree for FT101136, expanding the number of intervening generations from two to five in order to fit the most likely empirical relationship.

- For sub-Haplogroup FTC4333, the participants are not autosomal matches to others in their sub-Haplogroup. As mentioned previously, the chance of no autosomal match only reaches at least 50%, which is when a minimum of five intervening generations are present.

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[28] Donnelly, Kevin P (1983). The probability that related individuals share some section of genome identical by descent. Theoretical Population Biology, 23, 34-63.

- In FTC4333 the SNP/STR tree already had five intervening generations implied between the participants, so the autosomal information aligns with the Y-DNA-based assumptions for the tree. No adjustment to the tree is needed from these autosomal results.

- For sub-Haplogroup R-Y10443, the participants are not autosomal matches to others in their sub-Haplogroup. Y-STR data showed that BRAN15 and BRAN16 have a more recent common ancestor than their sub-haplogroup partner BRAN17. Autosomal results show that BRAN15 and BRAN16 are not autosomal matches for each other.

- As mentioned previously, the chance of no autosomal match only reaches 50% when at least five intervening generations are present. Accordingly, we adjust the intervening generations between BRAN15, BRAN and the MRCA (DYS533 13>12) from four generations to five generations.

- The autosomal relationship between sub-Haplogroup R-FTB27810 members and three of our Para-haplogroup members (BRAN12, BRAN13, and BRAN14) was described in the section on Kenyon Branan.

- The haplotree was adjusted to recognize that MRCA of BRAN8-14 and relationships and number of intervening generations were optimized to best fit the autosomal data within the constraints imposed by the SNP and STR results. The details of that optimization are provided in the appendices.

- Adjusting the haplotree to account for all the autosomal data stretches the tree from eight generations to eleven generations. Figure 8C summarizes the tree consolidating all the project DNA data. Note that we now permit the birthdates of the participants to be between 1920, 1950 and 1980 +/- 15 years.

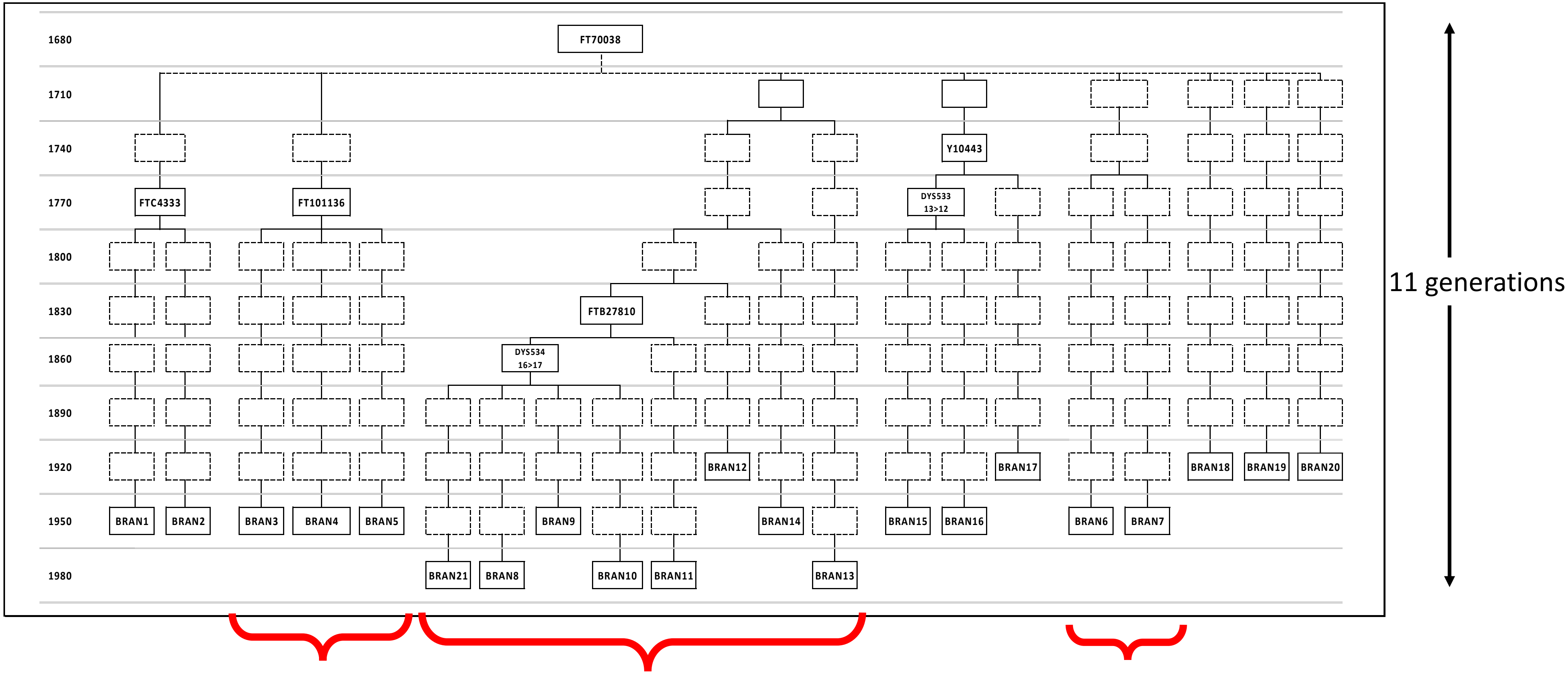
- The addition of generations to best fit the autosomal data moves the founding date of sub-Haplogroup R-FTB27810 backward from 1890 to 1830. Likewise, the founding date of our haplogroup R-FT70038 is estimated to move backward from 1740 to 1680, which independently aligns with Caron Brannon's reported birth date of 1683.

Haplotree adjusted with paper genealogy

The full haplotrees, applying paper genealogy to the DNA-based haplotree, are shown in Figures 8D (chronological alignment) and 8E (generational alignment). There are few edits to the haplotree generated by DNA data alone (Figure 8C).

The adjusted haplotree (Figures 8D and 8E), comprises eleven generations, matching the combined DNA analysis shown in Figure 8C. Neither DNA data nor paper genealogy definitively names the patriarch of R-FT70038.

Figure 8C: Chronological tree based on Y-DNA SNP, STR data and autosomal results



Additional generations

- Additional generations
- Inclusion of 3 parahaplogroup members

Additional generations

Branan, J. (2023). A similar-sounding surname sequel: haplotype R-FT70038.
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

Figure 8D: Chronological tree based on Y-DNA SNP, STR Data, autosomal results and paper genealogy

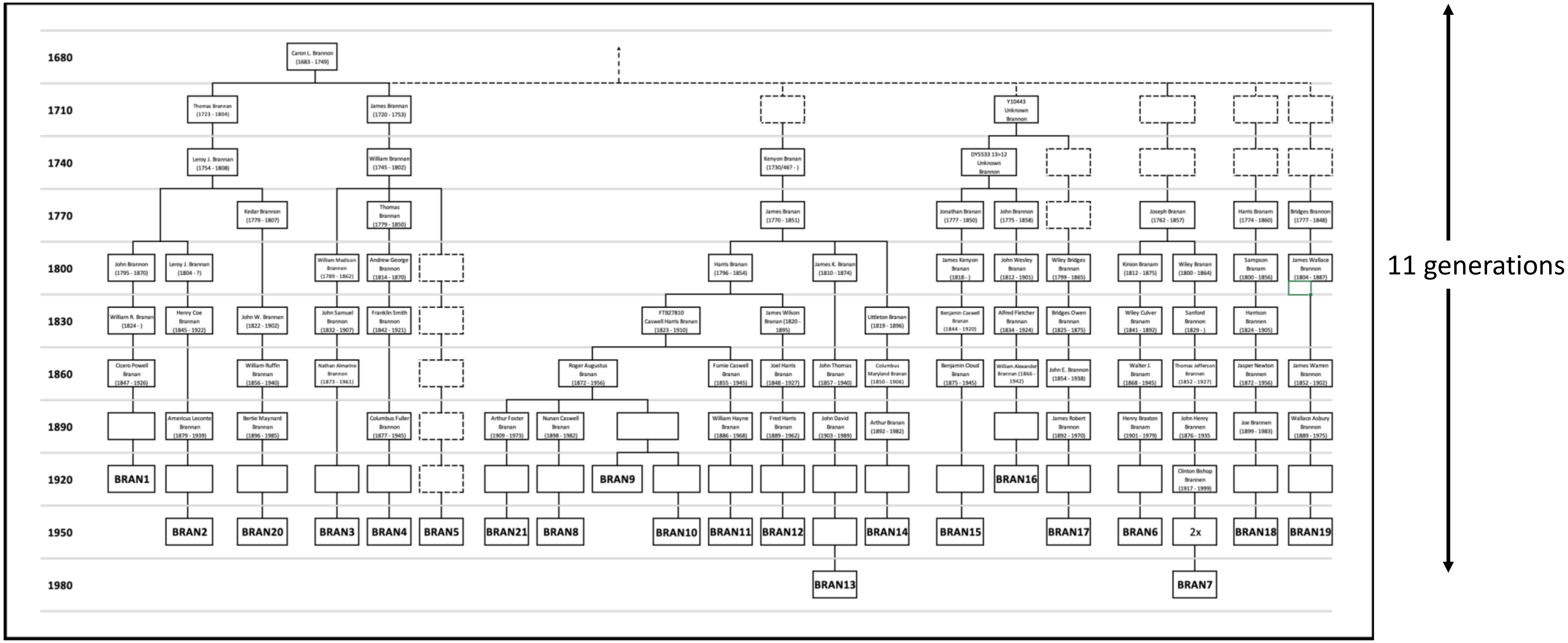


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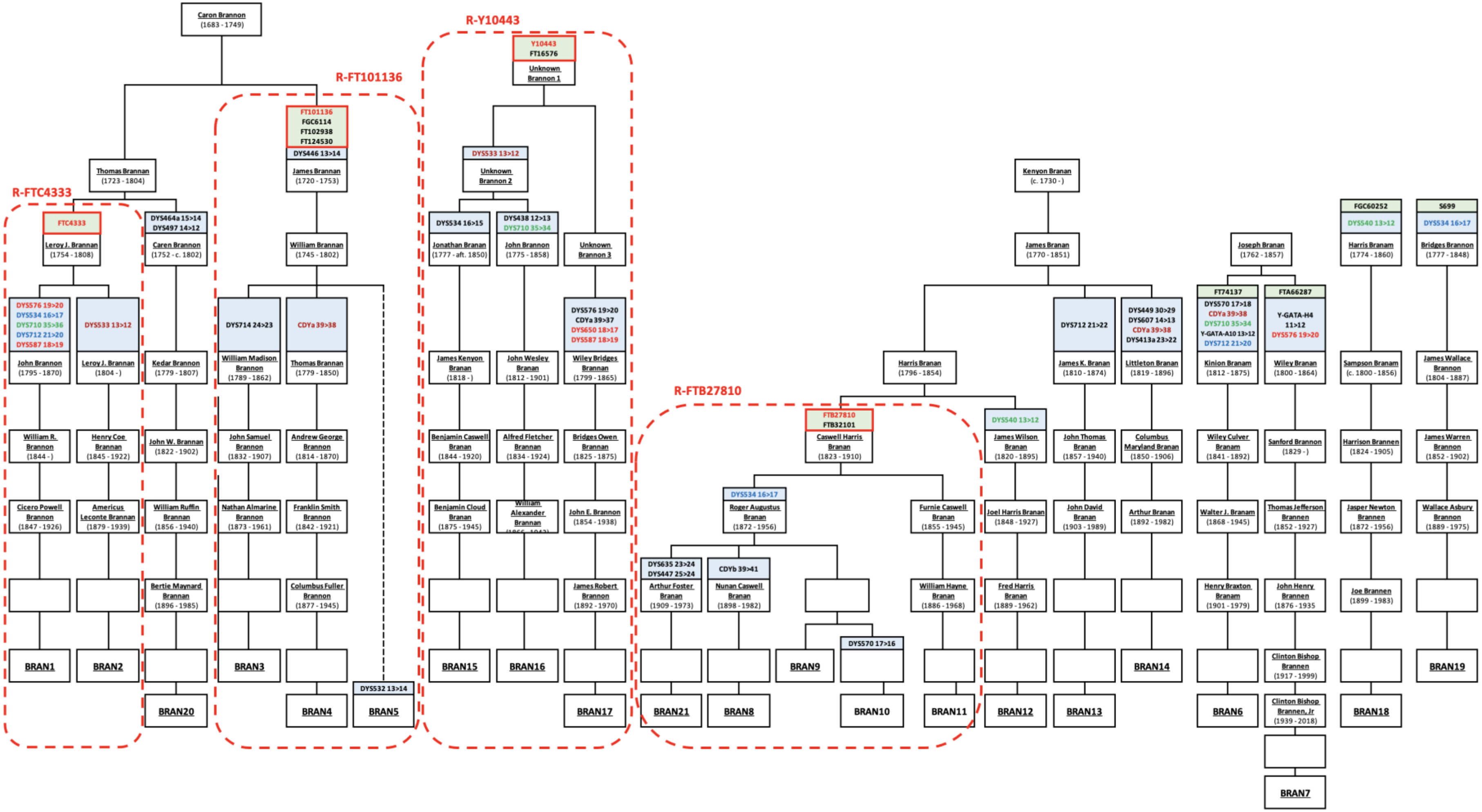
Figure 8E: Generational tree based on Y-DNA SNP, STR data, autosomal results and paper genealogy



Notes: Matching Y-SNPs are shaded green, and matching Y-STRs are shaded blue. The font is colored for the Y-STRs that are convergent elsewhere in the R-FT70038 haplotree .

Part III – Revisiting the patriarch Caron Brannon hypothesis

All of the project participants' lineages shown to belong to R-FT70038 have been traced by paper genealogy into the 18th century as shown in Figures 8D and 8E. Caron Brannon, the earliest named member in the haplogroup, had five sons. For Caron to be the patriarch of the whole haplogroup, plausible links must be established to four lines' MDKAs, Kenyon Branan, Joseph Branan, Harris Branam, Bridges Brannon, and the patriarch of sub-haplogroup R-Y10443 ('Unknown Brannon 1' in Figures 8D and 8E).

We look at each of Caron Brannon's sons in turn to check plausible links:

- Joseph Brannon died young, and his will indicates no wife or children. He is eliminated from consideration as a father of any para-haplogroup or sub-haplogroup lines.

- James Brannon was documented to have a single son, William, and all of his descendants belong to haplogroup R-FT101136. James and William are eliminated as a father of any line not belonging to R-FT101136.

- Thomas Brannon had five sons, James (b. 1742), Thomas, Caron, William, and Leroy. Leroy was shown to be the patriarch of R-FTC4333 and is therefore eliminated as a father of the four para-haplogroup lines. There is no documentation of James's family, but he is old enough to be a father candidate of Harris (b. 1774) or Bridges (b. 1777). James is too young to be the father of Kenyon or Joseph (b.1762). Thomas, Thomas Jr, James, and Caron are mentioned as grandchildren in Thomas's mother-in-law's 1754 will, but William is not mentioned. William is therefore too young to be the sire of one of our four para-haplogroup lines.

- Caron Brannon, Jr. and his wife Susanna had nine children and their births are well-documented.[8] The wills for two of Caron Jr.'s four sons, James (b. 1766) and Spencer (b. 1769), suggest that they had no male heirs.[29,30] No documentation beyond birth is found for Caron Jr's son Thomas Brannon (b. 1750) or William Brannon (b. 1756) – they are possible ancestors to any R-FT70038 para-haplogroup lines with the MDKA born after 1770, namely Harris Branam and Bridges Brannon. The lines of BRAN18 and BRAN19 could therefore descend through Caron Brannon Jr. The lines with the MDKAs of Joseph Branam and Kenyon Branan cannot.

- John Brannon, b. 1718 is undocumented after his birth. Accordingly, his birth date allows one to speculate that John is the MRCA for Joseph Branam (b. 1762), Harris

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[29] Virginia, US, Wills and Probate Records, 1652-1900, Volume 8, 1789-1794. Ancestry. https://www.ancestry.com/discoveryui-content/view/1517616:62347 : accessed 30 April 2023. Probate Place: Richmond, Virginia, USA. James leaves his estate to brother Spencer Branan and sister Barbary. No wife or children are mentioned.

[30] Virginia, US, Wills and Probate Records, 1652-1900, Volume 9, 1794-1822. Ancestry. Probate Place: Richmond, Virginia, USA. Link to image incorrect, manual paging required to image 38 of 777. Barbary Branan names brother Spencer as Executor.

> Branam (b. 1774), and Bridges Brannon (b. 1777). Kenyon Branan also could be John's son or grandson – recall that there is no record of Kenyon's birthdate which could range from c. 1710 - ca. 1749 based on his sole documented son James's birth date of 1770. Likewise, the whole haplogroup line R-Y10443 could descend through Caron's son John Brannon. However, the combined SNP and STR data discussed for haplogroup R-Y10443 shows us clearly that it is not possible for all of these suppositions to be simultaneously true.

The Y-STR mutation highlighted in Figure 6, DYS533 13>12, appears in the MDKAs for BRAN15 and BRAN16, both born in the 1770s and is central to our conclusions for the R-FT70038 haplotree. This mutation must be IBD from a common ancestor, designated 'Unknown Brannon 2' in Figure 6. 'Unknown Brannon 2', with a birth year ca. 1745, cannot be the patriarch for R-Y10443 because BRAN17 does not share the mutation. Therefore, the patriarch of R-Y10443, designated 'Unknown Brannon 1' in Figure 6 has a birth year of ca. 1715, approximately thirty years before the birth of 'Unknown Brannon 2'.

If 'Unknown Brannon 1' is a descendant of Caron Brannon, the only documented possibility is that 'Unknown Brannon 1' is actually John Brannon (b. 1718), son of Caron. Moreover, if John Brannon is the patriarch of R-Y10443, then the other para-haplogroup MDKAs shown in Figure 8E cannot have descended from John since they do not share that SNP mutation and are not a part of R-Y10443. The Caron Brannon patriarch hypothesis lives now in the realm of undiscovered and undocumented sons and grandsons to link to the documented lines.

The combined analysis of autosomal, Y-STR and Y-SNP data shows that the full tree should fit in around eleven generations, suggesting that the patriarch for R-FT70038 is Caron's father or grandfather. While any of the discovered para-haplogroup lines can descend directly from Caron Brannon, all of them cannot. The youngest of the para-haplogroup MDKA's, Harris Branam and Bridges Brannon could only descend from Caron's son John or through Caron's grandsons James (son of Thomas), Thomas (son of Caron Jr.) or William (son of Caron Jr.).

Figure 9 illustrates a simplified rendering of the R-FT70038 haplotree's remaining possible structures. Monte Carlo analysis of autosomal and Y-DNA STR data will identify the most likely option.

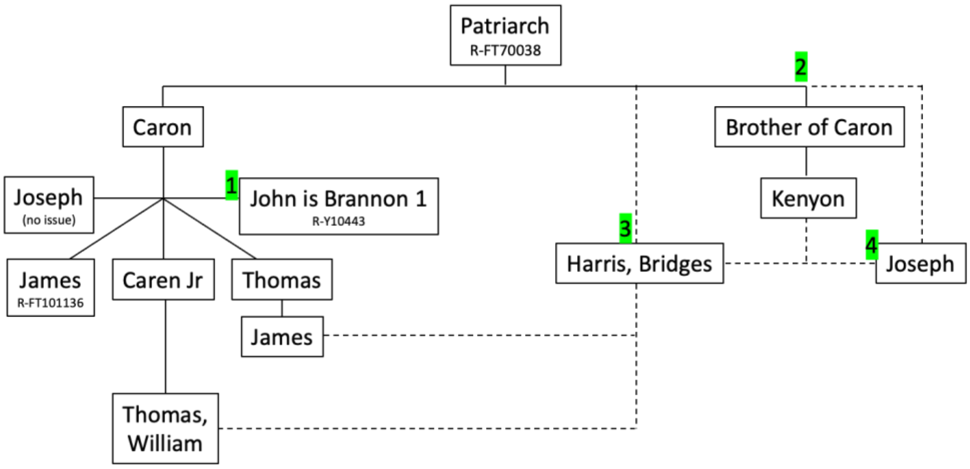
Part IV – Identification of the best fit haplotree via STR and autosomal DNA Statistics.

In Part II we used the Y-DNA STR and autosomal DNA result for each test participant to determine, individually, if they had shared common ancestors other than the patriarch and how many generations from the patriarch they are likely to be. This technique allowed the construction of a partial haplotree but could not discern between the various remaining permutations of haplotrees shown in Figure 9. In Part IV, we posit three of the haplotrees sketched in Figure 9. We then use Monte Carlo simulations of known STR and autosomal DNA statistics to assess the range of outcomes to be expected for STR 111-marker

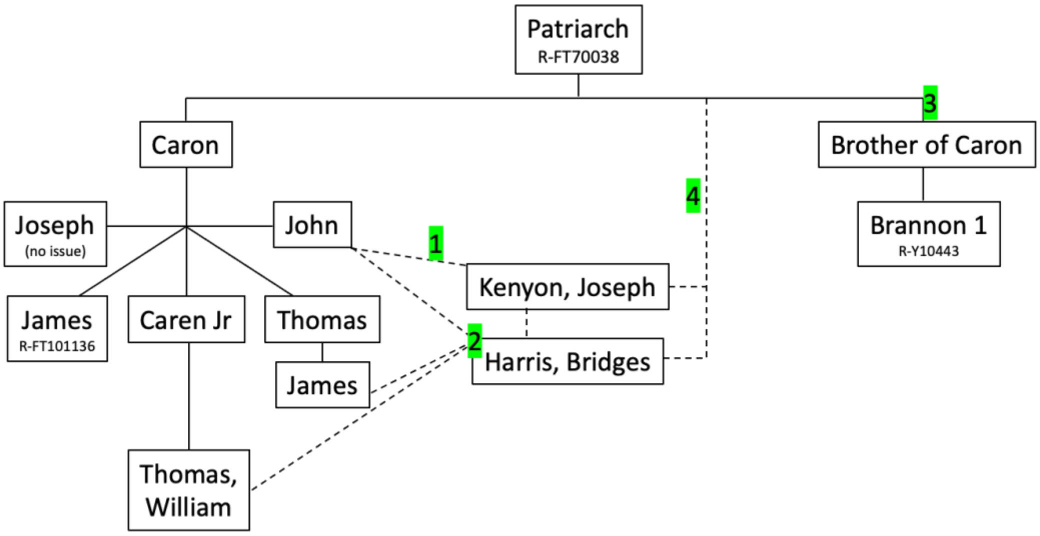
Branan, J. (2023). A similar-sounding surname sequel: haplotype R-FT70038.
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

mutations and number of autosomal matched pairs in the posited trees. Finally, we compare the actual observed number of STR marker mutations and autosomal matched pairs measured in the test participants. The closest match between posited tree simulations and actual data identifies which of the haplotrees is most likely.

Figure 9: Remaining candidates R-FT70038 haplotree structures



1. John (b. 1718), the son of Caron, is the R-FTC4333 patriarch
2. Kenyon (b. 1710 – 1750) is not listed as a named son of James, Caren Jr. or Thomas in their well-documented lineages
3. Harris (b. 1774) and Bridges (b. 1777) could be sons of Kenyon, Thomas, William, James, or descend through an undiscovered line to the patriarch
4. Joseph (b. 1762) may be a son of Kenyon or descend through an undiscovered line to the patriarch. He is too old to be a son of Thomas, William or James.



1. Kenyon (b. 1710 – 1750) could be a son or grandson of John (b. 1718). Joseph (b. 1762) could be John or Kenyon's son
2. Harris (b. 1774) and Bridges (b. 1777) could be grandsons of John, sons of Kenyon, or sons of Thomas, William, or James
3. Brannon 1 (b. c. 1715) is too old to descend from a son of Caron – must descend from the patriarch through a sibling of Caron
4. Kenyon, Joseph, Harris, and Bridges could descend through an undiscovered line to the patriarch

The compact trees (described in the following figures as 'John is Kenyon's father' and 'John is Y10443') postulate a single brother of Caron bearing a portion of the para-haplogroup lines. These compact trees are dependent as well on postulating that Caron's eldest son John bears another portion of the para-haplogroup lines. At the other extreme of possible trees, we test a simulation with multiple brothers of Caron, each individually siring a single line of the various para-haplogroup lines.

Each test participant, BRAN1-BRAN21, had a well-defined chance of experiencing an STR marker mutation for each of the 111 markers tested in each generation after the patriarch of the haplotree.[31] A Monte Carlo simulation[32] modelled the distribution of total Y-STR mutations expected in the project participants for the two most compact haplotrees and the most distributed haplotrees shown in Figure 10; note that actual test results showed forty-six Y-STR mutations.

The simulation distribution statistics from 2000-run Monte Carlo simulations for each compact haplotree are shown in Figure 11 on the left with blue bars. The average number of mutations predicted in both simulations is greater than the actual forty-six mutations found, but the difference is within one standard deviation – both trees are likely outcomes. The most distributed tree (described in the figures below as 'Six Separate Descendant Lines'), with independent lines drawn to the patriarch from Caron, the R-Y10433 patriarch, Kenyon, Joseph, Harris and Bridges has the best fit between the simulation average number of mutations and the actual value (actual result is +0.13 Standard deviations above the simulation average, also described as a z-score of 0.13).

Autosomal data can be used in a similar manner to test the various trees. It is well-known that autosomal matching between distantly related pairs is rare but is occasionally seen. The statistical likelihood of finding an autosomal match, shown in Table 2, enables a Monte Carlo simulation of the three candidate haplotrees to calculate the expected distribution of matching pairs found in autosomal DNA testing of the project members.

The distribution statistics for number of matches is shown on the right side of Figure 11 with orange bars. Across the haplogroup our actual autosomal testing found thirty matched pairs. Two thousand-run Monte Carlo analyses for each haplotree produced average numbers of matched pairs within two standard deviations of the thirty actual matched pairs.

Figure 11 compares both the STR mutation and autosomal match DNA simulation results for the three candidate haplotrees. Z-scores are then plotted for the actual DNA results versus simulation in Figure 12. In Figure 12, scatter plot of Y-STR vs Autosomal simulation A-scores, a perfect match between simulation and actual results would yield a point at the origin of the graph. The haplotree simulations for Kenyon as a son of John have the smallest Z-score vector of 0.9 and are therefore the best fit of the actual DNA data. This most likely haplotree, based on all of the DNA data and authenticated traditional genealogy data, is the outcome of this work and is shown in full detail in Figure 13. It is stressed that the other permutations of the haplotree shown in Figure 10 are should not be considered precluded by this analysis.

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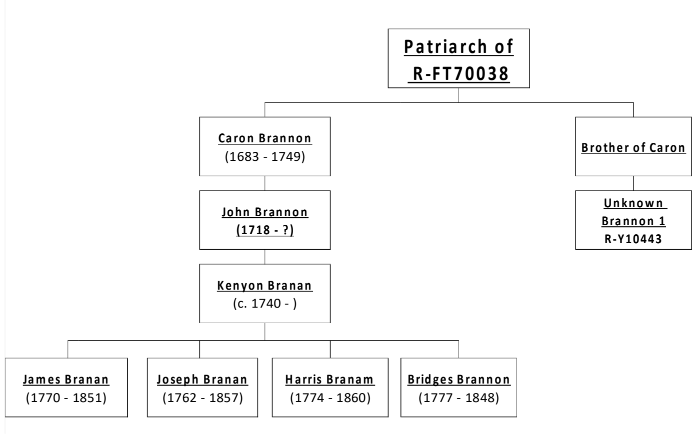
[31] Mutation Rates. International Society of Genetic Genealogy. https://drive.google.com/file/d/16LV9tBTXViPtNshnj_dxlTklCFutXqD2: Accessed 27 November 2022.

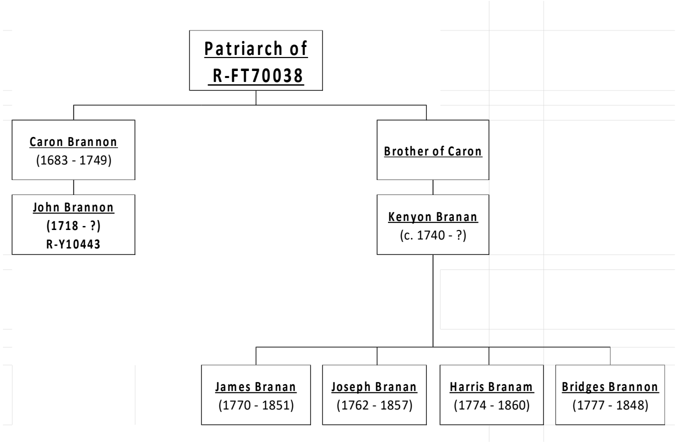
[32] How and why of running a simulation in excel. Adam. https://www.spreadsheetweb.com/simulation-in-excel/: accessed August 10, 2022.

Figure 10: Candidate haplotrees for Monte Carlo simulation analysis

Option 1 – John is Kenyon's Father



Option 2 – John is Y10443



Option 3 – Six Lines of Brothers for Caron

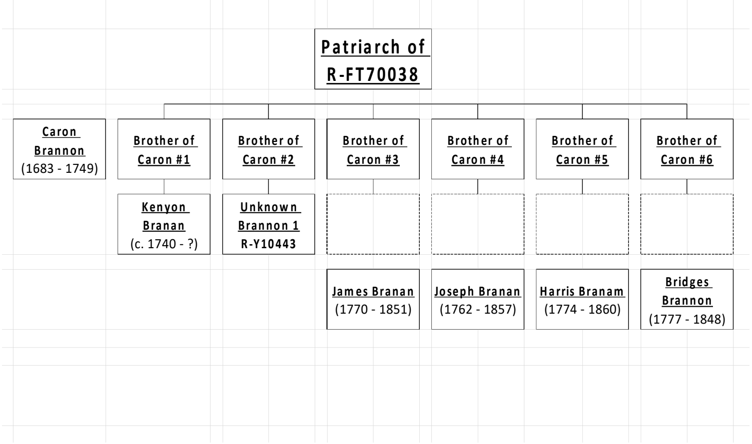
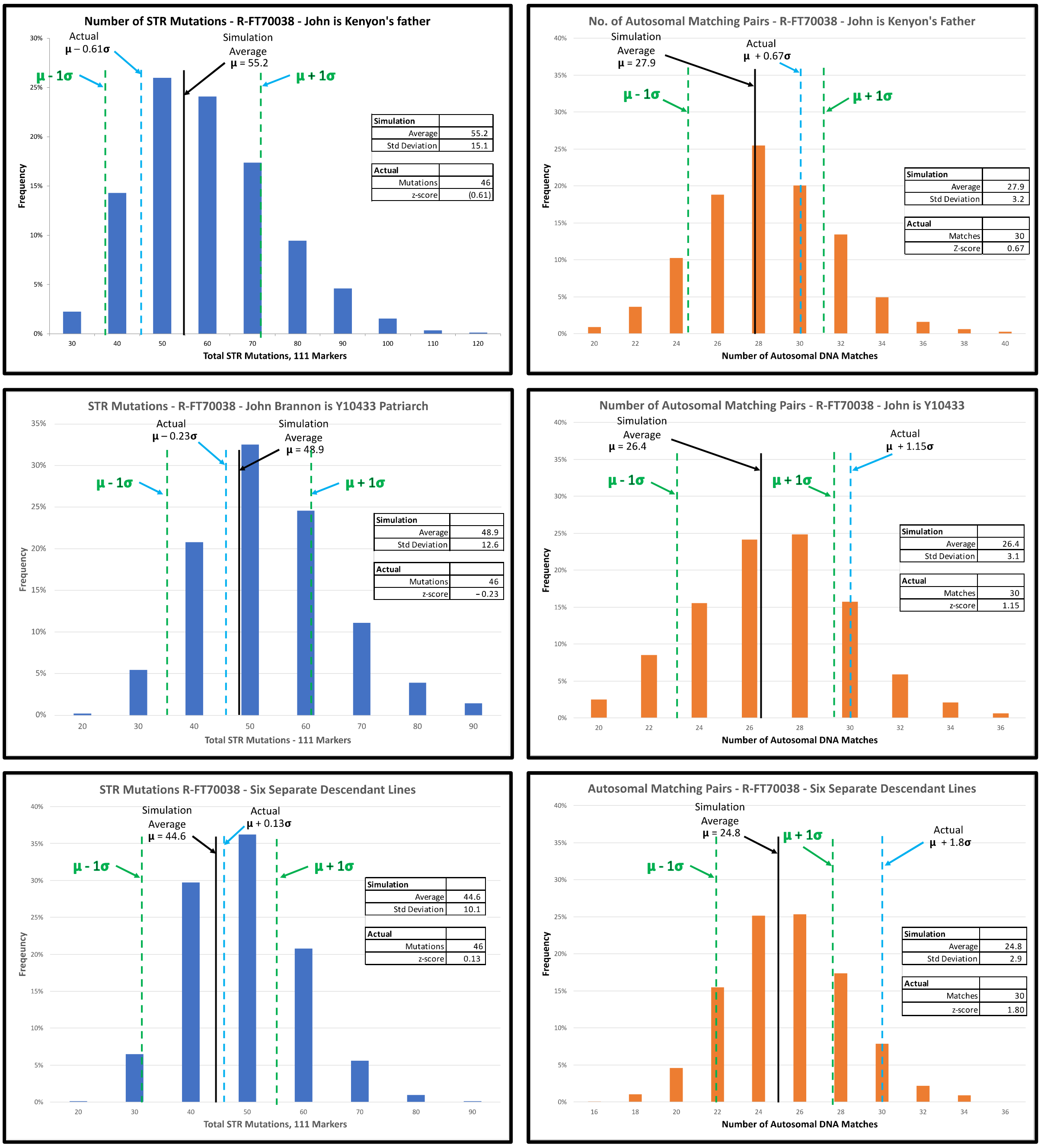


Figure 11: STR mutation and autosomal match simulations for candidate haplotrees



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The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

Figure 12: Statistical Assessment of three haplotrees favors Kenyon's descent through John Brannon

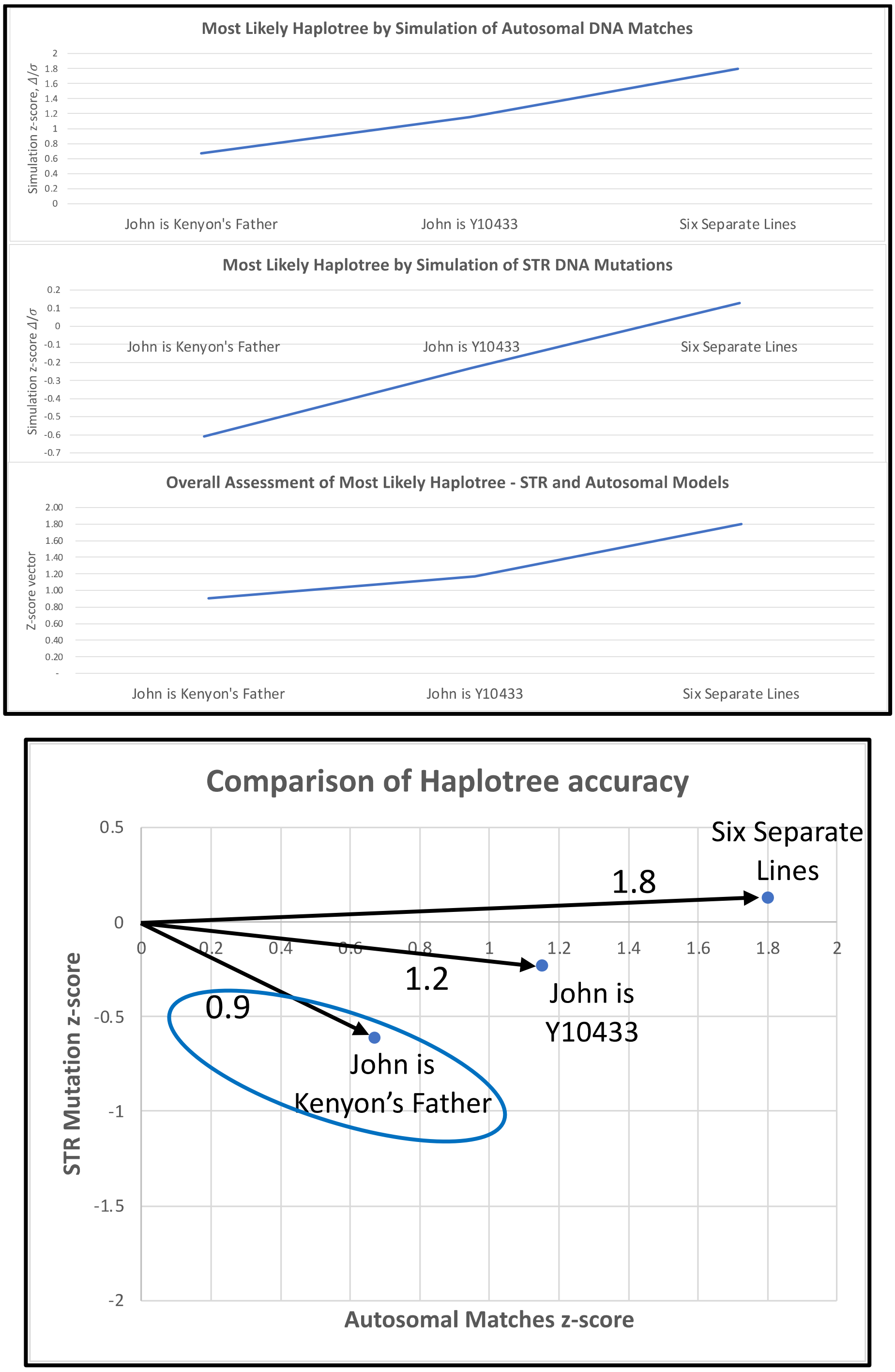
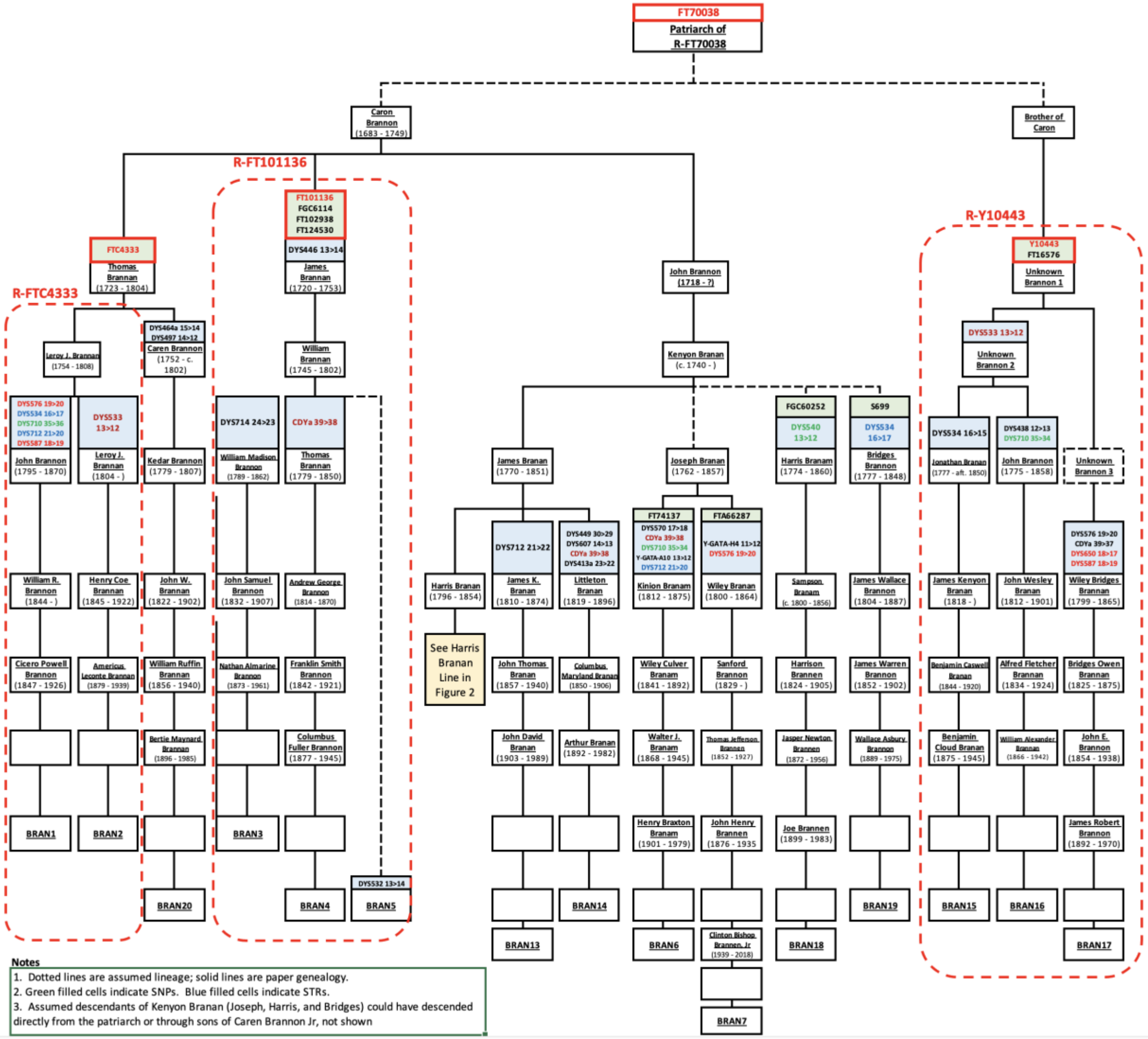


Figure 13 – Most likely R-FT70038 haplotree



Notes

1. Dotted lines are assumed lineage; solid lines are paper genealogy.
2. Green filled cells indicate SNPs. Blue filled cells indicate STRs.
3. Assumed descendants of Kenyon Branan (Joseph, Harris, and Bridges) could have descended directly from the patriarch or through sons of Caren Brannon Jr, not shown

Branan, J. (2023). A similar-sounding surname sequel: haplotype R-FT70038.
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

Part VI: The limits of similarly sounding surnames

Many of the BRAN lines have a long-standing identification with specific counties of Georgia in the United States. The R-FTC4333 haplogroup are the Gwinnett/Forsyth County BRANs. The R-FTB27810 BRANs and associated James Branan lines are of Wilkinson County. The R-Y10443 BRANs are of Henry County. The Joseph Branan line (SNPs FT74137 and FTA66287) are of Putnam County. Another BRAN line in Georgia is those of Bulloch County.

No Bulloch County BRANs participated in this project, but some relevant information was found. Several Bulloch County BRANs autosomally match BRAN6 of Putnam County. Like many of the lines in the project, the Bulloch County paper genealogy was strong back to the early 1800s but with no apparent paternal line link to members of R-FT70038. Unlike the R-FT70038 project participants, the Bulloch County BRANs most distant relatives were three brothers who immigrated together to Bulloch County from Ireland[33]. It was found that a Bulloch County BRAN who has previously had his Y-DNA tested belongs to Haplogroup R-M222 … FT429823[34]. Hence, not all longstanding BRAN families in Georgia are members of R-FT70038. A map depicting the associations of George BRAN haplogroups is shown in Figure 14.

Conclusions

Caron Brannon (b. c. 1683) is the MDKA of haplogroup R-FT70038 but is unlikely to have been the patriarch. DNA analysis suggests that the patriarch of R-FT70038 is most likely Caron's unnamed father or grandfather. NGS testing validated reported, albeit imperfectly documented, paper genealogy for two of the sons of Caron Brannon (Thomas and James). James is the patriarch of a new sub-haplogroup, R-FT101336. Thomas's son Leroy is the patriarch of a new sub-haplogroup, R-FTC4333.

Kenyon Branan's widely speculated fatherhood of Jonathan Branan and Wiley Bridges Brannan is disproved and a new sub-haplogroup R-Y10443 was discovered as the actual description of Jonathan and Wiley's line. The specific Y-DNA data generated in the testing is silent regarding Joseph Branan's speculated descendant relationship to Kenyon. Likewise, the Y-DNA data generated from the individual project participants is silent regarding a direct descent relationship for Kenyon from Caron Brannon.

However, the combined autosomal and Y-DNA data for all of the test results does restrict greatly the number of possible haplotrees describing the connection of the tested lines' MDKAs. Monte Carlo simulation of the possible haplotrees considering combined STR-mutation results and autosomal matched pairs across the whole haplogroup was used to identify the most likely haplotree. This best fit haplotree from the combined actual DNA results placed Kenyon Branan as the son of Caron Brannon's eldest son John. This analysis also placed the R-Y10443 sub-haplogroup descending through an unnamed brother of Caron

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[33] Kenan, Alvaretta (1967). The Kenan Family and some allied families of the compiler and publisher. Statesboro, Georgia: J.S Kenan II.

[34] Greer project. https://www.familytreedna.com/public/GREER?iframe=yresults: accessed 19 February 2023.

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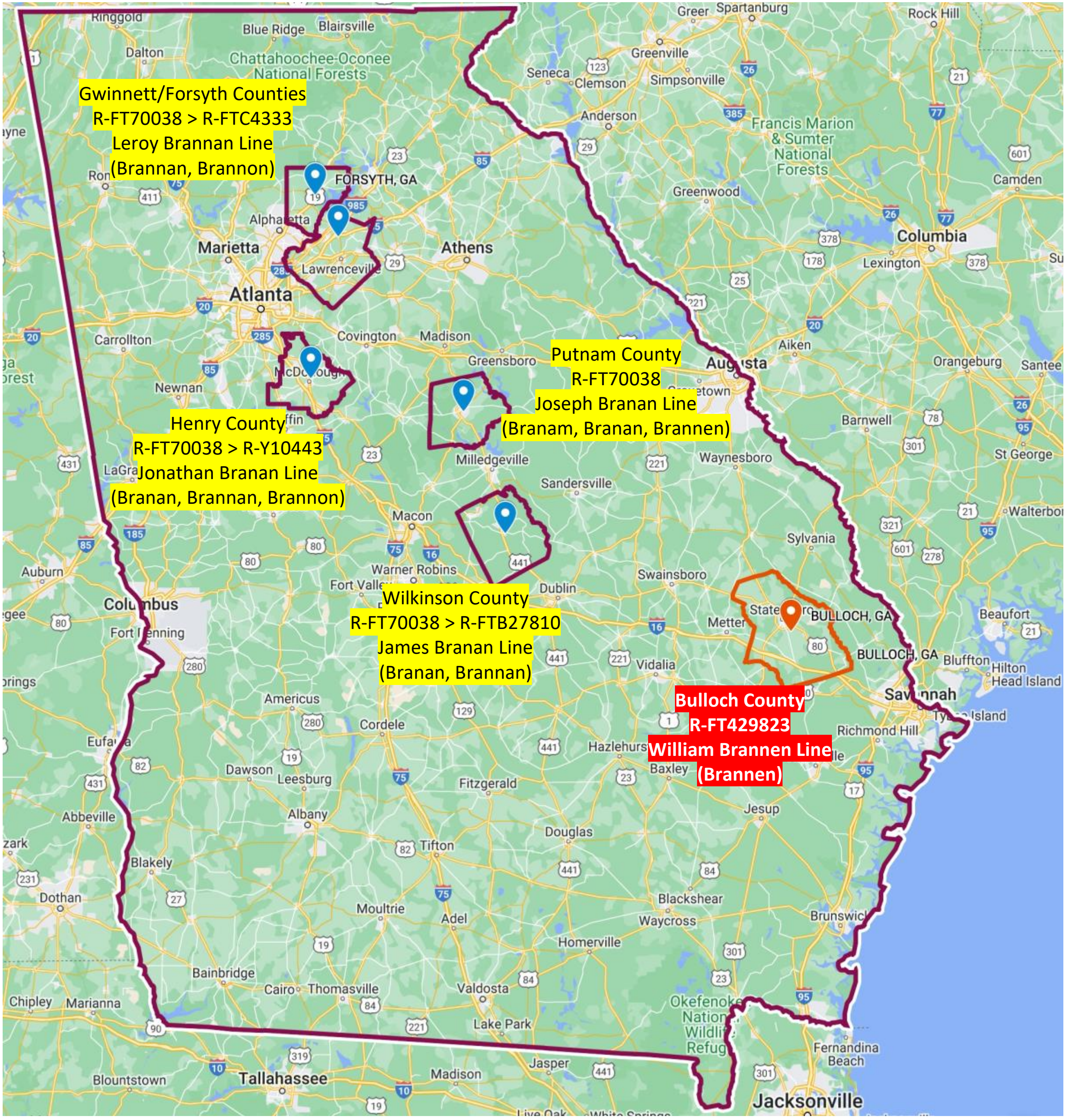
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

Brannon. The combination of DNA data and simulation analysis allowed us to sketch a timeline and haplotree that supports the strong genealogies, disproves the speculative ones, and provides insight into the most likely relationships to have occurred beyond the paper trail.

Figure 14: Georgia BRANs by county and haplotype



Acknowledgements

The author gratefully acknowledges the roles that Mike Fitzpatrick and Ian Fitzpatrick played in this article. Their initial hypothesis was the genesis of this project, and their expert guidance, encouragement and review of this work were central to its completion. The author also thanks the twenty-one BRAN project participants and in some cases their relations who authorized the DNA testing that allowed this work to progress to conclusion.

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The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 7 June 2023

A similar-sounding surnames sequel: haplogroup R-FT70038

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Genealogist, Billerica, MA, USA

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Appendices

1. Y-STR mutations matrix
2. Autosomal match matrix
3. Modifying the Y-SNP/STR haplotree by optimum use of autosomal match data
4. Monte Carlo simulation – Y-STR mutations
5. Monte Carlo simulation – number of autosomal matches

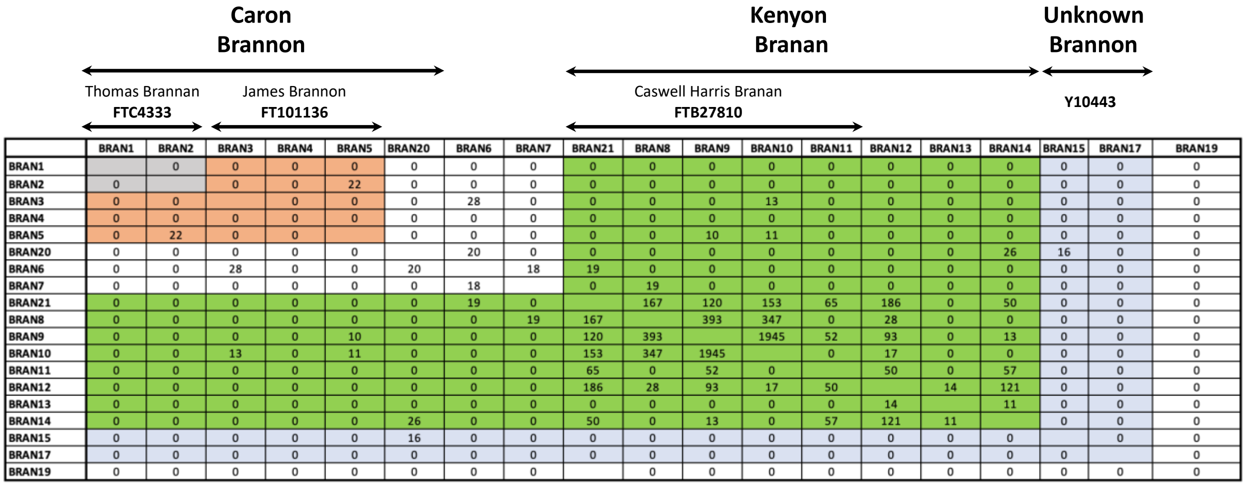
Branan, J. (2023). A similar-sounding surname sequel: haplotype R-FT70038.
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 9 June 2023

Appendix 1: Y-STR mutation summary matrix

	Project Participant - BRAN																					Mutations
STR Marker	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**Total Derived**
DYS447	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-1	1
DYS449	0	0	0	0	0	0	0	0	0	0	0	0	0	-1	0	0	0	0	0	0	0	1
DYS464a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-1	0	1
Y-GATA-H4	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
DYS607	0	0	0	0	0	0	0	0	0	0	0	0	0	-1	0	0	0	0	0	0	0	1
DYS576	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	3
DYS570	0	0	0	0	0	1	0	0	0	-1	0	0	0	0	0	0	0	0	0	0	0	2
CDYa	0	0	0	-1	0	-1	0	0	0	0	0	0	0	-1	0	0	-2	0	0	0	0	4
CDYb	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1
DYS438	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
DYS413a	0	0	0	0	0	0	0	0	0	0	0	0	0	-1	0	0	0	0	0	0	0	1
DYS534	1	0	0	0	0	0	0	1	1	1	0	0	0	0	-1	0	0	0	1	0	1	7
DYS446	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
DYS710	1	0	0	0	0	-1	0	0	0	0	0	0	0	0	0	-1	0	0	0	0	0	3
DYS540	0	0	0	0	0	0	0	0	0	0	0	-1	0	0	0	0	0	-1	0	0	0	2
DYS714	0	0	-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
DYS533	0	-1	0	0	0	0	0	0	0	0	0	0	0	0	-1	-1	0	0	0	0	0	3
Y-GATA-A10	0	0	0	0	0	-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
DYS712	-1	0	0	0	0	-1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	3
DYS650	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-1	0	0	0	0	1
DYS532	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
DYS635	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
DYS587	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
DYS497	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-2	0	1
Total Derived	5	1	2	2	2	5	2	2	1	2	0	1	1	4	2	3	4	1	1	2	3	46

Branan, J. (2023). A similar-sounding surname sequel: haplotype R-FT70038.
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 9 June 2023

Appendix 2: autosomal match matrix



Caron Brannon

Thomas Brannan **FTC4333**

James Brannon **FT101136**

Kenyon Branan

Caswell Harris Branan **FTB27810**

Unknown Brannon

Y10443

	BRAN1	BRAN2	BRAN3	BRAN4	BRAN5	BRAN20	BRAN6	BRAN7	BRAN21	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14	BRAN15	BRAN17	BRAN19
BRAN1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRAN2	0		0	0	22	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRAN3	0	0		0	0	0	28	0	0	0	0	13	0	0	0	0	0	0	0
BRAN4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRAN5	0	22	0	0		0	0	0	0	0	10	11	0	0	0	0	0	0	0
BRAN20	0	0	0	0	0		20	0	0	0	0	0	0	0	0	26	16	0	0
BRAN6	0	0	28	0	0	20		18	19	0	0	0	0	0	0	0	0	0	0
BRAN7	0	0	0	0	0	0	18		0	19	0	0	0	0	0	0	0	0	0
BRAN21	0	0	0	0	0	0	19	0		167	120	153	65	186	0	50	0	0	0
BRAN8	0	0	0	0	0	0	0	19	167		393	347	0	28	0	0	0	0	0
BRAN9	0	0	0	0	10	0	0	0	120	393		1945	52	93	0	13	0	0	0
BRAN10	0	0	13	0	11	0	0	0	153	347	1945		0	17	0	0	0	0	0
BRAN11	0	0	0	0	0	0	0	0	65	0	52	0		50	0	57	0	0	0
BRAN12	0	0	0	0	0	0	0	0	186	28	93	17	50		14	121	0	0	0
BRAN13	0	0	0	0	0	0	0	0	0	0	0	0	0	14		11	0	0	0
BRAN14	0	0	0	0	0	26	0	0	50	0	13	0	57	121	11		0	0	0
BRAN15	0	0	0	0	0	16	0	0	0	0	0	0	0	0	0	0		0	0
BRAN17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0
BRAN19	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0

Appendix 3: Modifying the Y-SNP/STR haplotree by optimum use of autosomal match data

In Figure 8C we presented a Haplotree which modified the Y-DNA Haplotree via the use of autosomal match data. In this Appendix we describe the approach and then discuss merits and shortcomings of that optimization of the autosomal match data. We will discuss the algorithm as applied to BRAN8 through BRAN14, which is the most complex network in the set. The other sets were optimized through inspection as previously described. For BRAN8 through BRAN14:

1. We start with the autosomal match matrix, segment length of shared DNA in cM from Figure 3.
2. We translate the shared segment lengths to most likely relationships from the data in Figure 2.
3. We use Donnelly's formulas for calculating the relevant matched pair relationships in our set and rewrite the matrix using that transformation[28]. This transformation has the utility of linearizing segment length versus number of separating generations.
   a. $k = 2s + t$ for sth cousins t times removed
   b. $k = n + 1$ for (great)^n uncle (uncle n times removed)
4. The resulting matrix is defined as the optimum autosomal set A, and is described the sum of k values above the diagonal:

$$S^{\Delta} = \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} f\left(i, j\right)$$

5. We seek a haplotree with a thusly transformed matrix, B, with k approaching the optimum autosomal set's k value. We define tree error for matrix B:

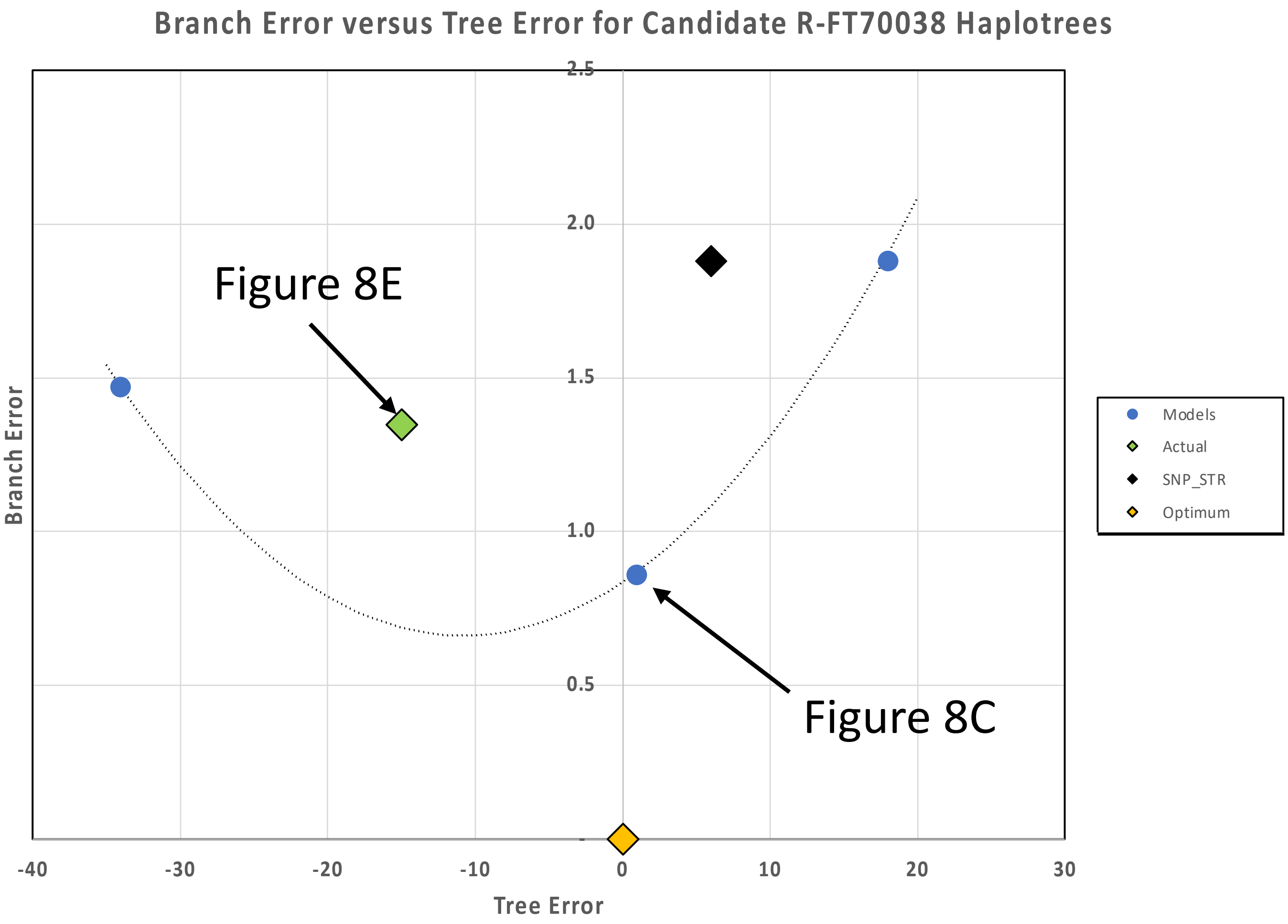
   Tree Error = $k_B - k_A$

6. We constrain the solution sets of haplotrees to adhere to the Y-SNP/STR tree, i.e., the para-haplotree members BRAN 12-14 will always have a more distant MRCA than the R-FT27810 members.
7. We also seek a haplotree with each autosomal pair k value as close as possible to the corresponding k value in the optimum autosomal set. We define Branch Error for the matrix B relative to matrix A, both n x n sized matrices:

$$\text{Branch Error} = \frac{\sum_{i=1}^{i=n}\sum_{j=1}^{j=n}\left(|k_{A(i,j)} - k_{B(i,j)}|\right)}{n^2}$$

Figure A is a graph of the resulting branch error versus tree error for five candidate trees. The Y-SNP/STR haplotree from Figure 8B is farther away from the optimum haplotree A than the tree constructed to optimize autosomal match results. The overall k-value of the Y-SNP/STR haplotree matches the optimum tree's total k-value quite well. However, many of its matched pairs are high above or high below the optimum case, driving large deltas in individual pairs. One of the three constructed trees is somewhat closer to the optimum tree than the actual tree based on Figure 8E, illustrating the natural variability. The full algorithm, including development of the tree and branch error values for the Y-SNP/STR haplotree is shown in Figure B and Figure C as an example.

Figure A: branch error versus tree error – autosomal data from the James Branan descendants



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The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 9 June 2023

The merit of this approach is that haplotree candidates can be compared objectively versus a standard on two dimensions: tree error, which is overall coverage of the space, roughly correlating with number of generations, and branch error, which measures how well the tree fits each and every matched pair. There are at least two shortcomings of this method, both associated with the definition of the optimum tree.

The first shortcoming is that the declaration of the optimum tree is based solely on the shared centimorgan project's statistics which are silent on the impact of 'no match' findings. The second shortcoming is that transforming a shared centimorgan finding into a specific relationship has ambiguity (e.g., should one assign a 13 cM match to a 5C3R or a 6C2R relationship?) and also ignores the variation reported in the Bettinger data.

British statistician George Box stated, 'all models are wrong, but some are useful.' The usefulness of this model is to suggest that eleven generations in the haplotree, not eight generations best fits the available data.

Figure B: Development of tree error for Y-SNP/STR tree

Development of Optimum Autosomal Tree k-value

Shared Autosomal segments, centimorgans

	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14
BRAN8		393	347	0	28	0	0
BRAN9	393		1945	52	93	0	13
BRAN10	347	1945		0	17	0	0
BRAN11	0	52	0		50	0	57
BRAN12	28	93	17	50		14	121
BRAN13	0	0	0	0	14		11
BRAN14	0	13	0	57	121	11	

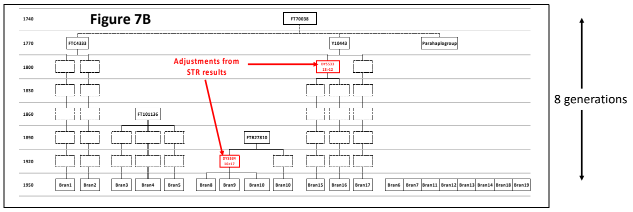
Most likely relationship

	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14
BRAN8		1C1R	!C!R		4C1R		
BRAN9	1C1R		U	3C1R	3C		6C2R
BRAN10	!C!R	U			6C		
BRAN11		3C1R			3C1R		3C1R
BRAN12	4C1R	3C	6C	3C1R		7C	2C1R
BRAN13				0	7C		8C
BRAN14		6C2R		3C1R	2C1R	8C	

Relatedness, k-value

	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14	K Total
BRAN8		3	3		9			15
BRAN9	3		1	7	6		14	28
BRAN10	3	1			12			12
BRAN11		7			7		7	14
BRAN12	9	6	12	7		14	5	19
BRAN13					14		16	16
BRAN14		14		7	5	16		
								104

Development Branch Error for SNP/STR based Haplotree



SNP/STR Matrix

	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14
BRAN8		B	B		6C		
BRAN9	B		B	1C	6C		6C
BRAN10	B	B			6C		
BRAN11		1C			6C		6C
BRAN12	6C	6C	6C	6C		6C	6C
BRAN13					6C		6C
BRAN14		6C		6C	6C	6C	

K - Figure 7B

	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14	K Total
BRAN8		0	0		12			12
BRAN9	0		0	2	12		12	26
BRAN10	0	0			12			12
BRAN11		2			12		12	24
BRAN12	12	12	12	12		12	12	24
BRAN13					12		12	12
BRAN14		12		12	12	12		
								110

Tree Error = 110 – 104 = 6

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The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 9 June 2023

Figure C – Development of branch error for Y-SNP/STR Tree

$$\frac{\sum_{i=1}^{i=n}\sum_{j=1}^{j=n}\left(\left|k_{A(i,j)} - k_{B(i,j)}\right|\right)}{n^2}$$

	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14
BRAN8		3	3		9		
BRAN9	3		1	7	6		14
BRAN10	3	1			12		
BRAN11		7			7		7
BRAN12	9	6	12	7		14	5
BRAN13					14		16
BRAN14		14		7	5	16	

$-$

	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14
BRAN8		0	0		12		
BRAN9	0		0	2	12		12
BRAN10	0	0			12		
BRAN11		2			12		12
BRAN12	12	12	12	12		12	12
BRAN13					12		12
BRAN14		12		12	12	12	

$(7)^2$

$=$

	BRAN8	BRAN9	BRAN10	BRAN11	BRAN12	BRAN13	BRAN14
BRAN8	0	3	3	0	3	0	0
BRAN9	3	0	1	5	6	0	2
BRAN10	3	1	0	0	0	0	0
BRAN11	0	5	0	0	5	0	5
BRAN12	3	6	0	5	0	2	7
BRAN13	0	0	0	0	2	0	4
BRAN14	0	2	0	5	7	4	0

49

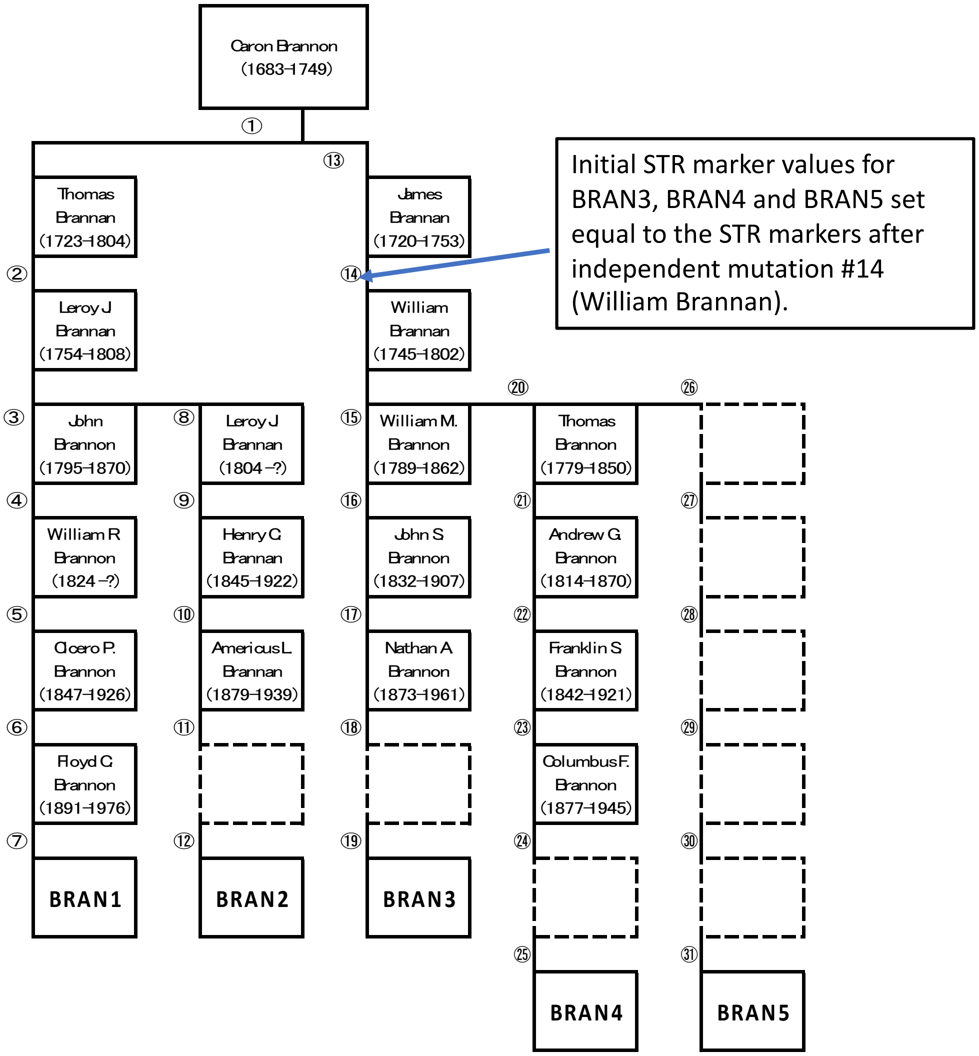
$$= \frac{(3+3+3+3+1+5+6+2+3+1+5+5+5+3+6+5+2+7+2+4+2+5+7+4)}{49}$$

$$= 1.88$$

Appendix 4: Y-STR Monte Carlo simulation

Each generation represents know mutation opportunities on each of 111 STR markers. Figure D illustrates a haplotree with 31 mutation opportunities. The most likely haplotree in Figure 13 has 125 total mutation opportunities, so each run of the simulation calculates 125 generationally sequential mutation opportunities for each of the 111 markers. A 2000-run simulation was performed in Microsoft Excel using the random number generator function, RAND(), for each mutation opportunity. In Figure 20, as an example, the BRAN 1 and BRAN3 lines are simulated with initial values for each Y-STR marker in the initial generation. All other BRAN simulations, BRAN2, BRAN4 and BRAN5 take their initial values from the appropriate generation of the simulations for BRAN1 and BRAN2. In our models we used 'zero' as the modal value for the Y-STR marker.

Figure D – Technique for Simulating IBD Mutations



Initial STR marker values for BRAN3, BRAN4 and BRAN5 set equal to the STR markers after independent mutation #14 (William Brannan).

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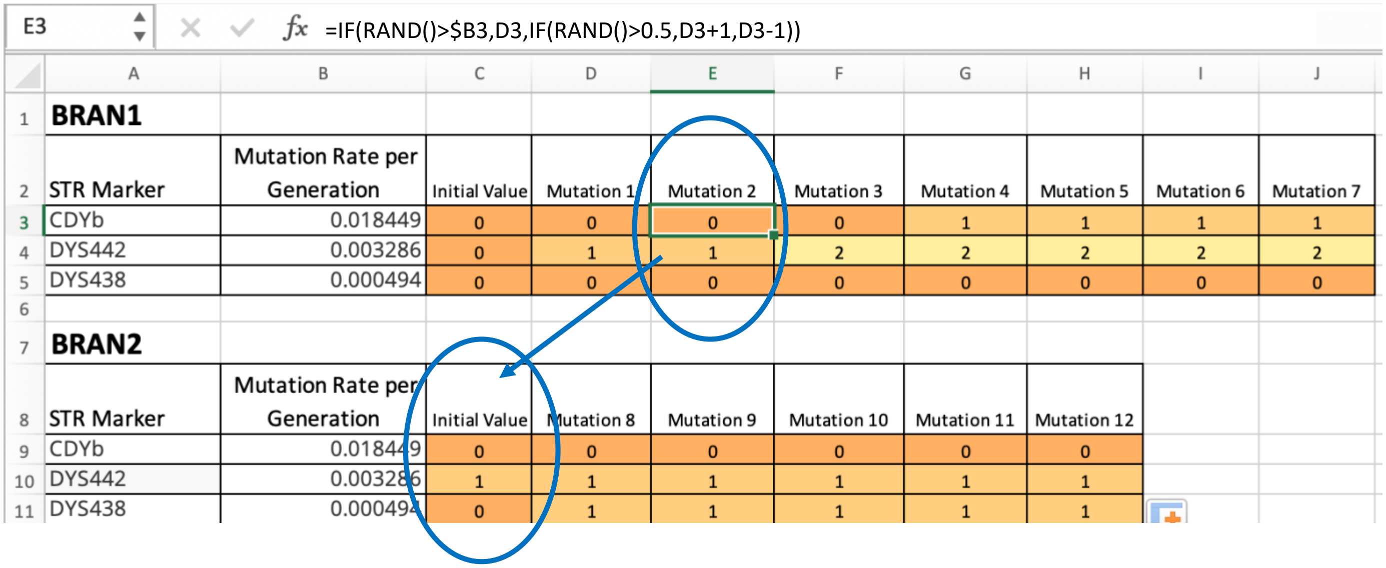
The Journal of the Fitzpatrick Clan Society 4, 11-44. doi:10.48151/fitzpatrickclansociety01323, Ver1, 9 June 2023

Figure E illustrates in more detail the simple simulation based on a small portion of the tree shown in Figure D. The mutation formula for cell E3 references the mutation rate for the Y-STR Marker CDYb (0.018449 per generation) and returns cell D3 marker value for all random numbers > 0.018449. If the random number generated is <0.018449 then the equation increases or decreases the Y-STR marker value by 1. In all cases, BRAN2's initial values for Y-STR markers are set equal to BRAN1's mutation #2 result (Leroy J Brannan). In this example for CDYb, BRAN1 has a mutation in mutation #4, but BRAN2 does not. For DYS442, BRAN1 has a mutation in mutation #1 and mutation #3 – the value of the marker after mutation #2 is 1 which is passed along to BRAN2 as the initial value of the marker. Note that BRAN1's mutation #3 change has no impact on BRAN2. For DYS438, BRAN2's initial value changes in mutation #8, while BRAN1 has no mutation.

Figure E – Equations for Monte Carlo simulation of Y-STR mutations in R-FT70038 haplotree



E3 =IF(RAND()>$B3,D3,IF(RAND()>0.5,D3+1,D3-1))

BRAN1

STR Marker	Mutation Rate per Generation	Initial Value	Mutation 1	Mutation 2	Mutation 3	Mutation 4	Mutation 5	Mutation 6	Mutation 7
CDYb	0.018449	0	0	0	0	1	1	1	1
DYS442	0.003286	0	1	1	2	2	2	2	2
DYS438	0.000494	0	0	0	0	0	0	0	0

BRAN2

STR Marker	Mutation Rate per Generation	Initial Value	Mutation 8	Mutation 9	Mutation 10	Mutation 11	Mutation 12
CDYb	0.018449	0	0	0	0	0	0
DYS442	0.003286	1	1	1	1	1	1
DYS438	0.000494	0	1	1	1	1	1

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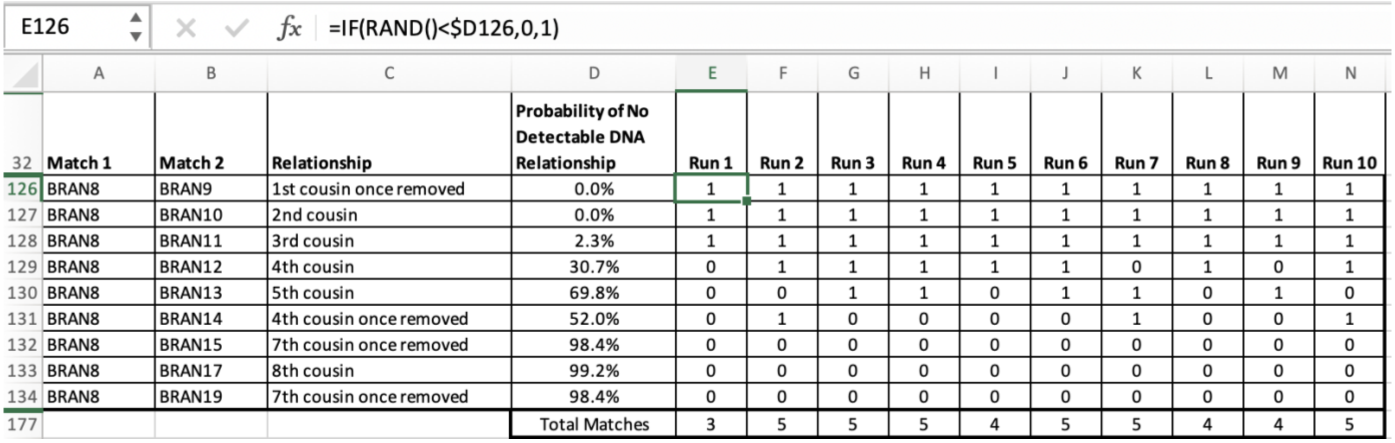
Appendix 5: Autosomal DNA Monte Carlo simulation

For any pair of individuals, there is a reported probability of no detectable shared DNA, as shown in Figure 2. Figure F shows as an example a match simulation created for BRAN8 versus a subset of members of the R-FT70038 Haplotree. As in our Y-STR Monte Carlo simulations reported in Appendix 4, we used the random number generator function in Microsoft Excel to determine if shared DNA would be detected for each pair in each run. For the ten runs shown for BRAN8 in Figure F, the number of autosomal matches ranged from three to five. The formula for the indicated cell E126 is visible as reference. This approach was expanded to encompass all 19 autosomal test results over 2000 runs of the model to generate the statistics reported in Figure 11 in the main text.

Figure F: Autosomal DNA assessment of number of matches for haplogroup members



=IF(RAND()<$D126,0,1)

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
32	**Match 1**	**Match 2**	**Relationship**	**Probability of No Detectable DNA Relationship**	**Run 1**	**Run 2**	**Run 3**	**Run 4**	**Run 5**	**Run 6**	**Run 7**	**Run 8**	**Run 9**	**Run 10**
126	BRAN8	BRAN9	1st cousin once removed	0.0%	1	1	1	1	1	1	1	1	1	1
127	BRAN8	BRAN10	2nd cousin	0.0%	1	1	1	1	1	1	1	1	1	1
128	BRAN8	BRAN11	3rd cousin	2.3%	1	1	1	1	1	1	1	1	1	1
129	BRAN8	BRAN12	4th cousin	30.7%	0	1	1	1	1	1	0	1	0	1
130	BRAN8	BRAN13	5th cousin	69.8%	0	0	1	1	0	1	1	0	1	0
131	BRAN8	BRAN14	4th cousin once removed	52.0%	0	1	0	0	0	0	1	0	0	1
132	BRAN8	BRAN15	7th cousin once removed	98.4%	0	0	0	0	0	0	0	0	0	0
133	BRAN8	BRAN17	8th cousin	99.2%	0	0	0	0	0	0	0	0	0	0
134	BRAN8	BRAN19	7th cousin once removed	98.4%	0	0	0	0	0	0	0	0	0	0
177				Total Matches	3	5	5	5	4	5	5	4	4	5

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