

Journal: [www.jogg.info](http://www.jogg.info)

Originally Published: Volume 12, Number 2 (Summer 2024)

Reference Number: 122.003

# Y-DNA-CONFIRMED DESCENDANTS OF DOCUMENTED 1600S IMMIGRANT HUBERT PETTY: COMPARISON OF THEIR PHYLOGENETIC HIERARCHY WITH THEIR PATRILINEAL FAMILY TREE

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# YDNA-CONFIRMED DESCENDANTS OF DOCUMENTED 1600S IMMIGRANT HUBERT PETTY: COMPARISON OF THEIR PHYLOGENETIC HIERARCHY WITH THEIR PATRILINEAL FAMILY TREE

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## Abstract

Documentation in support of immigrant Hubert Petty and his arrival in Colonial America in 1652, of his only son, Thomas Petty (1673-1750), and of Thomas's six sons, is presented. Conventional genealogical research on 26 members of the FTDNA Petty Surname Y-DNA Project is presented as evidence of their direct descent from Hubert Petty through his only son, Thomas, and one of three of Thomas's sons. Y-SNP test results are presented for assigning the Project members' most recent common ancestor, Thomas, their shared haplogroup, I-BY34474, and as confirmation of their interrelationships with one another. A conventional patrilineal descendant tree for Hubert Petty is merged with the corresponding haplotree in such a way as to allow the phylogenetic hierarchy of the members' genetic results to be clearly correlated with their conventional family tree structure. The use of the "Rule of Three" Y-DNA testing strategy in the selection of testers is presented, and its advantages are discussed.

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## Introduction

One of the lineages in the Family Tree DNA (FTDNA) Petty Surname Y-DNA Project ("Project") consists of the direct descendants of a 17th century English immigrant to Colonial America, Hubert Petty, which was determined roughly 50 years ago through extensive conventional genealogical research by late Project member James Winter Petty, AG (1948-2020). An FTDNA Big Y test in 2017 established James's haplogroup as I-BY34474. Around 2021 a concerted effort was begun to expand this portion of the Project from the roughly 15 members then sharing James's I-BY34474 haplogroup. Using Bill Wood's "Rule of Three" (Wood, 2019) to help identify and select new living descendants of Hubert Petty for Big Y-700 testing, we have now nearly doubled the number of participants who fall under the I-BY34474 haplogroup, and whose Y-SNP results have begun to reveal their phylogenetic hierarchy, genetically confirming specific levels of relatedness between one another and to their most recent common ancestor (MRCA), Hubert's only son, Thomas Petty. In conjunction with this study, conventional genealogical research was used to further document the pedigrees of 25 additional Big Y testers, and connect them to Hubert Petty.

This combination of Y-SNP genetic testing and conventional genealogical research – a classic application of Genetic Genealogy – has allowed us to achieve four important interim goals on the way to reaching our ultimate goal, which is to have our tree of known Hubert Petty descendants fully genetically characterized (see 'The Value of Full Genetic Characterization' in the Discussion section). These interim goals are: (1) establish likely generational connections between an early ancestor and his living descendants (using conventional genealogical research); (2) establish a hierarchy of ancestors' haplogroups through Y-SNP testing of multiple well-

documented descendants (using combined genetic testing and conventional genealogy); (3) confirm the biological connections between suspected, presumed, and even well-documented descendants and their early ancestors, as well as each other, through their Y-SNP test results (requires genetic testing); and (4) directly correlate the phylogenetic hierarchy of their genetic results with their conventional family tree structure (using combined genetic testing and conventional genealogy). This last point in particular provides a clear demonstration of the synergistic effect of combining the two methodologies, and coordinated colorization of both family tree and haplotree charts is used to enhance the visualization of this effect.

## Methods

### Conventional Genealogical Research

The defining genealogical research that led to the identification of Hubert Petty as the immigrant ancestor of the line of Pettys herein discussed was carried out in the late 1960s through the '70s by late professional genealogist and Project member James Winter Petty, AG (1948-2020), in accordance with standard genealogical research practices of that pre-internet period. Tax records, wills, land documents, and other primary sources were examined either as originals or facsimiles where they reside, or as microfilm/microfiche images of the originals located at the Family Search Library (formerly the Genealogical Society Library of the Church of Jesus Christ of Latter-day Saints) in Salt Lake City, Utah. Each of the ancestors in James's line from his father to Hubert Petty was thereby identified and documented.

Recent genealogical research on other branches of this line's family tree, performed largely in conjunction with this study and carried out by conventional methods utilizing online access to primary and secondary sources, has been used to identify and document the patrilineal ancestry of 25 additional members of the Project to Hubert Petty, through his only son Thomas (abt. 1673-1750, m. Catherine Garton), and one of three of Thomas and Catherine's six sons (Thomas, William or James).

### Y-DNA Testing and Results

All Y-DNA test kits used in this study (mainly Big Y-700 ("Big Y"), but also Y-37, Y-67, and Y-111), are genetic analysis products from Family Tree DNA ("FTDNA" (FTDNA, 2023)). After purchasing and receiving a Sample Kit, each tester returned his sample to FTDNA, where it was analyzed, and the results returned to the tester. When the testers joined the Petty Surname Project, their results became available to the Project administrator(s). Interpretation of the analysis results was assisted by applications provided on the FTDNA website, such as "Discover" (FTDNA-Discover, 2023), but is ultimately the authors. In the family tree chart images shown below, Big Y testers are identified by their anonymized FTDNA test kit number and by their FTDNA-designated haplogroup (RLP, 2024 "Designated" Haplogroup).

#### *Big Y Testers*

Prior to 2019 thirteen men had been identified through FTDNA's Big Y test results to fall under the I-BY34474 haplogroup; one of BY34474's subclades, BY120617, had been identified by that time as well. Since then, 16 additional Big Y testers have been shown to fall under the I-BY34474 haplogroup. (Of these 29 Big Y testers, only 26 are currently either active or deceased members of the Project. The results of resigned or otherwise inactive (other than deceased) members of the Petty Surname Project are not included in this paper's Figures, Results, or Discussion.) With these additional test results - many from "targeted" relatives (see [Genetic Testing](#)

Strategy: The Rule of Three in the next section and The Rule of Three in the Discussion section) - three levels of subclades below BY34474 have now been revealed, with the number of unique terminal SNPs having reached a total of 13. (The KEY in Fig. 1b will assist in visualizing the Levels, as well as the SNPs belonging to each. See also “Haplogroup Levels” in the Discussion section.)

## Genetic Testing Strategy: The Rule of Three

As originally presented (Wood, 2019), the Rule of Three describes its three Y-DNA testers as (#1) an initial Big Y tester, (#2) a close relative (brother, father/son, uncle/nephew, or 1<sup>st</sup> cousin), and (#3) a more distant relative (2<sup>nd</sup> or 3<sup>rd</sup> cousin or great uncle, or a 4<sup>th</sup> or greater cousin). It further describes the purpose of each tester’s results.

The first tester provides:

- (a) a list of SNPs and unnamed variants that are unique to one paternal profile
- (b) identifies SNPs/variants seen for the first time

The second tester’s results:

- (a) begin to build the Family Clade
- (b) can help to name any unnamed variants
- (c) begin to break up blocks of phylogenetic equivalents

The third tester’s results will:

- (a) confirm the results of the first tester
- (b) continue to break up blocks of equivalents

The possibility of extending the Rule to include more distant relatives (through more distant cousins) is alluded to (“Additional Big Y Candidates” (Wood, 2019, p. 15), and we’ve found this concept useful. Additionally, we have found slight modifications of the originally presented Rule, consisting of a re-worded #3 tester description and more clearly specified extensions, to be advantageous. Thus, testers #1 and #2 are as originally defined, but #3 would be selected from one of the next two generations (2<sup>nd</sup> or 3<sup>rd</sup> cousin, or similar generational relative such as grandfather or great uncle, if available). The first “extended” tester (#4) would be a 4<sup>th</sup> or 5<sup>th</sup> cousin. As such, his results would continue to break up further blocks of equivalents, but this tester’s results could alternatively provide the possibility of establishing a new genetic branch in the family tree, which would utilize the descendants of a brother of the original tester’s 2<sup>nd</sup> or 3<sup>rd</sup> great grandfather. Additional (extended) testers (#5 and beyond) may follow the same 2-generation pattern of more distant cousins to augment the original branch, or they may continue to build on the newly established branch (as just described). (For an older #1 tester, considering a grandchild or grandnephew, as for what might be considered a “#0” tester in an expanded Rule of Three, could be useful as well.)

## Average Interval Between Mutations

Although an average 3-generation interval between mutations (based on the long-term average for new mutations of around 75 years (YDNA Warehouse, n.d.), equating to roughly three average generations of 25 years each (RJ Wang, 2024)) is often assumed in genealogical studies, in this study, birth year and generational information from the Project’s members and their ancestors, combined with the FTDNA Time Tree’s (FTDNA Time Tree, 2023) very approximate Y-SNP origination estimates, are in closer agreement with a roughly 60 year and two average (30 year) generation interval between Y-SNP mutations over the roughly 300-year time span

of this study. (This additionally supports the 2-generation average interval implied in Wood's Rule of Three (op. cit.)) These values have provided a useful guideline for identifying and selecting those Project members' relatives whose Big Y test results would be most likely to provide greater help in the chronological resolution of equivalent SNPs in the branches of our Hubert Petty tree.

## Results

### Conventional Genealogy

#### *Identification of Hubert Petty as the Immigrant Ancestor of James Winter Petty*

Late Project member James Winter Petty, AG, was able to trace his own Petty family line back 9 generations to his immigrant ancestor, who he identified and documented as Hubert Patey/Patty/Petty. (These and other surname spellings have been encountered for Hubert in the older literature, though most of his recent descendants have settled on either "Petty" or "Pettesy"). James published much of his research in a quarterly newsletter he started in 1976 called *The Petty Papers*, and readily shared his findings with others researching this Petty lineage. In Vol. 1, No. 2 (Petty, 1976) James presented extensive details on the life of Hubert's only son, Thomas Petty (Gen 2 in the pedigree below), conclusively connecting him to Hubert, and providing documented evidence for his six sons and three daughters. These relationships had also been described in a May 1974 letter sent to a Petty researcher in Texas, Katherine Reynolds (almost exactly 50 years prior to the submission of this article for publication), and although the letter appeared in Ms. Reynolds' 4 volume treatise "The Petty Family," (Reynolds, 1976), James's findings were unfortunately not utilized in her published pedigree of this Petty family line (with the result of its not being entirely correct). In subsequent genealogical research, James was able to identify and document Hubert as his earliest New-World ancestor, and determine his entire Petty line as follows.

- Generation 1. **Hubert Petty** Bef. 1634 (Engl.) – 1687 (Col. VA), arr. Colonial Maryland 1652, m. (1) Rebecca (Unk.) bef. 1667, (2) Faith (Unk.) aft. 1673*
- Gen 2. **Thomas Petty** Abt. 1673 (Col. VA) – Abt. 1750 (Col. VA), m. C(K)atherine/Kat Garton abt. 1700*
- Gen 3. **James Petty** Aft. 1721 (Col. VA) – 1806 (SC), m. Martha Clanton Abt. 1742*
- Gen 4. **Thomas Petty** 1765 (Col. NC) – 1842 (TN), m. Jane Cowan Darwin 1789*
- Gen 5. **Robert Cowan Petty** 1812 (TN) – 1856 (OK Ter.), m. Margaret Jefferson Wells 1831*
- Gen 6. **Robert Thomas Petty** 1842 (TN – 1904 (UT), m. Julia Ann Wright 1865*
- Gen 7. **William Henry Petty** 1874 (UT Ter.) – 1964 (UT), m. Ann Eliza Beers 1900*
- Gen 8. **Russell Beers Petty** 1901 (UT) – 1968, (UT) m. Josephine Volker 1923*
- Gen 9. **Robert William Petty** 1924 (IL) – 2015 (UT), m. Medalou Winter 1946*
- Gen 10. **James Winter Petty** 1948 (CA) – 2020 (UT), m. Mary E. Gleason 1972*
- Gen 11. Living son of James W. Petty and Mary E. Petty. (Additional personal information withheld.)*
- Gen 12. [Members of this generation of James Winter Petty's line are withheld.]*

#### *Expanding Hubert Petty's Descendant Tree*

James Winter Petty's research determined that Hubert Petty had only one son, that Thomas married Catherine Garton, that Thomas and Catherine had six sons and three daughters, and that his own line descended from their next-to-youngest son, James (m. Martha Clanton) (op. cit.). Most Project members, however, though they were generally confident of who their more recent ancestors were, had not completed the extensive conventional genealogical research needed to identify and document their early ancestors, and could usually only speculate as to from which son, grandson, and great grandson of Thomas and Catherine Petty they descended. (Their Big Y test results proved that they descended from Thomas Petty (and by extension, his father Hubert), but these results could not (prior to this study) conclusively differentiate which of Thomas's sons (or their further descendants) they descended from) - which is critical for tying the Y-SNP test results unequivocally to the conventional genealogical results.

An effort was therefore made to complete the conventional genealogies of each of the Project's Big Y testers back to Thomas Petty, and their ancestors were thereby identified and documented. A family tree incorporating these genealogical results and including extensive documentation, has been created on Ancestry.com and is posted on the rlpetty1046 account (rlpetty1046 (2024)). (This publicly accessible but un-editable tree has been augmented with hundreds of additional identified and documented descendants of Hubert Petty as well.)

A graphic version of Hubert's descendant tree for the members of the Project and their ancestors, is shown in **Fig. 1d**, below. **Figures 1a, 1b**, and **1c** are three sections of the full tree: Left Side, Middle Portion (with KEY), and Right Side, respectively. Due to its size and complexity, the full tree image is provided mainly for its overall view, while the three sections allow the descendants' names and other information to be more readily visualized.

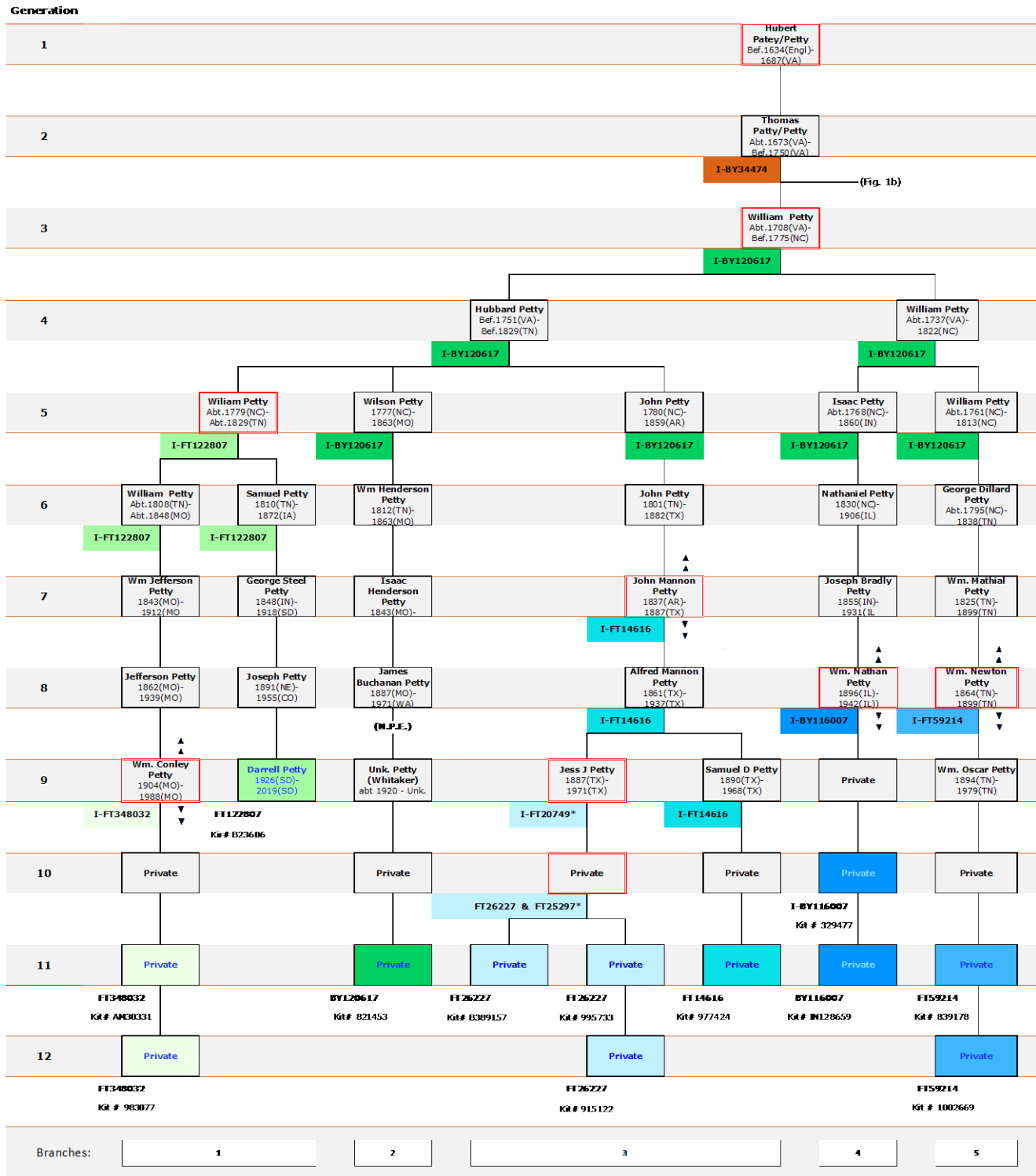
The vertical time scale of the tree is generation based. Hubert's descendants are identified by name, along with birth and death years and their respective locations (states), all in black font, except for the most recent two or three generations in most branches. These are usually labeled "Private," and their details not included due to privacy concerns; Y-SNP testers are labeled in **blue** font. For testers who are now deceased, their name and other details are shown, unless privacy is still considered a concern.

Genetic identifiers (haplogroups and SNPs) are incorporated into this tree as well. The names of the terminal SNPs measured in living individuals (some of whom are now deceased) are shown - with no background color - below the colored boxes representing the testers themselves. FTDNA Kit Numbers are provided (below the haplogroup name) as anonymized identification for each project member. The color used for each tester's box and/or information is associated with his measured haplogroup. Thus, the haplogroup names with colored backgrounds below deceased descendants with un-colored boxes, indicate that those men either inherited that haplogroup, or were individuals with whom that haplogroup is likely to have originated (see Assignment of Haplogroups in the **Discussion** section, below). The boxes representing the latter men additionally have a double red-colored outline. Note however that these assignments can be speculative (refer again to Assignment of Haplogroups in the **Discussion** section). Descendants without a haplogroup label are presumed to share the haplogroup of the most recent haplogroup-labeled ancestor above them.

In summary, Big Y testers are represented by colored boxes - labeled "Private" when the tester is still living - and have colorless-background SNP labels, while their ancestors are represented by uncolored boxes and colored-background haplogroup labels. Uncolored boxes labeled "Private" may be either living or deceased

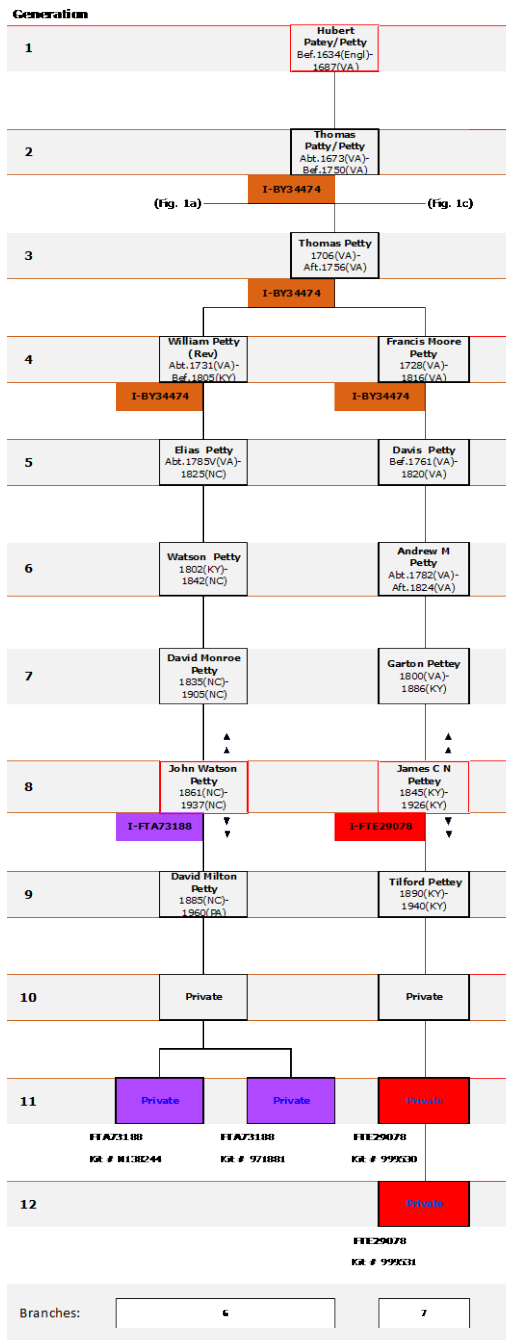
descendants of Hubert Petty, but will not have taken a Big Y test. The KEY (in Fig. 1b) provides, in addition to explanatory information, a ready reference as to which colors are associated with which haplogroups.

**Figure 1a.** Hubert Petty Descendant Tree (Left Side).



\* Equivalent SNPs: Assignment occurring in 'Rule of Three Limitations'

**Figure 1b.** Hubert Petty Descendant Tree (Middle Portion), with Key

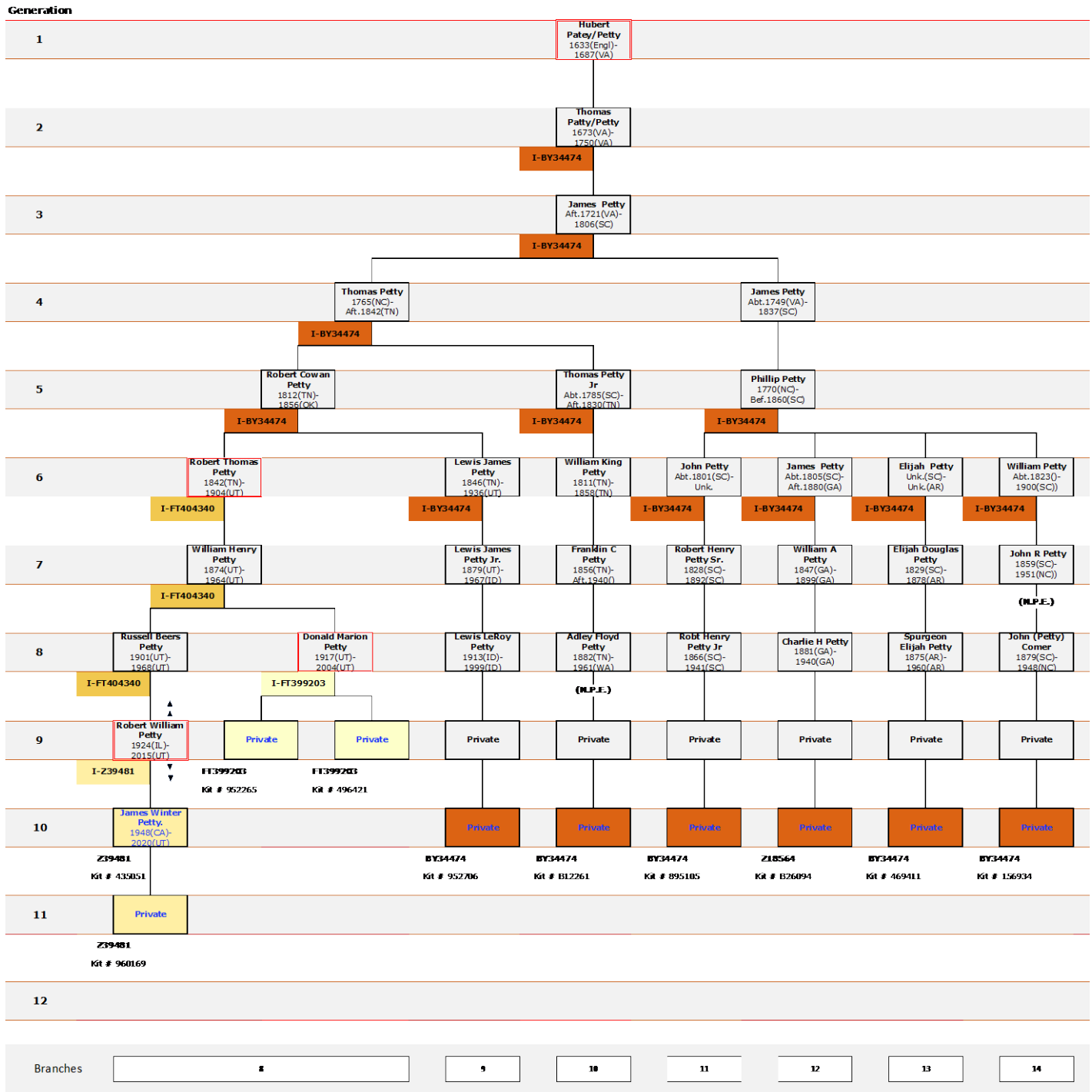


**KEY**

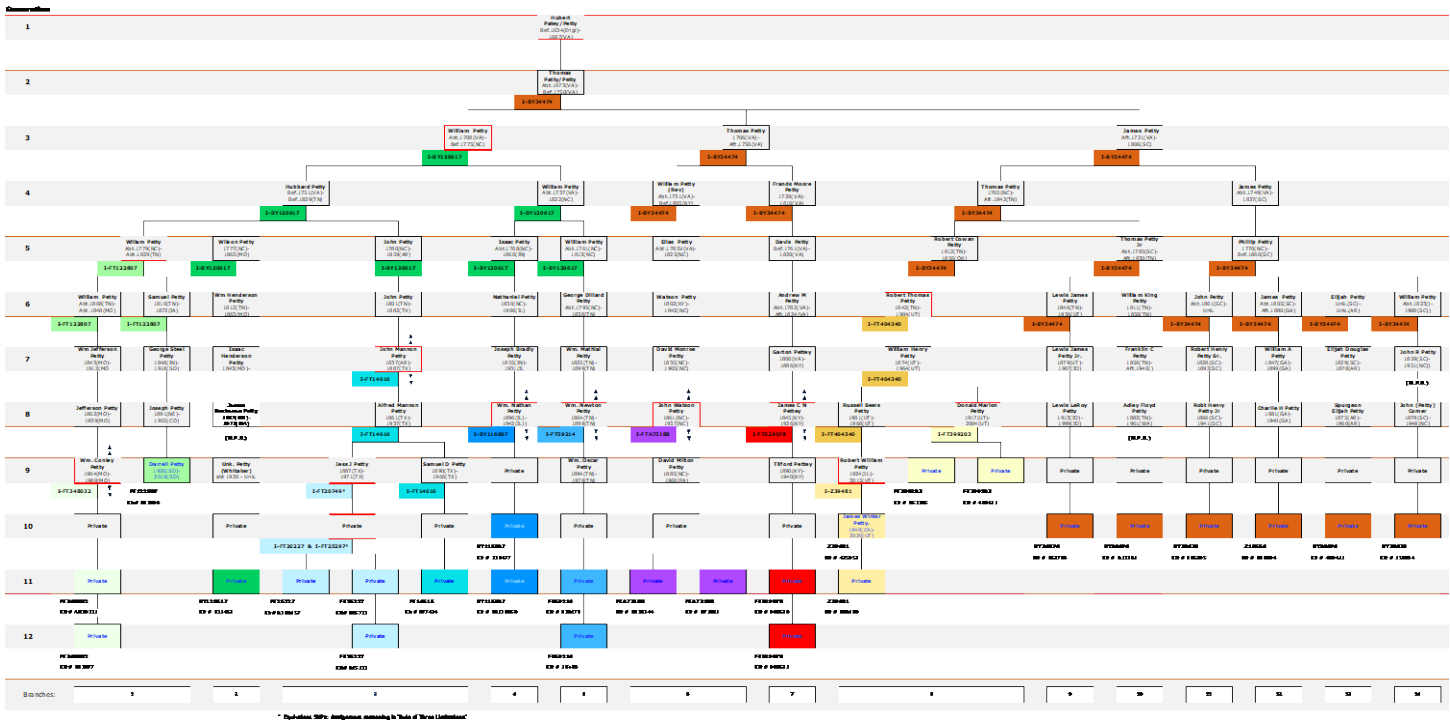
Box Contents	Haplog. Level	Box Shadings (Big Y Testers and Branch SNP Mutations/Haplogroups)							
Ancestor Name:	1	BY34474							
Birth Yr (State) - Death Yr (State)	2	BY120617		FTA73188	FTE29078	FT404340			
<b>Double Red Outline:</b> Possible ancestor with whom new haplogroup was formed	3	FT122807	FT14616	BY116007	FT59214	Z39481		FT399203	
	4	FT348032	FT26227						
<b>Haplogroup (Terminal SNP):</b> <i>Measured</i> if background is uncolored; <i>Presumed</i> if background is colored <b>Name in blue:</b> Y-DNA test performed, member of Petty Surname Project <b>Name in black:</b> Y-DNA test NOT performed (usually deceased ancestors)									



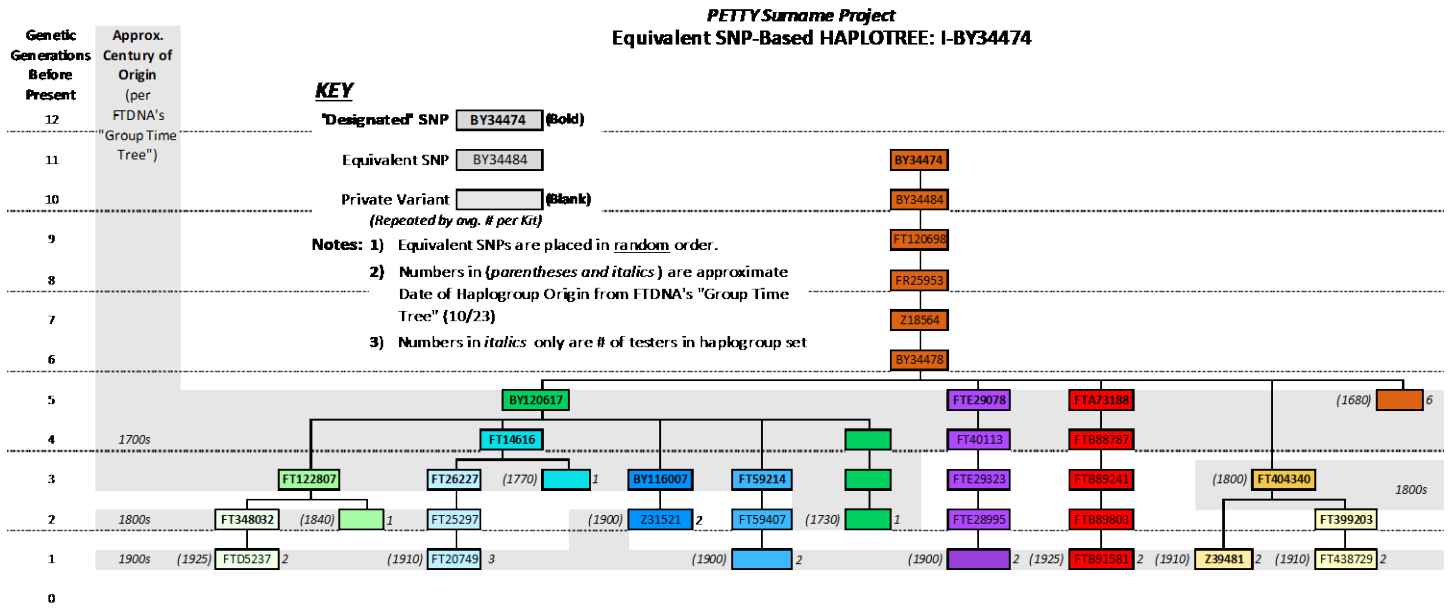
Figure 1c. Hubert Petty Descendant Tree (Right Side)



**Figure 1d.** Descendants of Hubert Petty (Full Tree). (Scaled for overall view, not intended for identification of individual descendants.) Box colors are correlated with genetic identifiers (haplogroups/SNPs): see KEY in Figure 1b, above. See also Figure 2, below.)



**Figure 2.** Haplotype of I-BY34474 and its subclades. (Haplotype colors are coordinated with box colors in Figures 1a, 1b, 1c and 1d.)



## Y-DNA Results.

### Y-STR Test Results

Y-STR results are much less precise than Y-SNP results in identifying relatively close interrelationships between testers, and other than in this section, are not used in this study. However, these results, which are provided in the lower-level Y-37, Y-67, and Y-111 tests (with the number indicating the number of STR values measured), can be useful in suggesting approximate relationships (with a higher number of measured STRs being more useful than a lower number), and are important as a lower-cost option for ruling out more distant connections. (Over 700 STR values are provided along with the SNP results in the Big Y-700 test.)

I-M253 is the ancient haplogroup (approximate origin around 4500 years ago) under which the Big Y testers fall, and is the “predicted” haplogroup of 6 testers in the Project who have only taken one of the lower-level tests (four having taken the Y-37 test, one the Y-67, and one the Y-111). Comparing the values of the first 37 measured STRs in the 26 Big Y testers, the 37 values match in all but five of the them. In each of these 5 testers, one of their 37 STR values differs from the mean of the value of the same STR for all the of the testers – which is referred to as a genetic difference (“GD”) of 1. This means that for the 26 men in this study, who range from close relatives to 9<sup>th</sup> cousins, their first 37 STR values are all either an exact match, or only one STR is different. In the six low-level testers, one has a GD of 1 in his first 37 STRs, and the rest are exact matches. Results from testing only 37 STRs are not considered highly reliable at predicting close relationships, but this comparison would suggest that all of these low-level testers are at least somewhat related to the Big Y testers, and that upgrading to Big Y should be encouraged.

The Y-67 and Y-111 testers also have a GD of 1, though with more STRs having been tested. Having especially the Y-111 tester upgrade to Big Y would appear to be even more likely to result in the identification of a new member of the Hubert Petty Clan.

### Haplotree

**Figure 2**, the “Haplotree of I-BY34474 and its subclades,” (above, loosely patterned after FTDNA’s Block Tree (FTDNA-BlockTree, 2023), but more compact, with a more pronounced tree structure), shows the branches of and interconnections between the haplogroups determined for Hubert Petty’s direct male descendants. As with the Block Tree, the vertical scale of the chart is in “genetic generations,” each of which is associated with a named haplogroup (either “designated” or phylogenetic equivalent) and/or un-named private variants. Shown on either side of the last equivalent SNP (or the last private variant if there are any, or the named terminal SNP if there are neither equivalent SNPs nor private variants) in a haplogroup set (with “set” referring to a group of associated designated and equivalent haplogroups and their accompanying private variants), are the estimated year of formation (FTDNA-TimeTree, 2023) for the most recent SNP of the set (left side), and the number of testers with the designated haplogroup (right side). Equivalent SNPs and average numbers of private variants per tester are represented as well.

At the first Level (see “Haplogroup Levels” in the Discussion section) *beneath* BY34474 (and its equivalent SNPs) (Level 2), four subclades have been identified, which, with their respective associated subclades, account for 20 of the Project’s 26 members. (The remaining 6 retain the BY34474 haplogroup). The four Level-2 subclades are BY120617 (12 members), FTA73188 (2 members), FTE29078 (2 members), and FT404340 (4 members). There are no additional subclades below FTA73188 and FTE29078, but FT403340 has two, and BY120617 has four. The

Level-3 subclades below BY120617 are FT122807, FT14616, FT59214, and BY116007. The Level-3 subclades below FT404340 are Z39481 and FT399203. Subclades FT122807 and FT14616 each have one additional (Level-4) subclade, consisting of haplogroups FT348032 and FT26227, respectively.

### *Rule of Three Results.*

We have (arbitrarily) defined a branch of the Hubert Petty descendant tree as the shortest series of at least 5 generations below a branching point, which provides a set of 14 logical and appropriate branches of from 5 to 9 generations. The Branch numbering is shown at the bottom of **Figures 1a-d**, and is used as the primary row in the **Branch Table** (shown under the 'Rule of Three Applied' in the Discussion section, where the Rule of Three results are discussed in detail.

## Discussion

### Visualizing Correlations Between the Descendant Tree and Haplotree

We've melded the portion of Hubert Petty's descendant tree derived from conventional genealogical research on specific branches of his tree, with its corresponding (though incomplete) haplotree derived from the Y-SNP testing of living members of those same specific branches, by incorporating genetic indicators from the haplotree into the descendant tree. The result is what we've referred to here as Hubert Petty's descendant tree (**Fig. 1d** and its sub-sections (**1a, b, and c**)), but the incorporated color-coded genetic indicators make it much more than just a descendant tree. In the combination tree – the layout of which is dictated by the genealogy, of course, but also by the genetics – makes it easy to follow the flow of genetic changes from the clan haplogroup to its subclades, to their subclades, and so on, by following the color changes, while still maintaining the family tree structure. By adding a graphic distinction between "normal" generations and those with which genetic mutations are likely to have occurred (boxes with double red-lined borders), the timing of those mutations can also be visualized and associated with specific sections of the branch. This layout also makes it very easy to recognize which branches are in most need of additional Y-SNP testing – and which generations (i.e., distance of cousins) would be likely choices to fulfill this need.

### Making the Connection between Surname Lineage and Haplogroup.

James Winter Petty's meticulous conventional genealogical research in the late 1960s and '70s (referenced and summarized above) uncovered and verified Hubert Petty as his immigrant (and earliest known) ancestor, and Thomas as Hubert's only son. In 2015, after many more years of conventional genealogical research on the Petty surname and Hubert Petty's origins, with the hope of being able to break through remaining brick walls, James took a Y-DNA test from FTDNA and joined the Petty Surname Project. Two years later he upgraded to their Big Y test, which revealed his terminal SNP to be BY34474. The 26 current members of this group, each descending from one of three of Thomas's six sons, all share the I-BY34474 haplogroup, confirming Thomas, born about 1673, as the most recent common ancestor of the group.

Other "sibling" SNPs of BY34474 (Y78878 and FT186158), subclades of their parent haplogroup (I-Y24458), are known to be associated with surnames other than Petty (RLP (2024)), increasing the likelihood of Hubert carrying the BY34474 SNP, though this is not possible to prove at this time. Nevertheless, we've chosen to designate I-BY34474 as the Hubert Petty "Clan haplogroup."

## Haplogroup Levels and the Phylogenetic Hierarchy of Y-SNP Results

(We have found it convenient to use “Levels” in discussing SNP hierarchy here, rather than the “upstream” and “downstream” terminology.)

(Please refer to the **KEY** in **Figure 1b** – “Hubert Petty Descendant Tree (Middle Portion), with Key” – for a table showing the Levels for the 12 Haplogroups determined from work related to this study.)

### *Level 1: I-BY34474*

I-BY34474, the Hubert Petty “Clan haplogroup,” is designated the *Level 1* haplogroup.

### *Levels 2 – 4*

With several early Big Y testers being (fortuitously) somewhat closely related to each other (in the 4<sup>th</sup> – 7<sup>th</sup> cousin range) – and also being (unknowingly) descendants of the same grandson of Hubert Petty (William, abt. 1708-1775) – the first subclade of BY34474 (I-BY120617) was revealed not long after the determination of BY34474 itself (see *Rule of Three Summary and Extension*, below), establishing *Level 2*. As the Rule of Three strategy was recognized and began to be applied (see below), *Level 2* saw a small increase in haplogroups, and an additional level was revealed (*Level 3*), with the number of haplogroups in that level beginning to increase significantly. Securing #3 testers for a few branches added more haplogroups to *Level 3*, and revealed two in *Level 4*.

## The Rule of Three

In early 2021 the Petty Surname Project was experiencing a surge in interest, and thanks to an effort to recruit more Big Y testers, the portion of the Project associated with the Hubert Petty Clan (those under the haplogroup I-BY34474) was growing especially quickly. About this same time, we became aware of the “Rule of Three,” (Wood, 2019) and began using it as a guide for identifying and targeting those relatives of Project members whose tests would be likely to provide the greatest help in further genetic characterization of their individual branches of the tree. (These would generally be relatives with documented placement in the family tree, whose Big Y test would be likely to chronologically resolve one of a branch’s equivalent haplogroups, and not just duplicate an earlier haplogroup.) Although strictly speaking we’ve only been able to fully apply this Rule in three of our branches thus far (see Branch Table, below), it’s instructive to include the single- and double-tester branches as well in discussing the use of the Rule and the results it has provided.

### *Rule of Three Applied*

As is readily seen in the **Figure 1a** and **1c** descendant tree charts, not all of our testers fit the “strict” definitions of the Rule of Three. Slight variations of the categories have been utilized, necessitated by difficulties in (a) locating individuals who fit the exact category definitions and/or (b) convincing them to test. Test results of the 26 members of this study have nevertheless allowed the identification of 12 haplogroups in three levels below the Clan haplogroup, as shown in the Branch Table, and described in the subsequent breakdown of the results by number of testers.

## Branch Table

Branch:	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Color(s):	Greens	Deep Grn	Turquoise	Dark Blue	Med. Blue	Purple	Red	Yellows	Brown	Brown	Brown	Brown	Brown	Brown
MRCA	William Petty	Wilson Petty	John Petty	Isaac Petty	William Petty	Ilias Petty	Francis M Petty	William H Petty	Lewis J Petty	Thomas Petty	John Petty	James Petty	Elijah Petty	William Petty
Measured SNPs:	FT122807 FT348032	<b>BY120617</b>	FT41616 FT26227	BY116007	FT59214	FTA73188	FTE29078	FT404340 FT399203 Z39481	<b>BY34474</b>	<b>BY34474</b>	<b>BY34474</b>	<b>BY34474</b>	<b>BY34474</b>	<b>BY34474</b>
RoT Testr(s):	1,2,3	1	1,2,3	1,2	1,2	1,2	1,2	1,2,3	1	1	1	1	1	1

(This Table is intended to be used in conjunction with the descendant tree charts, Figures 1a – 1d.)

1. *Single Testers.* For the seven branches with just a single tester (*tester #1* in the Rule of Three) – Branches 2 and 9 - 14 – the measured haplogroups would, due to the limited genetic resolution provided by a single tester, be expected to be a more distant (upper-level) haplogroup, and this is seen to be the case, with the tester’s early ancestor (at the top of his numbered branch) sharing his measured haplogroup. In Branches 9 - 14 this is the Clan haplogroup (I-BY34474), and in Branch 3 it’s a (still upper-level) subclade of the Clan haplogroup (I-BY120617).
2. *Two Testers.* In all the other seven Branches, a close relative of the initial tester (*tester #2* in the Rule of Three), at least, has taken the Big Y test. Of the four two-tester-only branches in this group of seven, in one pair (Branches 6 and 7) each branch has a subclade of the Clan haplogroup I-BY34474 (I-FTA73188 and I-FTE29078, respectively), and in the other pair (Branches 4 and 5) each branch has a subclade of the clan haplogroup’s subclade (I-BY120617): I-BY116007 and I-FT59214, respectively.

Interestingly, in these two pairs of branches (6/7 and 4/5), the fact that the measured haplogroups are pairs of subclades of the Clan Haplogroup (BY34474) and its own subclade (BY120617) (I-FTA73188 and I-FTE29078, and I-BY11607 and I-FT59214, respectively) means that the MRCA for each branch pair had to be the Clan Haplogroup and its immediate subclade, respectively. This in turn tells us that the MRCA of the double branch 4/5 must have inherited that SNP from his father, William Petty, Sr. (1708-1775), and since William Sr.’s father, Thomas Petty (as has been previously described) had haplogroup I-BY34474, the I-BY120617 haplogroup must have originated with William Sr. From similar reasoning, the son of Thomas Petty (1673-1750), Thomas Jr. (1706 – 1756), must have retained the Clan Haplogroup, and likely passed it on to his sons, Rev. William Petty and Francis Moore Petty. (See also the section [Assigning of Haplogroup Origins to Likely Ancestors](#), below.)

3. *Three Testers (+).* In the one three 3-tester *only* branch (Branch 1), the Rule of Three is followed closely, although the third tester is a 3<sup>rd</sup> cousin twice removed – probably more similar to a 4<sup>th</sup> or 5<sup>th</sup> cousin than 2<sup>nd</sup> or 3<sup>rd</sup>. The “plus” testers in Branches 3 and 8 are not #4 testers, but rather additional “close” relatives. The third tester in these two branches (completing the Rule of Three) is essentially a 2<sup>nd</sup> or 3<sup>rd</sup> cousin (or a 1<sup>st</sup> cousin once removed in the case of Branch 8). Additional subclades are revealed in these branches, with Branches 1 and 3 each having two new successive SNPs below BY120617 (FT122807 and FT348032, and FT41616 and FT26227, respectively). Branch 8, with its two pairs of close relatives, has revealed three new SNPs, one a subclade of BY34474 (FT404340), and two being subclades of FT404340 (FT399203 and Z39481).

## *Rule of Three Extensions*

Extending the Rule of Three beyond tester #3 can be used to identify additional haplogroups in a branch, up to the point where all equivalents and unnamed variants have been identified (the ultimate goal of our project – see **Introduction**). A 4<sup>th</sup> tester (#4), for example, would be a 4<sup>th</sup> or 5<sup>th</sup> cousin of the initial tester, and would be expected to continue breaking blocks of equivalents in that branch. Alternatively, the 4<sup>th</sup> tester could become the initial tester of a new branch of the tree. This could also apply to a 6<sup>th</sup> or 7<sup>th</sup> cousin, which was the case in Branches 4 and 5. Thus, when a 6<sup>th</sup> cousin of the father (of the father/son pair of testers) in Branch 5 was tested, a brother (Isaac Petty, 1768-1860) of the father's 4<sup>th</sup> great grandfather (William Petty, 1761-1813) became the head of that cousin's branch (Branch 4); when the father of that cousin tested, he was the #2 tester of that new branch.

So far though, our Project has unfortunately not been able to locate a #4 tester for any of its branches.

## *Rule of Three Limitations and Alternative Scenarios*

It should be pointed out that even having completed the Rule of Tree in the three branches discussed above, more SNPs still need to be named (private variants) and/or chronologically characterized (phylogenetic equivalents), with the total number of SNPs that can be uncovered by additional testers in a given branch being, as mentioned, dependent on the total number of unnamed private variants plus the number of equivalent SNPs existing in that branch. Using Branch 3 (turquoise colors) as an example and referring to **Figure 2**, haplogroup I-FT26227 still has two equivalent SNPs (FT25297 and FT20749), and I-FT14616 still has one private variant. With the tested descendant of Samuel D Petty having SNP FT14616 and the descendants of Jess J Petty having a subclade of FT14616, it's clear that Jess and Samuel's father, Alfred Mannon Petty, must have had the FT14616 SNP as well, so the not-fully-characterized mutations of FT14616 (a private variant and three equivalent SNPs) would appear to have originated within generations 9 and 10 (Jess and Samuel, and their sons, respectively). This happens to be author RLP's own branch, and it's personally known that Alfred Mannon Petty had only the two sons shown, Jess and Sam, and that Jess and Sam each had two sons – though one of Jess's sons died before adulthood. (His other son is the author's father, Sid.) For Sam's sub-branch, there's a clear solution to having his private variant named, and that's to have another of his grandsons tested. Since all three of Jess's tested descendants, including his only two grandsons, share the FT26227 haplogroup and its equivalents, all three equivalent SNPs must have originated in Jess and/or Sid. But with Jess and Sid, along with Sid's brother, all having passed away, and both of Sid's sons (and a grandson) having tested and been shown to share the three equivalent SNPs, chronologically differentiating the three SNPs would seem to be impossible. In **Figures 1a** and **1d**, Jess has been assigned one of the three SNPs (FT20749) and Sid the other two (FT25297 and FT26227), but this is largely speculation. Sid was, however, a fighter pilot in World War II (RLP, knowledge passed directly from father), so considering the increased time spent at higher altitudes while flying, an increased likelihood of Sid having multiple mutations – as suggested by the two SNPs assigned to Sid – is not unreasonable. Chronological differentiation of the three equivalent SNPs, however, doesn't appear to be possible.

## *Rule of Three Summary*

Test results in this study confirm the tenets of the Rule of Three, and clearly demonstrate its ability to help uncover a branch's recent haplogroups. Several ways of fulfilling the Rule with a third tester of intermediate generational distance have been demonstrated, and extension of the rule beyond three testers has been

described. There are some practical aspects of applying this rule that may be useful as well. First, testing of a close relative (tester #2) is not only an important component of the Rule, as it immediately results in the naming of most (if not all) private variants, but, assuming the relative is available, it's often the easiest starting point for an initial Big Y tester to begin the genetic resolution of his own branch of his larger family tree. Second, thanks to the wide variety of alterations possible to the "strict" rule categories, our study has demonstrated different ways of completing the rule with a third tester of intermediate distance - and many additional ways remain. Finally, we've demonstrated various possibilities for extending the "Rule" by adding additional testers based on average mutation intervals and other criteria.

## Assignment of Haplogroup Origins to Likely Ancestors

When a new haplogroup is revealed in a new tester, the question arises as to when and with whom that haplogroup might have originated. (This was already touched on in the Rule of Three Limitations and Alternative Scenarios section.) Thanks to the genealogies of the Petty Project members having been determined, we've been able to use the known branching in the family tree, along with rough estimates of the time of SNP formation provided by the FTDNA Time Tree app (FTDNA-TimeTree, 2023)), to help determine the originator of the SNP and thus the haplogroup's placement in the descendant tree. For instance, the first subclade of the Clan haplogroup identified, BY120617, was observed in a known descendant of Thomas and Catherine's son William (1707-1775). Since William's father (Thomas) was already known to have the Clan Haplogroup, the formation of BY120617 was considered to have occurred with William, or possibly one of his early descendants. Known descendants of William's two sons, Hubbard and William Jr., however, were also shown to have the BY120617 terminal SNP, so it was clear that it had to have originated with the birth of William (Sr.) himself (abt. 1708) – which is coincidentally close to the Time Tree's median estimate of 1730. Similar reasoning was applied to determine with whom each haplogroup is most likely to have originated. (Most of these determinations, denoted by the double-red outlined boxes in the family tree charts (**Figures 1a-d**), are well-reasoned estimates, based largely on known branching patterns in the tree, and are most likely no more than a generation off. Those located in branches without nearby sub-branching, however, could vary by multiple generations either way, as indicated by the arrow symbols next to their double red-colored box outlines.)

## The Value of Full Genetic Characterization

The discovery of new haplogroups in a group of related men is important in determining - and especially in confirming - their exact relationships, and can lead to the confirmation of extended family relationships. Uncovering a specific haplogroup sequence in a group of tested men provides confirmation of the sequential relationship of the men – such as a series of cousins from close to distant – and these men then may connect each of their shared ancestors (e.g., 2<sup>nd</sup> cousins are related through a shared grandfather, 4<sup>th</sup> cousins are related through a shared great-great grandfather, etc.), thus connecting their genealogical lineage to the genetic sequence. Tying several related haplogroup sequences to one another through shared haplogroups then grows the haplotree, which is similarly correlated with the physical family tree through conventional genealogical research. In this way the value of initially short haplogroup sequences in confirming genealogical relationships is magnified to the confirmation of family-wide relationships that were previously unknown or only suspected.

Using the Rule of Three, known relatives of current members of the Petty Surname Project have been targeted, recruited, and tested, enhancing the correlations between known biological connections and their



corresponding genetic connections. It is the Project's long-term goal to achieve full genetic characterization of all known branches of its Hubert Petty descendant tree – which means naming all private variants and chronologically resolving every equivalent haplogroup. Achieving this (rather lofty) goal would allow any man who descends from Hubert Petty (whether he's aware of it or not) to be, first, confirmed as Hubert's descendant, but further, have his exact place in the Hubert Petty Clan identified - simply by taking a Big Y or other Y-SNP test.

Thus far, only James Winter Petty's five-generation, two-haplogroup branch, from his great grandfather (William Henry Petty) to his son, has reached this goal. (Testing of one of James's 2<sup>nd</sup> cousins (grandsons of Donald Marion Petty) will likely distinguish the FT399203 SNP from its phylogenetic equivalent (FT438727), expanding James's fully characterized branch to 5 generations and 4 haplogroups.) Other sub-branches are approaching a similar level of success though, and the effort to extend their characterized range to even further generations is well under way.

## Conclusions

The research described in this paper has resulted in the creation and genetic confirmation of a 12-generation descendant tree for the 17<sup>th</sup> century English immigrant to America, Hubert Petty, through a combination of conventional genealogical research and Y-SNP genetic testing. It has also provided genetic and genealogical evidence confirming 26 of Hubert's living descendants. Being shared by all these descendants, the haplogroup I-BY34474 has been assigned to, and is offered as the Clan haplogroup of, Hubert Petty. The descendants' haplogroups, presented graphically in both their color-coded Y-haplotree and their correlated descendant tree, have allowed the confirmation, as well as clear visualization, of their relationships to Hubert and their interrelationships between themselves. The advantages of following the "Rule of Three" to enhance genetic characterization of the descendant tree have been demonstrated as well.

## Acknowledgements

This study would not have been possible without the cooperation and contributions of the members of the FTDNA Petty Surname Y-DNA Project, and they are gratefully acknowledged. We'd like to acknowledge two of our Project members in particular, Terry Embrey and Ross Petty, who generously agreed to review this manuscript, and the JoGG reviewers as well, whose many suggestions have, we believe, significantly improved the accuracy, readability, and other aspects of the originally submitted manuscript. Finally, we are especially indebted to our late project member, professional genealogist James Winter Petty, without whose groundbreaking research into his own ancestors this study could never have happened.

## Conflicts of Interest

The authors declare no conflicts of interest in their contributions to this study, and specifically declare no commercial or business interests in the FamilyTreeDNA organization (FTDNA) or any other genealogical testing or consulting company. However, authors RLP and MEGP do acknowledge their volunteer positions as co-administrators of FTDNA's Petty Surname Y-DNA Project. Author MEGP acknowledges past association, but no current involvement, with the no-longer active genealogy firm Heirlines Family History and Genealogy of Salt Lake City, Utah.

## References

- FTDNA (2023). *FamilyTreeDNA*. <https://www.familytreedna.com>
- FTDNA-BlockTree (2023, December). *Block Tree (Introduction)*. <https://help.familytreedna.com/hc/en-us/articles/4402744197647-Big-Y-Block-Tree-Introduction#accessing-the-block-tree-0-0>
- FTDNA-Discover(2023). *Discover™*. <https://discover.familytreedna.com/y-dna/I-BY34474/tree>
- FTDNA-TimeTree (2023, December). *TimeTree - I-BY34474*. <https://discover.familytreedna.com/y-dna/I-BY34474/tree>
- Petty, J. W. (1976, October). *Thomas Petty of Orange County, Virginia (ca 1675-1750)*, The Petty Papers, V. 1, #2, pp. 22-26. Retrieved from The Petty Papers: a genealogical research quarterly. (Available through LDS Family Search Libraries, or contact [rlpetty@mac.com](mailto:rlpetty@mac.com) - not available online.)
- Reynolds, K. (1976). *The Petty Family*, Vol. IV, p. 260. Retrieved from The Petty Family: <https://www.familysearch.org/library/books/records/item/600649-the-petty-family-v-04?offset=>
- RJ Wang, S. A. (2024). *Human Generation Times, Sci Adv, 9:1*. Retrieved from Pub Med: <https://pubmed.ncbi.nlm.nih.gov/36608127/>
- RLP (2024). "Designated" Haplogroup. *Refers to the haplogroup assigned to the tester by FTDNA from a group of phylogenetically equivalent haplogroups.*
- RLP (2024a). Haplogroups I-Y78878 and I-FT186158. *These sibling haplogroups of BY34474 (subclades of I-Y24748) are seen to be associated with the Mumford/Momphard surname, and Stetler and Patty surnames, respectively, in members of the Petty Surname Y-DNA Project.*
- rlpetty1046 (2024). [Ancestry.com](https://www.ancestry.com), User ID: rlpetty1946; public tree: Hubert Petty Family Tree.
- Wood, B. (2019). *Big Y-700 and the Rule of Three*. Retrieved from Facebook: <https://www.facebook.com/groups/1009907362494357/search/?q=BiGY-700%20and%20The%20Rule%20of%20Three%20>
- YDNA-Warehouse. (n.d.). *YDNA Warehouse: Estimated Years/SNP*. Retrieved from ydna-warehouse statistics: <https://ydna-warehouse.org/statistics.html>