Report on the VAN_TUYL Surname Project Y-STR Results

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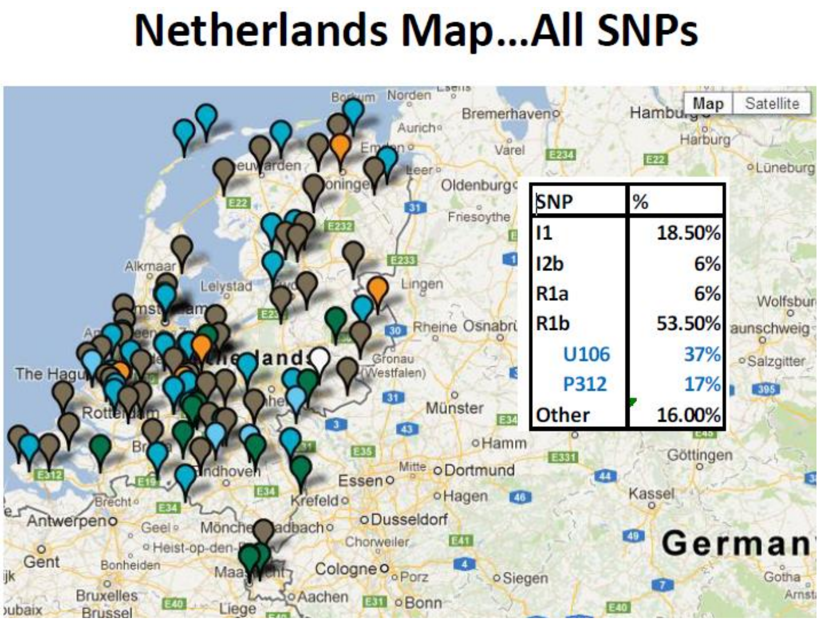
Abstract: Recent data for one more descendant of Ott van Tuyl has been added to the project, bringing the total number of Gameren Van Tuyl descendants tested to eight; six in the U.S. and two in The Netherlands. The two Dutch descendants are descended through Geerlof Otten van Tuyl [VTC IXa/A1], the brother of immigrant Jan Otten van Tuyl [VTC IXb/1]. The latest data show that all known Dutch descendants can be distinguished from all known American descendants by two Y-STR mutations, DYS-390 and DYS-449, and that the American Van Tuyls can be identified as descendants of either Abraham Jansz [1.1] or Isaac Jansz [1.2] on the basis of one Y-STR mutation, DYS-389b [DYS389ii – DYS389i]. Ancient ancestors of the Van Tuyl family have been traced to R1b-P312>>DF27>>ZZ12>>Z2552>>YP4295, a descendant branch of the western European R1b-P312 subclade.

Summary

Eight men named "Van Tuyl" (or various spellings thereof) have now been tested for Y-chromosome Short Tandem Repeats [Y-STR] and Single Nucleotide Polymorphisms [SNPs]. SNP Results indicate they are all members of the P312/DF27 subclade, a group closely associated with Western Europe and the British Isles, and that the Van Tuyl family to which they belong is in no way related to the noble family Van Tuyll van Serooskerken.[1]



Netherlands Map...All SNPs

SNP	%
I1	18.50%
I2b	6%
R1a	6%
R1b	53.50%
U106	37%
P312	17%
Other	16.00%

Fig. 1 – The Van Tuyls belong to haplogroup R1b/P312, the third most common SNP haplogroup associated with ancestry in The Netherlands. This clade came into existence some 130 generations (~4000 years) ago. The Most Recent Common Ancestor [MRCA] for the six tested men is Ott van Tuyl of Gameren, The Netherlands, who lived in the 17th century.

Prehistoric Van Tuyls

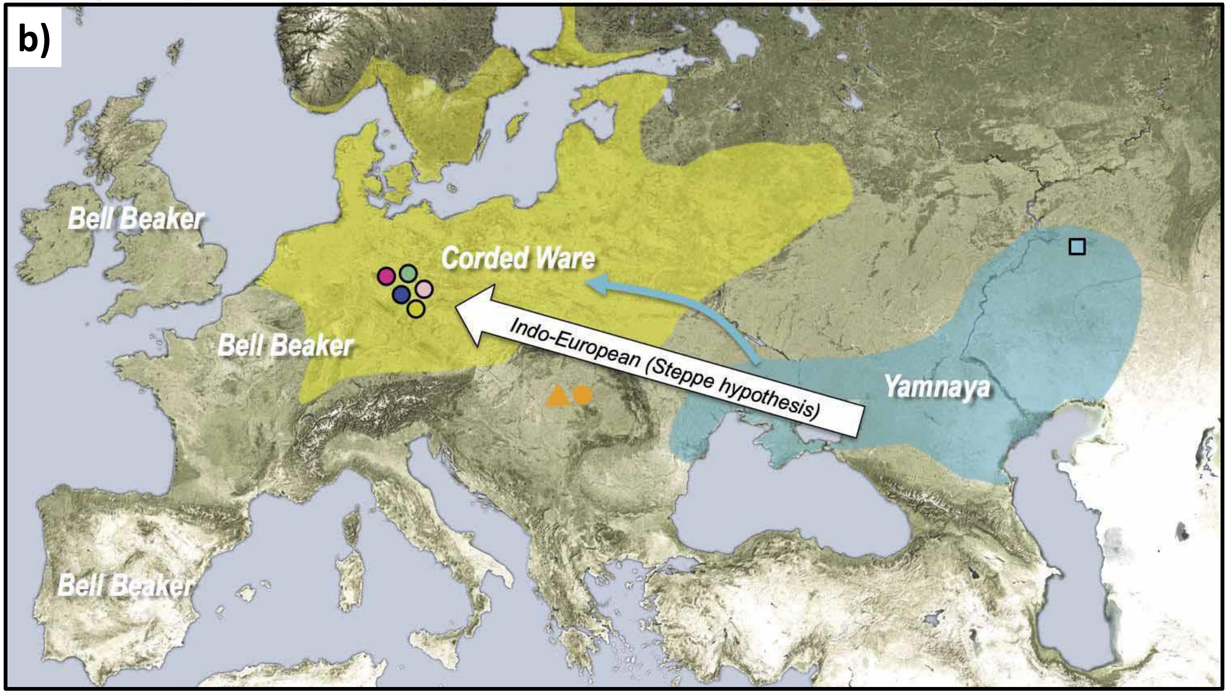


Fig 2 – Settlement of Europe from the East.[2] About 9000 – 7000 years ago, Anatolian farmers settled in Europe, introducing agriculture to the continent which was then sparsely occupied by hunter-gatherers, with whom they interbred. Starting about 4500 years ago, the Yamnaya people of the Pontic steppes brought horses, two-wheeled chariots, and their DNA to Europe. These people were probably the ancestors from which the R1b-P312 haplogroup - including the Van Tuyls – descended.

Recent SNP test results on Rory Van Tuyl, which are virtually certain to be identical to those of all VAN_TUYL project participants, indicate we have accumulated several additional known SNPs after P-312: P312>DF27>Z2552>YP4295[3]. But the most informative map of our prehistoric roots is still that of the main subclade, P-312, shown below:

Western Europe and British Isles: P-312 SNP

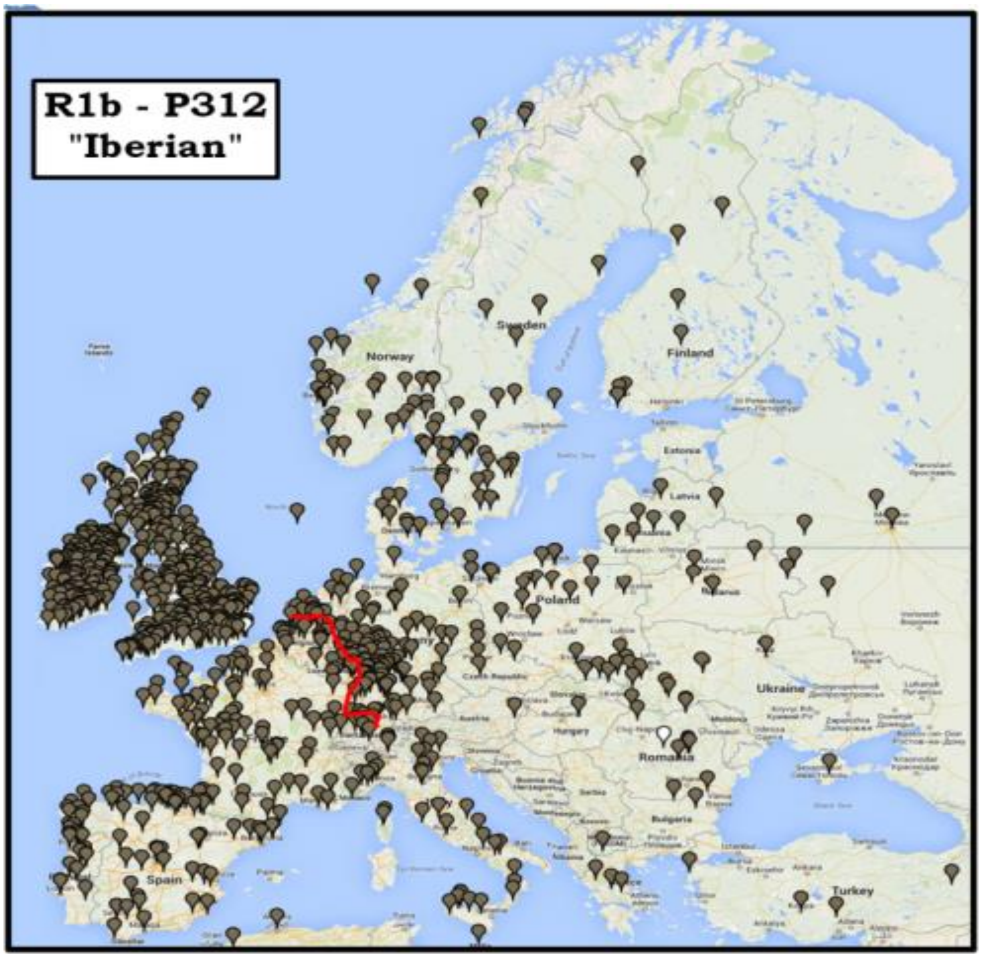


Fig. 3 – A distribution of the known ancestors for FTDNA customers testing positive for P-312 shows concentrations in Iberia, France and the Rhine River Basin (Red line), as well as the British Isles. (Most FTDNA customers are descended from the British Isles, hence the greater density of points in Britain). The common ancestor for this SNP haplogroup is over 4000 years in the past and may be associated with the Celtic inhabitants of ancient Europe. Recent DNA obtained from ancient German skeletons indicates that R1b-P312 was in Western Europe by 2000 BCE.[4]

Van Tuyl Y-SNP Findings

Amateur genetic genealogists have obtained DNA identification of SNP mutations on the Y-chromosome, and have aggregated their findings over a period of 10 years or so in an effort to tease out their genetic family trees extending back to prehistoric times. These SNP (Single Nucleotide Polymorphism) mutations occur at just one location on the Y chromosome, and once having occurred are extremely unlikely to ever change again. Thus, these SNP mutations form an indelible record of each man's genetic heritage extending back to the dawn of humanity. In contrast to the Y-STR record, where mutations occur once in hundreds of generations and are reversible, these SNP mutations occur much less frequently and are essentially permanent. But making sense of the vast zoo of SNP mutations requires a huge effort from hundreds or thousands of people. Various online groups have formed around a number of SNP haplotypes, with members mostly being descended from western European (and British Isles) males. Some groups – notably Scottish descendants – have discovered shared mutations which occurred as recently as hundreds of years ago. But most groups have only been able to form a coherent picture of male-line genetic relationships that occurred no later than the bronze age, about 4000 years ago. This is still very much a work in progress. Someday these records may become useful to records-based genealogists. But for now, they just give us a glimpse of who our ancient ancestors may have been long before written records were kept.

In the case of the Van Tuyl family, we have been represented by a DNA sample contributed by Rory Van Tuyl (there is no need for additional samples since we all descend from a single individual within historical times and hence share the same ancient Y chromosome SNP mutations). Our ancient heritage can be viewed on the graphic on the next page, which shows the entire spectrum of known European SNP mutations as of 2016.

Our SNP History from about 5000 years ago is:

P311>> P312>>ZZ11>>DF27>>ZZ12>>Z2552>> YP4295>>A6457>>BY3232

SNP mutation P311 is common to all western European men in the most common European haplogroup, R1b.

P312 is characteristic of the "Iberian" subclade, whose descendants originate from the Rhine River valley and to the west, including the British Isles.

DF27>>ZZ12>>Z2552 are other commonly-occurring SNPs descendant of P312, with no particular geographic identification

YP4295 is a SNP which so far has been found in five individuals, A6457 & BY3232 in only two.

Many yet-to-be-discovered SNPs lie down the road on the way to Ott van Tuyl, our most recent Common Ancestor.[5]

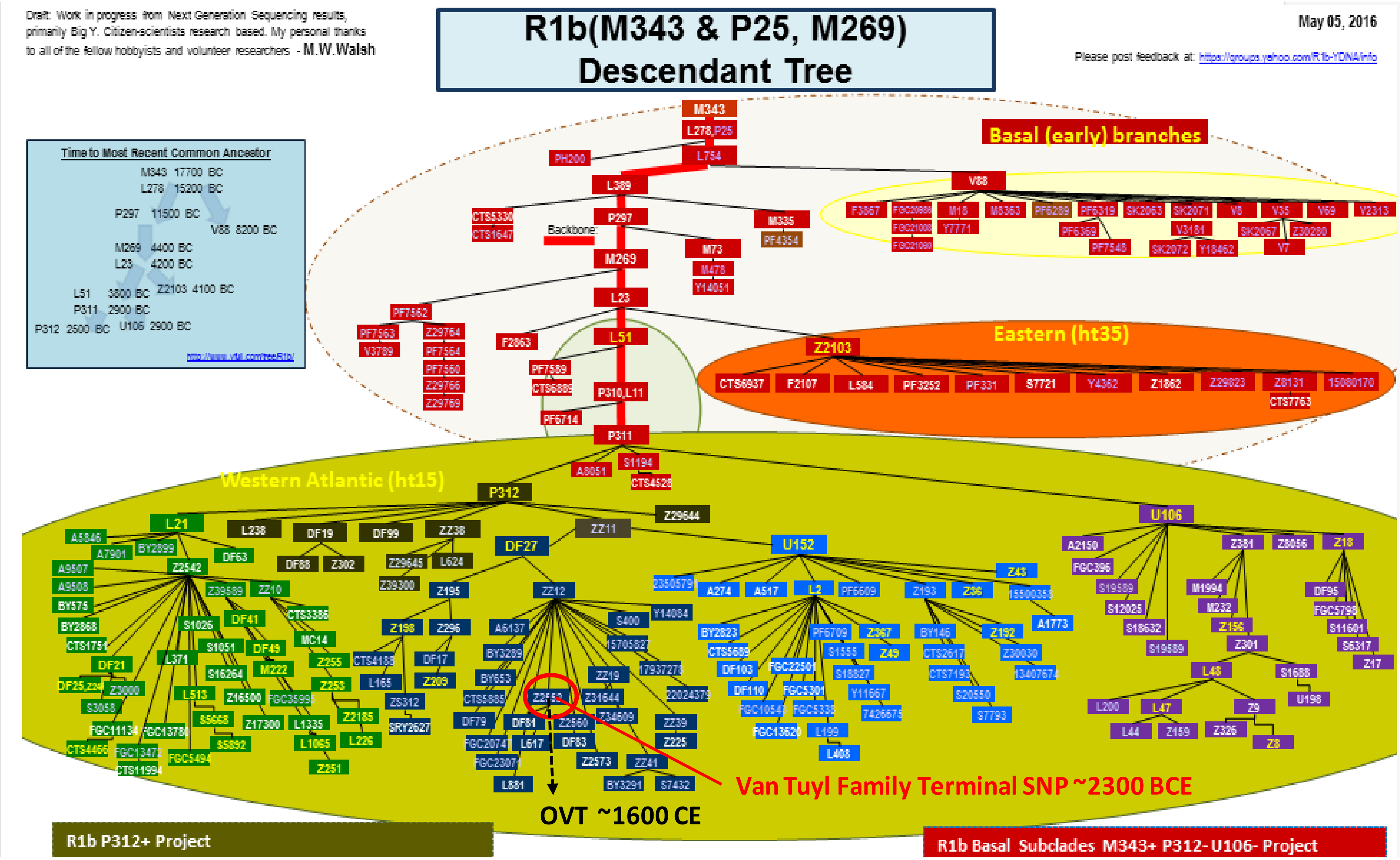
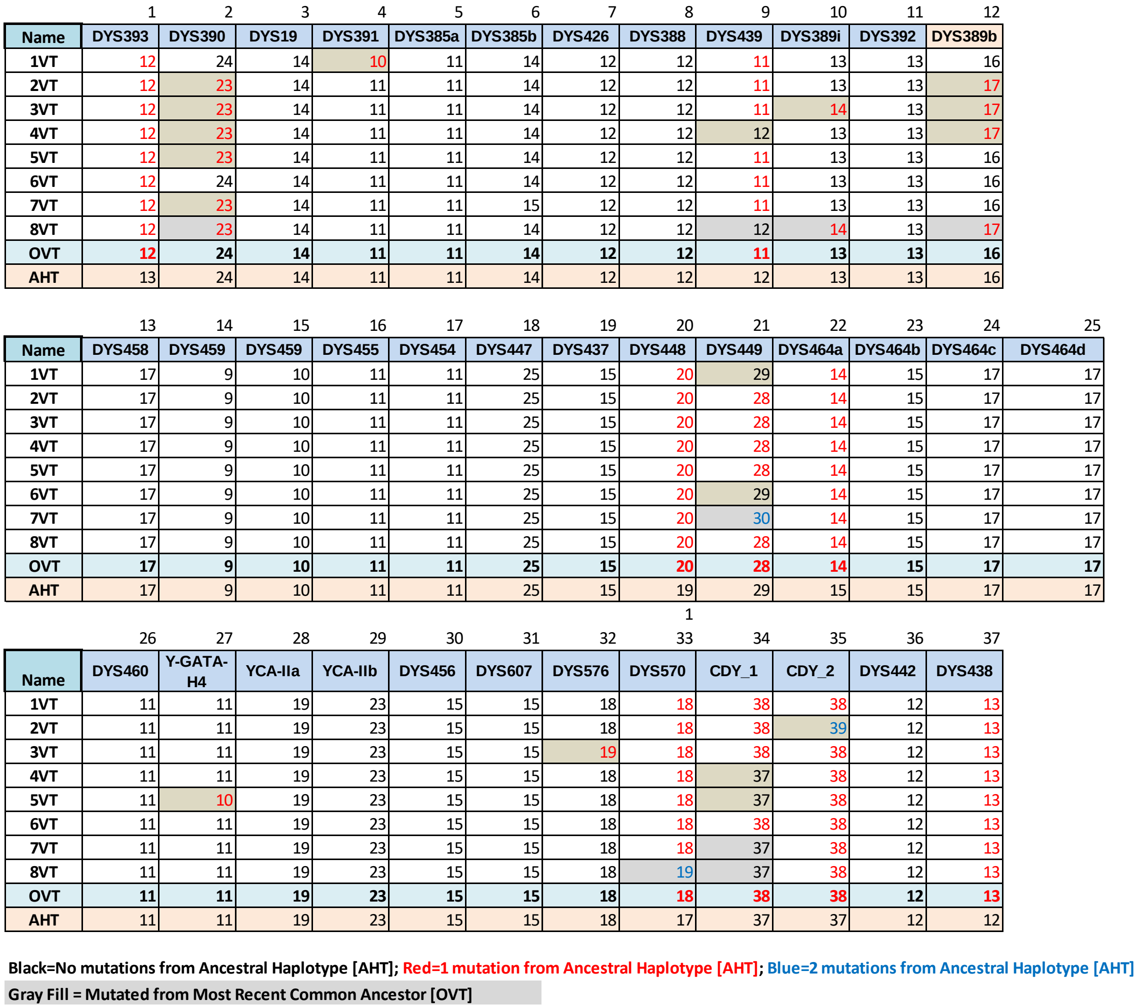


Fig. 4 – Ancient Y-SNP phylogeny of European males in Haplogroup R1b.[6] The Ancestral Haplotype for Western European males is called R1b-P31. Van Tuyls can trace their genetic line to mutation Z2552, which occurred over 4000 years ago. In the millennia between Z2552 and our MRCA Ott van Tuyl, a number of additional mutations will have occurred, but only a few are yet known.

The Van Tuyl Y-STR Findings

The Y-STR test which clearly shows the relatedness of the seven project members measures benign minor variations on the Y-chromosome, the part of the genome that controls the conversion of a fetus to the male sex after 6 to 7 weeks of gestation. These variations simply count the number of times certain inactive 4-letter segments of the genetic code repeat themselves in the Y-Chromosome. In contrast to the *Genes*, the active parts of the Y-chromosome which determine sex characteristics, these *short tandem repeats* mutate fairly rapidly, on the order of once every 100 - 900 generations at each location [usually referred to as a *locus* (pl. loci)]. By measuring 37 of these loci and searching for certain evolved combinations of STRs (called ***haplotypes***), we can identify related men with high accuracy. Y-STR numbers for the 8 members of the VAN_TUYL project are shown here:



	1	2	3	4	5	6	7	8	9	10	11	12
Name	**DYS393**	**DYS390**	**DYS19**	**DYS391**	**DYS385a**	**DYS385b**	**DYS426**	**DYS388**	**DYS439**	**DYS389i**	**DYS392**	**DYS389b**
1VT	12	24	14	10	11	14	12	12	11	13	13	16
2VT	12	23	14	11	11	14	12	12	11	13	13	17
3VT	12	23	14	11	11	14	12	12	11	14	13	17
4VT	12	23	14	11	11	14	12	12	12	13	13	17
5VT	12	23	14	11	11	14	12	12	11	13	13	16
6VT	12	24	14	11	11	14	12	12	11	13	13	16
7VT	12	23	14	11	11	15	12	12	11	13	13	16
8VT	12	23	14	11	11	14	12	12	12	14	13	17
OVT	**12**	**24**	**14**	**11**	**11**	**14**	**12**	**12**	**11**	**13**	**13**	**16**
AHT	13	24	14	11	11	14	12	12	12	13	13	16

	13	14	15	16	17	18	19	20	21	22	23	24	25
Name	**DYS458**	**DYS459**	**DYS459**	**DYS455**	**DYS454**	**DYS447**	**DYS437**	**DYS448**	**DYS449**	**DYS464a**	**DYS464b**	**DYS464c**	**DYS464d**
1VT	17	9	10	11	11	25	15	20	29	14	15	17	17
2VT	17	9	10	11	11	25	15	20	28	14	15	17	17
3VT	17	9	10	11	11	25	15	20	28	14	15	17	17
4VT	17	9	10	11	11	25	15	20	28	14	15	17	17
5VT	17	9	10	11	11	25	15	20	28	14	15	17	17
6VT	17	9	10	11	11	25	15	20	29	14	15	17	17
7VT	17	9	10	11	11	25	15	20	30	14	15	17	17
8VT	17	9	10	11	11	25	15	20	28	14	15	17	17
OVT	**17**	**9**	**10**	**11**	**11**	**25**	**15**	**20**	**28**	**14**	**15**	**17**	**17**
AHT	17	9	10	11	11	25	15	19	29	15	15	17	17

	26	27	28	29	30	31	32	1 33	34	35	36	37
Name	**DYS460**	**Y-GATA-H4**	**YCA-IIa**	**YCA-IIb**	**DYS456**	**DYS607**	**DYS576**	**DYS570**	**CDY_1**	**CDY_2**	**DYS442**	**DYS438**
1VT	11	11	19	23	15	15	18	18	38	38	12	13
2VT	11	11	19	23	15	15	18	18	38	39	12	13
3VT	11	11	19	23	15	15	19	18	38	38	12	13
4VT	11	11	19	23	15	15	18	18	37	38	12	13
5VT	11	10	19	23	15	15	18	18	37	38	12	13
6VT	11	11	19	23	15	15	18	18	38	38	12	13
7VT	11	11	19	23	15	15	18	18	37	38	12	13
8VT	11	11	19	23	15	15	18	19	37	38	12	13
OVT	**11**	**11**	**19**	**23**	**15**	**15**	**18**	**18**	**38**	**38**	**12**	**13**
AHT	11	11	19	23	15	15	18	17	37	37	12	12

Black=No mutations from Ancestral Haplotype [AHT]; Red=1 mutation from Ancestral Haplotype [AHT]; Blue=2 mutations from Ancestral Haplotype [AHT]

Gray Fill = Mutated from Most Recent Common Ancestor [OVT]

Fig. 5 – Y-STR table for members of the VAN_TUYL surname project as of May, 2016. Participants are numbered 1VT – 8VT; OVT is the most recent common ancestor Ott van Tuyl; AHT is the ancestral haplotype R1b-P311, from which the Van Tuyls evolved (as inferred from modern measurements). Entries shaded in gray indicate mutations since the Most Recent Common Ancestor [MRCA] Ott van Tuyl. Entries in Red show where Van Tuyls differ from the ancient ancestral haplotype, and form the basis for a unique *Van Tuyl Haplotype* which identifies men descended from OVT with a high degree of certainty.

Locus	Ancestral Haplotype		Van Tuyl Haplotype	Selection Ratio	Avg. Gen to Mutation
HT Mode				44	
DYS-393	13	>>>>>>>>	12	33	455
DYS-438	12	>>>>>>>>	13	29	625
DYS-448	19	>>>>>>>>	20	18	862
DYS-570	17	>>>>>>>>	18	3	158

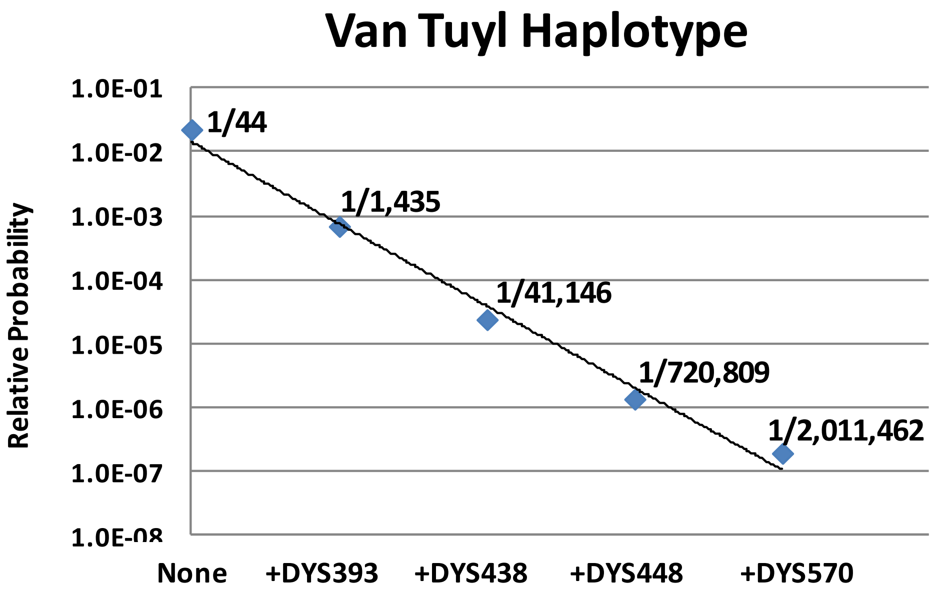
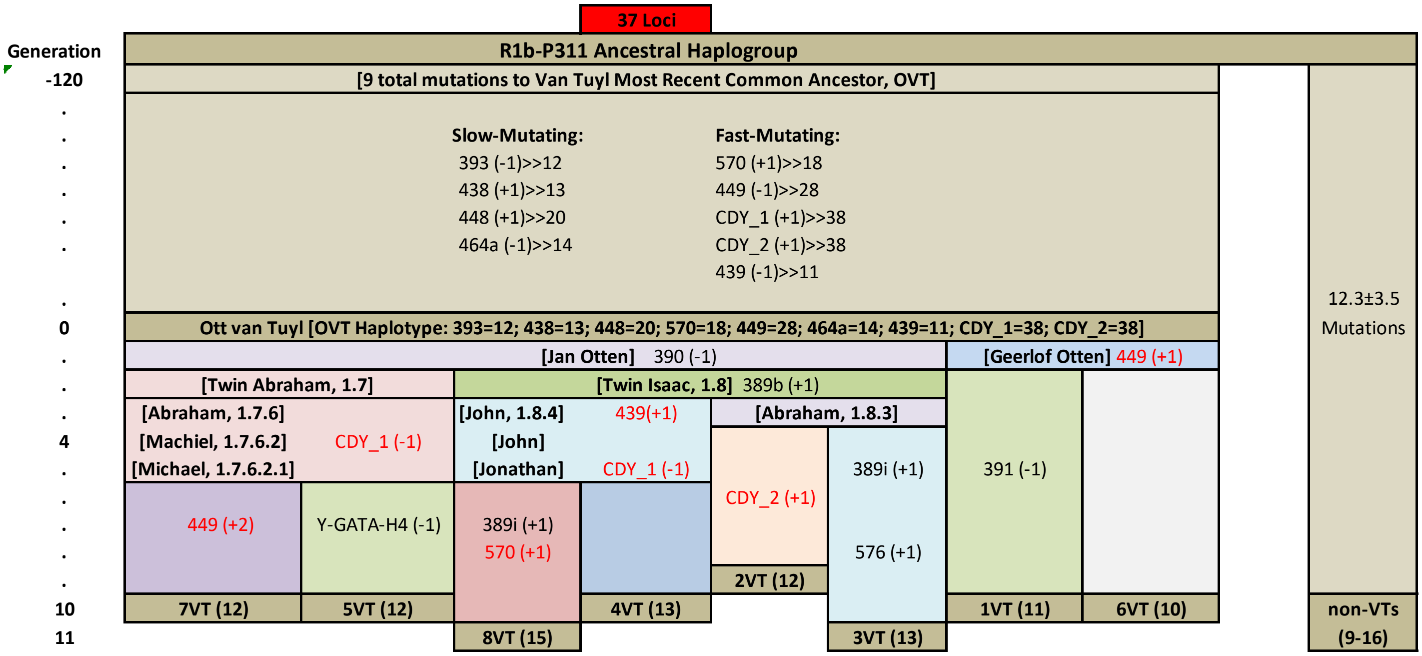


Fig. 6 – The revised Van Tuyl Haplotype consists of 4 loci which have mutated since the ancient ancestral group some 4000 years ago. All members of today's VAN_TUYL project possess DYS393, DYS438, DYS448 and DYS570 STR values characteristic of the family. The odds of this combination occurring *somewhere* in the population are 1:2,011,462. The odds that any ***particular man*** who is ***not*** a descendant of OVT would possess this combination of Y-STRs are infinitesimal. As the number of group members has increased, new variations have appeared at loci that were previously part of the Van Tuyl Haplotype, leaving only 4 loci identical for all 7 project participants. But the four remaining loci have rare alleles that are slowly-mutating. So the Van Tuyl Haplotype is still very selective and able to predict descent from Ott Van Tuyl of Gameren very reliably.

Combining the DNA data with records-based genealogy (including recent genealogy relating 4VT & 8VT), and assuming that the twins Abraham and Isaac were fraternal, we expanded the phylogenic tree to include the all eight participants, 1VT – 8VT:



Loci from OVT Haplotype which have NOT mutated since [OVT]: DYS393 [12]; DYS448 [20]; DYS464a [14]; DYS438 [13]

Loci from OVT Haplotype which have mutated at least once since [OVT]: DYS570; DYS449; DYS439; CDY_1; CDY_2

Fig. 7 – Phylogenic Tree of the 8 Van Tuyl project members, showing the number of STR mutations for each from the MRCA (OVT) and from the Ancestral Haplotype. The average number of mutations since ancient times for men of our ancestral haplotype in the general population was 12.3; for American Van Tuyls it was 12.8, for Dutch Van Tuyls 10.5, for all Van Tuyls 12.25. The average mutations since ancient times for Van Tuyls prior to OVT were one in 13 generations; after OVT the mutations occurred once in 2.9 generations on average for the American branch, once in 6.7 generations for the Dutch branch. Such variations in rate are common, due to the random nature of the process. The average genetic distance between Van Tuyls is 2.4±2.2 mutations; the Genetic distance between Van Tuyl and non-related men descended from the ancestral haplogroup some 4000 years ago is 24.2±3.7 mutations.

This phylogeny assumes that Abraham and Isaac Van Tuyl (b. 1681) were fraternal twins.[7]

Y-STR mutations characteristic of each sub-branch have emerged: For descendants of Twin Abraham it is CDY_1 (-1); Twin Isaac 389b (+1); Jan Otten (American branch) 390 (-1); Geerlof Otten (Dutch branch) 449 (+1). Further down the line, we see that descendants of John Van Tuyl (4VT and 8VT) are characterized by 439 (+1) and CDY_1 (-1). So we now have a series of "fingerprints" with which to identify which branches future members of unknown ancestry may belong to.

Discussion

We now have three major branches of the family represented in the DNA project:

1. The Dutch Branch [1VT, 6VT] descended from Ott van Tuyl through Geerlof Otten van Tuyl of Gameren;
2. The American Revolutionary Branch [2VT, 3VT, 4VT] descended from twin Isaac Van Tuyl [VTC 1.8] of central Staten Island;
3. The Loyalist Branch [5VT, 7VT] descended from twin Abraham Van Tuyl [VTC 1.7] of north Staten Island.

These three branches are characterized by the following Y-STR values:

	DYS393	**DYS438**	**DYS448**	**DYS570**	**DYS390**	**DYS449**	**DYS389b**
Ott van Tuyl	12	13	20	18	24	28	16
Dutch Branch	12	13	20	18	24	29	16
Abraham VT Branch	12	13	20	18	23	28/30	16
Isaac VT Branch	12	13	20	18	23	28	17

With the addition of 8VT to the project we now have a clear marker for the descendants of Jan (John) Van Tuyl [1.8.3a.1]. Both 4VT and 8VT are known to be descended from this early pioneer of the Minisink area of New York. They share the mutation 11>>12 at locus DYS439, a clear marker for their sub-branch of the descendants of Twin Isaac.

So future project members who carry the Van Tuyl signature haplotype [DYS393=12; DYC438=13; DYS448=20; DYS570=18] can be sorted into one of these three branches based on the above findings. The Dutch Branch has the VT Haplotype plus DYS449=29. The Abraham VT branch has the VT Haplotype plus DYS390=23 and DYS389b=16. The Isaac VT branch has the VT Haplotype plus DYS390=23 and DYS389b=17. Descendants of John VT will have DYS439=12.

Conclusion

Eight male Van Tuyl genetic relatives, representing two major branches of the American Van Tuyl family and two major branches of the Dutch family have now been characterized by Y-STR haplotype analysis. This genetic analysis is entirely consistent with the records-based genealogy of these men, and should be of help to others who wish to understand their place in the Van Tuyl family tree.

In addition, we now know the pattern of SNP mutations that characterize the ancient ancestors of the family van Tuyl in the European Bronze Age, some 4300 years in the past. Future SNP mutation findings may enable us to track this ancient lineage to more recent ancestors.

References

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[1] The family Van Tuyll van Serooskerken is in the R1b-U106 subclade, the family van Tuyl is in the R1b-P312 subclade. http://www.roryvantuyl.com/PDFs/VT-VTVS%20summary.pdf

[2] Haak, W. et al., "Massive migration from the steppe was a source for Indo-European languages in Europe," *Nature* (2015) **522,** 207-211, doi:10.1038/nature14317

[3] YFull.com (retrieved 5/9/2016. Only two instances of the terminal SNP YP4295 have been detected, though all members of the VAN_TUYL project share this haplotype.

[4] For additional information on the ancient Celts, see: http://roryvantuyl.com/PDFs/Celts%20Paper.pdf

[5] Williamson, A., "The Big Tree" http://www.ytree.net/DisplayTree.php?blockID=31 (Accessed 3/9/2016)

[6] Walsh, M.W., R1b Project Gateway, https://www.familytreedna.com/groups/r-1b/about/results (accessed 5/12/2016)

[7] A modern study of Dutch women over 40 showed that more fraternal twins were produced than identical twins: http://www.tweelingenregister.org/nederlands/verslaggeving/NTR-publicaties_2010/Hoekstra_FS_2010.pdf