

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 six; four in the U.S., 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.

Summary

Six men named “Van Tuyl” or “Van Tyle” 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 P-312 Clade, 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

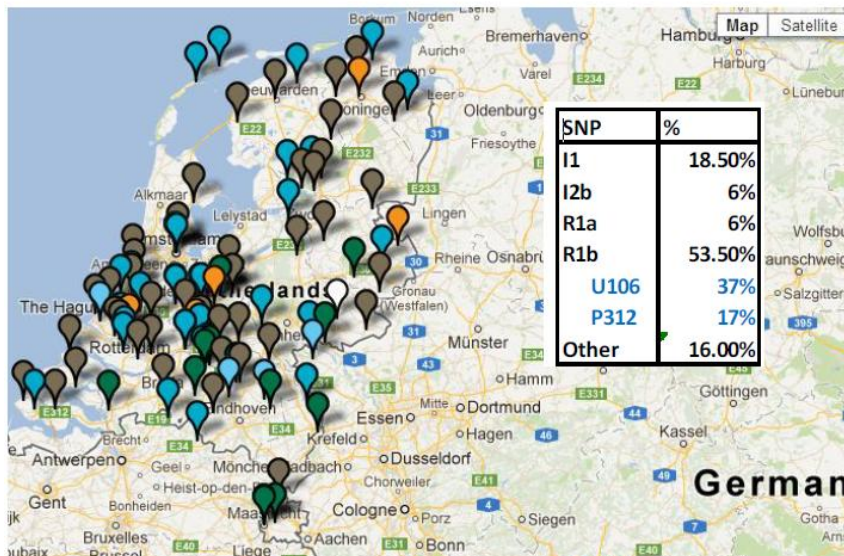


Fig. 1 – The Van Tuyls belong to haplogroup R1b/P312, the third most common SNP haplogroup associated with ancestry in The Netherlands. This clade came into existence some 130 generations (~4000 years) ago. The Most Recent Common Ancestor [MRCA] for the six tested men is Ott van Tuyl of Gameren, The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

¹ <http://www.roryvantuyl.com/PDFs/VT-VTVS%20summary.pdf>

Prehistoric Van Tuyls

Recent SNP test results on Rory Van Tuyl, which are certain to be identical to those of all VAN_TUYL project participants, indicate we have accumulated one additional known SNP after P-312. It is named DF-27. A map of its distribution is shown below:

Western Europe and British Isles: DF-27 SNP

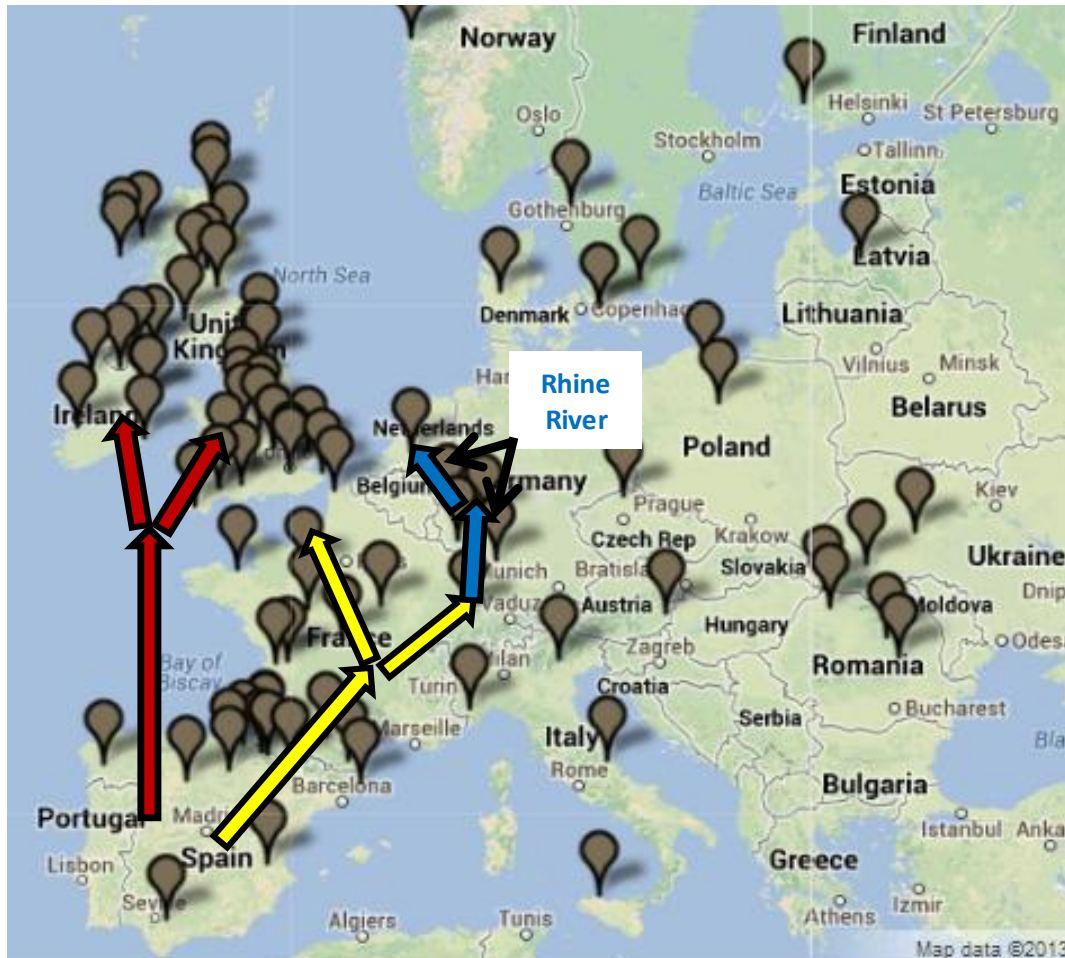


Fig. 2 – Recent tests show the Van Tuyls have accumulated both the P-312 SNP and the DF-27 SNP, which is descended from P-312. A distribution of the known ancestors for FTDNA customers testing positive for DF-27 shows concentrations in Iberia, France and the Rhine River Basin, as well as the British Isles (most FTDNA customers are descended from the British Isles). Possible migration routes are indicated with colored arrows.

The DNA ancestral distribution corresponds pretty well with archaeological data for the *Bell Beaker Culture*, a group of Celtic people who employed certain implement designs from 2900 BC to 1800 BC. Here is a map of the Beaker Culture's extent, based on archaeological finds:



Fig. 3 – The Bell Beaker Culture's extent in the period 2900 BC – 1800 BC.² This corresponds generally with the presumed date of origin for the P-312 and DF-27 SNP mutations, which probably occurred between 1300 and 2000 BC.

One possible interpretation of these maps is that the Bell Beaker People - Celts of the R1b haplogroup – spread overland from Spain to Middle Europe then along the rivers and coastlines before sailing to the British Isles. The Van Tuyls would have been of the group which descended the Rhine from Switzerland to the North Sea.

² http://en.wikipedia.org/wiki/Bell_Beaker_culture

The Van Tuyl Y-STR Findings

The Y-STR test which clearly shows the relatedness of the six 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 6 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
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
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	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
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

Fig. 4 – Y-STR table for members of the VAN_TUYL surname project as of August, 2013. Participants are numbered 1VT – 6VT; OVT is our ancestor Ott van Tuyl; AHT is the ancestral haplotype from which we 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	R1b1a2a1a1 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
DYS-439	12	>>>>>>>	11	2	299
CDY_1	37	>>>>>>>	38	2	116

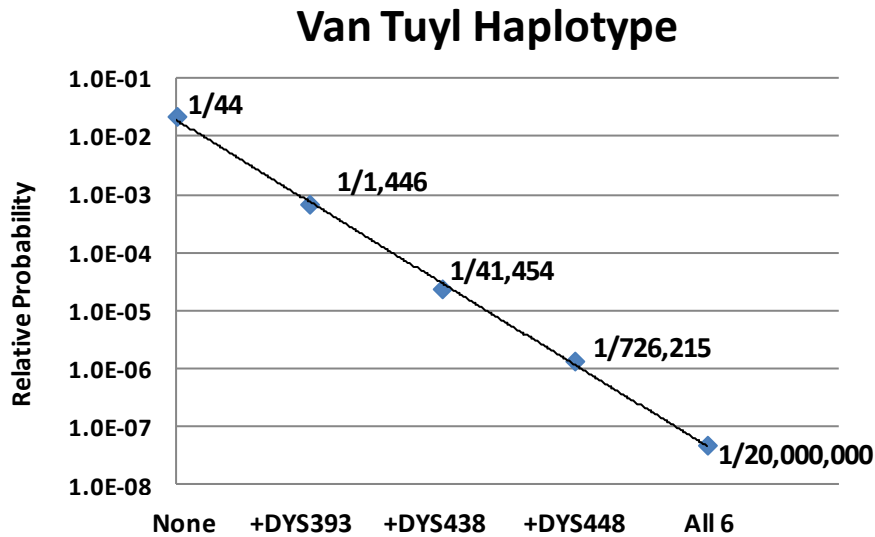


Fig. 5 – The revised Van Tuyl Haplotype consists of 6 loci which have mutated since the ancient ancestral group some 4000 years ago [DYS-449 has been removed since Dutch and American branches have different values]. All members of today’s VAN_TUYL project possess DYS393, DYS438, DYS448 and DYS570 STR values characteristic of the family. The odds of this combination occurring *somewhere* in the population are 1:2,178,000. The odds that any *particular man* who is *not* a descendant of OVT would possess this combination of Y-STRs are infinitesimal.

Combining the DNA data with records-based genealogy (including recent work on 4VT – 6VT), and assuming that the twins Abraham and Isaac were fraternal, we expanded the phylogenetic tree to include the all six participants, 1VT – 6VT:

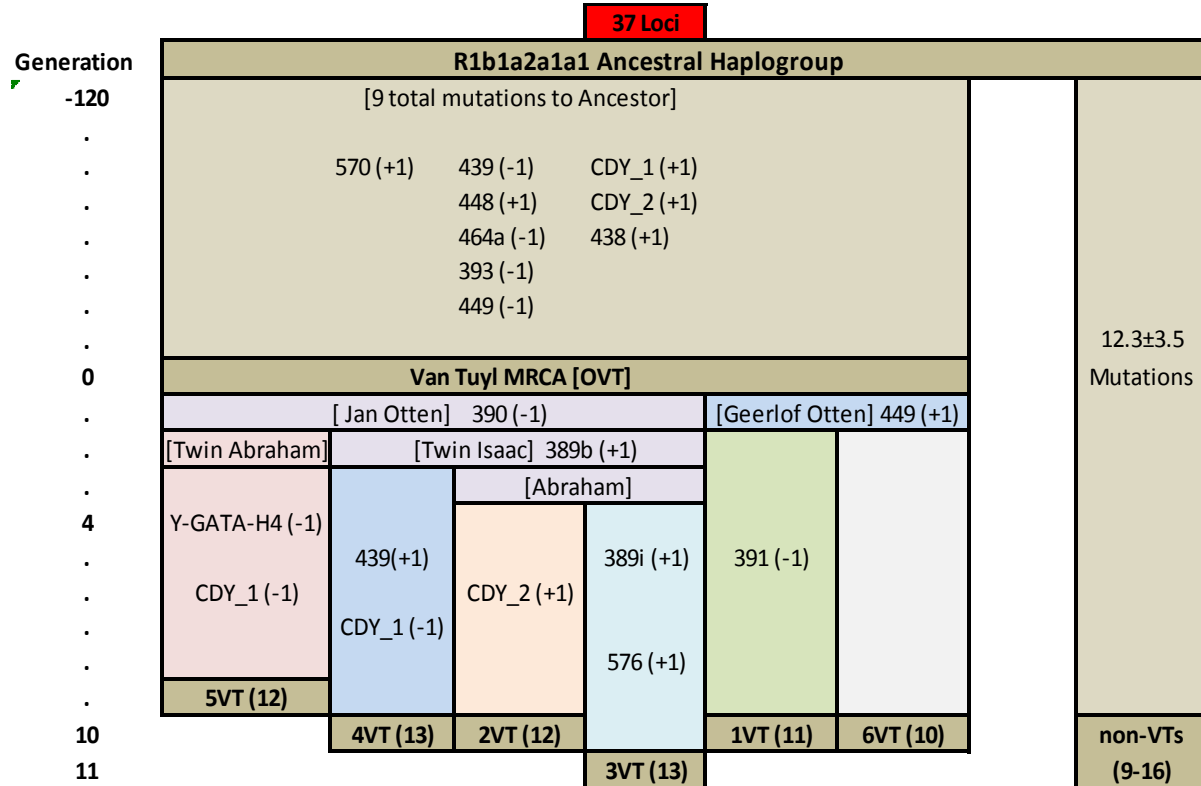


Fig. 4 – Phylogenetic Tree of the 6 Van Tuyts, showing the number of STR mutations for each from the MRCA (OVT) and from the Ancestral Haplotype. The average mutations since ancient times for men of our ancestral haplotype in the general population were 12.3; for Van Tuyts it was 11.8. The average mutations since ancient times for Van Tuyts prior to OVT were one in 13 generations; after OVT the mutations occurred once in 5.5 generations on average. Such variations in rate are common, due to the random nature of the process. The genetic distance between Van Tuyts is 4.6 ± 1.5 mutations; the Genetic distance between Van Tuyt and non-related men descended from the ancestral haplogroup some 4000 years ago is 24.1 ± 3.7 mutations. This phylogeny assumes that Abraham and Isaac Van Tuyt (b. 1681) were fraternal twins.

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;
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] 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	16
Isaac VT Branch	12	13	20	18	23	28	17

So future project members who carry the Van Tuyl signature haplotype [DYS393=12; DYS438=13; DYS448=20; DYS570=18] can be sorted into one of these three branches based on the above findings.

Conclusion

Two major branches of the American Van Tuyl family have now been characterized by Y-STR haplotype analysis, along with the Dutch Gameren Branch from which they are descended, If Dutch or American Van Tuyls of unknown genealogy present themselves, the VAN_TUYL surname project should be able to help them research their origins.