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## Modern Technology Confirms a Transatlantic Family Connection:
### Results of the Van Tuyl DNA Project

*The family van Tuyl of Gameren descends from Heer Gijsbrecht van Tuyl of 14th century Gelre, many of whose descendants moved to the Bommelerwaard in the 15th century and settled in Gameren in the 16th century. Today's descendants of this family are believed to have descended from the Gameren farmer Ott Jansz van Tuyl (b. ~1606) through his son Geerlof Otten (b. 1626-1635). Most Americans born with the name "Van Tuyl" are believed to have descended from Geerlof's brother Jan Otten van Tuyl (b. 1636-1641), who left Gameren in 1662 and arrived in Nieuw Amsterdam in 1663. The connection between the Gameren and American Van Tuyls was established genealogically in the 1990s and has now been confirmed through Y-chromosome testing of four American and two Dutch descendants of Ott Jansz van Tuyl.*

**Rory Van Tuyl**

### A New tool for Historical and Genealogical Detectives

Human history is based on written and oral records, some of which have been passed down for thousands of years. Often, the history based on these records is a matter of interpretation. And usually, emphasis is placed on famous people, places and events. Family history is also based on written and oral records. But these records are often incomplete and sometimes inaccurate, so family historians must exercise great care and keen judgment in constructing their histories. DNA testing offers a way to verify (or refute) records-based genealogical connections and to establish connections where no records exist. During the 19th and 20th centuries, several Americans with the name "Van Tuyl" sought records-based confirmation of their roots. In the late 20th century, with the advent of modern communications technology, we were able to expand the American tree and to connect these Van Tuyls to their Dutch relations in the Bommelerwaard.

The advent of affordable DNA testing in the 21st century - along with techniques for analyzing the genetic records carried in the DNA of every person- gave us an opportunity to confirm our genealogical results and to test the efficacy of certain DNA tests against a family tree connecting people with up to 21 generations of separation.

This paper describes the application of two types of DNA testing – SNP analysis and Y-STR analysis – to the family history of the family van Tuyl in The Netherlands and North America.

**SNP Test Results:**

In 2012 and 2013, we collected DNA samples from the Y-chromosomes of four Van Tuyl men in the United States and two in The Netherlands, all of whom claimed direct male-line descent from Ott Jansz van Tuyl of Gameren (b. ~1606). First, their Y-chromosomes were scanned to determine a characteristic pattern of slowly-mutating variations at single points in the DNA sequence. Mutations in these *Single Nucleotide Polymorphisms* [SNPs] occur very infrequently, and once such a mutation has occurred, it is unlikely to ever change again. As a consequence, these SNPs become markers identifying all male descendants of a common ancestor. Every male will carry a sequence of SNPs, some of them acquired over 100,000 years ago, others hundreds or thousands of years ago. The particular combination of SNPs carried by an individual is referred to as his *haplotype*. Men who share a *haplotype* are members of a *haplogroup*. Subdivisions of *haplogroups* are called *subclades*.

All the Van Tuyl men tested in this project belong to haplogroup R1b, subclade L11 (R1b-L11). This is the most common subclade for Western Europeans. About half of modern Dutch men belong to R1b-L11, whose defining SNP mutation dates back to the European Neolithic age some 130±35 generations (~4000 years) before the present. Since that time, new SNP mutations have occurred. The family van Tuyl first accumulated the mutation P312 from an ancient forbear whose descendants now comprise about 17% of the Dutch population. Subsequently, the Van Tuyls accumulated mutation DF27 but failed to accumulate Z196, implying their R1b *subclade* must be shared by about 3% of today's Dutch population. Figure 1 shows the distribution in Europe for known ancestors of men who share the Van Tuyl subclade, R1b-DF27 (without Z196). Figure 2 shows that four men of subclade R1b-DF27 had ancestors born near the Bommelerwaard.


**Fig. 1 – Reported locations for the earliest ancestors of men sharing the exact SNP haplotype of the family van Tuyl (R1b including P312 and DF27 mutations, but not the Z196 mutation). Points shown in Red correspond to the approximate extent of the proto-Celtic *Bell Beaker Culture* which existed during the period 2900 BC – 1800 BC at about the same time these SNP mutations occurred. Many DF27 ancestors clustered along the Rhine River from Switzerland to the Waal delta. (Data is from participants in the Family Tree DNA R1b-DF27 project).[1]**

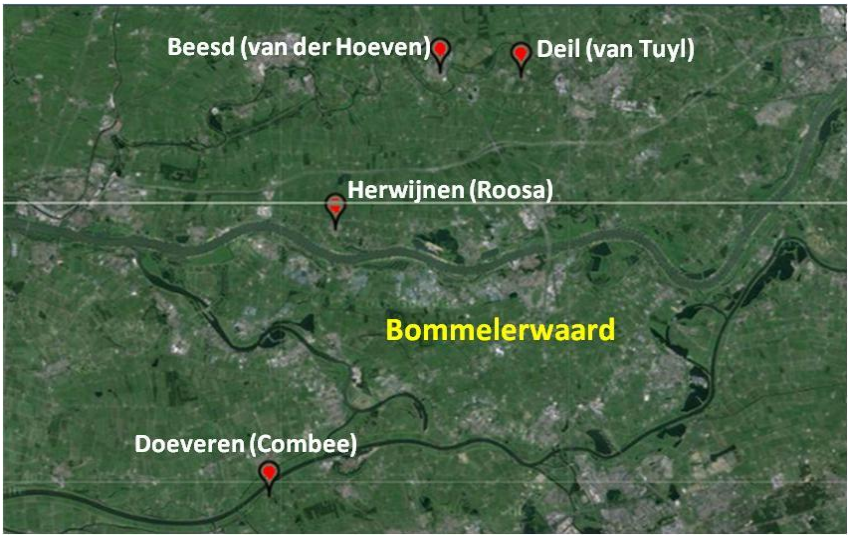


**Fig. 2 – Reported locations for R1b-DF27 ancestors near the Bommelerwaard. (Data is from participants in the Family Tree DNA R1b-P312 project).[2]**

SNP analysis is not selective enough to identify descendants of a particular ancestor within genealogical times (<20 generations). But it can identify those who are **not** members of this family. One American man named Van Tuyl joined the Van Tuyl DNA project and was shown to carry the I1 haplotype, implying he was descended from completely different ancestors than were the Van Tuyls. Detailed genealogical analysis pointed to a his great-grandfather born in 1852 in upstate New York and adopted by a childless Van Tuyl couple as the apparent source of this non-Van Tuyl DNA. Further analysis of his Y-STR haplotype showed that he very likely was descended from another Dutch-American family living in the neighborhood of the Van Tuyl couple in the 1850s.[3]

Quite significantly, SNP analysis was able to show that the family van Tuyll van Serooskerken is completely unrelated to the descendants of Ott Jansz van Tuyl. They are members of the subclade R1b-U106, whereas the family van Tuyl is R1b-P312. The most recent common ancestor of these two families – if there is one – must have lived about 4000 years ago!

**Y-STR Test Results:**

SNP mutation haplotypes can identify groups of men who share a common ancestor thousands of years in the past, but cannot identify relationships within the genealogical period stretching back 20 generations. To solve this problem, we must use another property of the Y-chromosome: the *Y chromosome Short Tandem Repeat* (Y-STR). Every chromosome possesses regions where short blocks of nucleotides with identical patterns repeat themselves in tandem. Fig. 3 illustrates an example of the Y-STR and shows how certain numbers of repeats are common and others are rare. The Y-STRs have mutation rates much higher than do SNPs, which are essentially static. The number of repeats in a sequence can change in a single generation, but on average these changes occur in tens to hundreds of generations. By examining a significant number of Y-STR Loci, we can find patterns that have emerged in such a way as to uniquely identify men who share a common ancestor within genealogical times. As long as there has been an uninterrupted chain of paternity associated with a family name inherited through the paternal line, family names and Y-STR haplotypes should correlate.

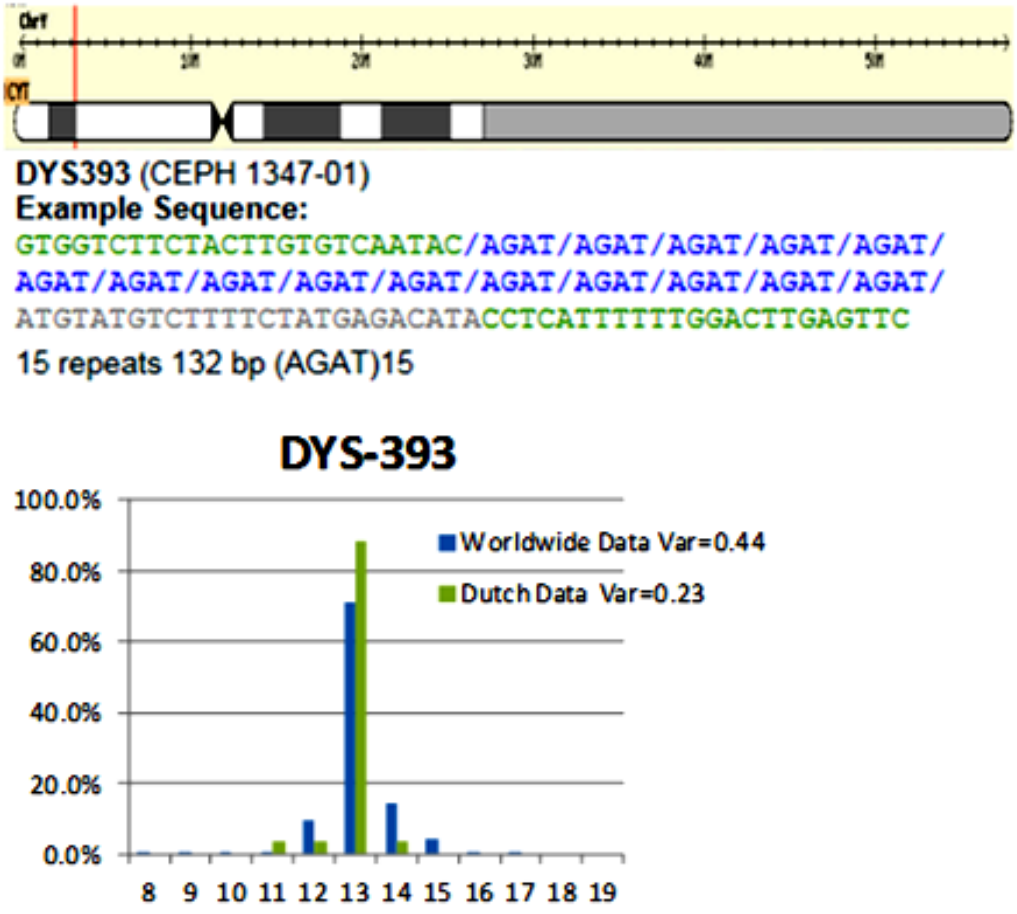


**Fig. 3 – Example of a Y-chromosome short tandem repeat [Y-STR]. At the locus marked on the chromosome with a red line, there exists a series of four-nucleotide repeats. The number of these repeats occurring in tandem can be counted and used to partially identify a person's genome. The frequency of occurrence for the number of repeats at this particular locus, DYS-393, is shown for worldwide data and for data from Dutch males. The most frequently-occurring number of repeats for this Y-STR locus is 13. The family van Tuyl has 12 repeats for DYS-393, a characteristic that is rare worldwide and even rarer for Dutch men. When several loci exist with rare numbers of repeats in a single person, the probability of finding another person with the same combination of repeats becomes very low unless those people share a common ancestor within genealogical times (<20 generations).**

Using the services of the genetic testing company *Family Tree DNA*[4], we tested the six members of the Van Tuyl DNA project, all of whom claimed descent from Ott Jansz van Tuyl of Gameren (b. ~1606). We found that a 37 locus Y-STR test was sufficient to positively determine their relationship, or lack of relationship. As we had hoped, all 6 men tested positive for membership in the genetic family van Tuyl. Using this data, we were able with high confidence to derive a combination of Y-STR values that can clearly identify a man as a Van Tuyl descendant. We call this combination the *Van Tuyl Haplotype*. Table 1 shows these four loci whose Y-STR values have mutated from the ancestral pattern in a way apparently unique to the family van Tuyl. The odds of this combination appearing by random chance are about 1 in 2 million. But since the odds that a citizen of the world is named "Van Tuyl" is probably one is several million, the chances that one of them is *not* a descendant of Ott Jansz van Tuyl yet nevertheless carries the Van Tuyl haplotype purely by chance is one in several trillion: virtually impossible.

| Y-STR Locus | Voorouders Haplotype | Mutatie | Van Tuyl Haplotype | Gem. Generaties tussen Mutaties |
|---|---|---|---|---|
| DYS-393 | 13 | >>>>>>> | 12 | 455 |
| DYS-438 | 12 | >>>>>>> | 13 | 625 |
| DYS-448 | 19 | >>>>>>> | 20 | 862 |
| DYS-570 | 17 | >>>>>>> | 18 | 158 |

**Table 1 – The core loci of the *Van Tuyl Haplotype*. These four mutations are extremely rare. The average number of years between mutations is expected to vary from 158 to 862, making this haplotype very stable through the generations. Taken together, the odds of this combination occurring by random chance *somewhere* in the population are 1:2,000,000. The odds that anyone named *Van Tuyl* would possess this combination of Y-STRs by random chance are infinitesimal.**

There are in total seven Y-STR loci that are informative as to the family relationships between these project members. Besides the four loci where all project members have identical Y-STR values, there are three that not all share. The pattern of these three loci identifies whether the person is a descendant of Geerlof Otten van Tuyl (the Dutch branch) or of Jan Otten van Tuyl (the American branch). Furthermore it appears to be possible to tell from which of two American branches a Van Tuyl man descended. These results are shown in Table 2.

| | Short Tandem Repeat Loci [Y-STR] | | | | | | |
|---|---|---|---|---|---|---|---|
| | DYS393 | DYS438 | DYS448 | DYS570 | DYS390 | DYS449 | DYS389b |
| Ott Jansz van Tuyl | 12 | 13 | 20 | 18 | 24 | 28 | 16 |
| Nederlandse 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 |

**Table 2 – Seven Y-STR Loci pertinent to the family van Tuyl and the branches of the family they identify. Values for the ancestor Ott Jansz van Tuyl are inferred from his descendants. Four loci are identical for all branches of the family and taken together form the core of the *Van Tuyl Haplotype*. The Dutch branch is identified by the DYS449 mutation where one STR is added, increasing the total from 28 to 29. The two American branches share a mutation of DYS390 from 24 to 23 which can therefore be used to discriminate between Dutch and American family members. The American descendants of Isaac Van Tuyl share a mutation of DYS-389b from 16 to 17 and can therefore be identified as distinct from the American descendants of Abraham Van Tuyl.**

Figure 4 illustrates the phylogeny of the family van Tuyl, with a timeline in years and number of generations. The SNP and Y-STR mutations in each branch are included.

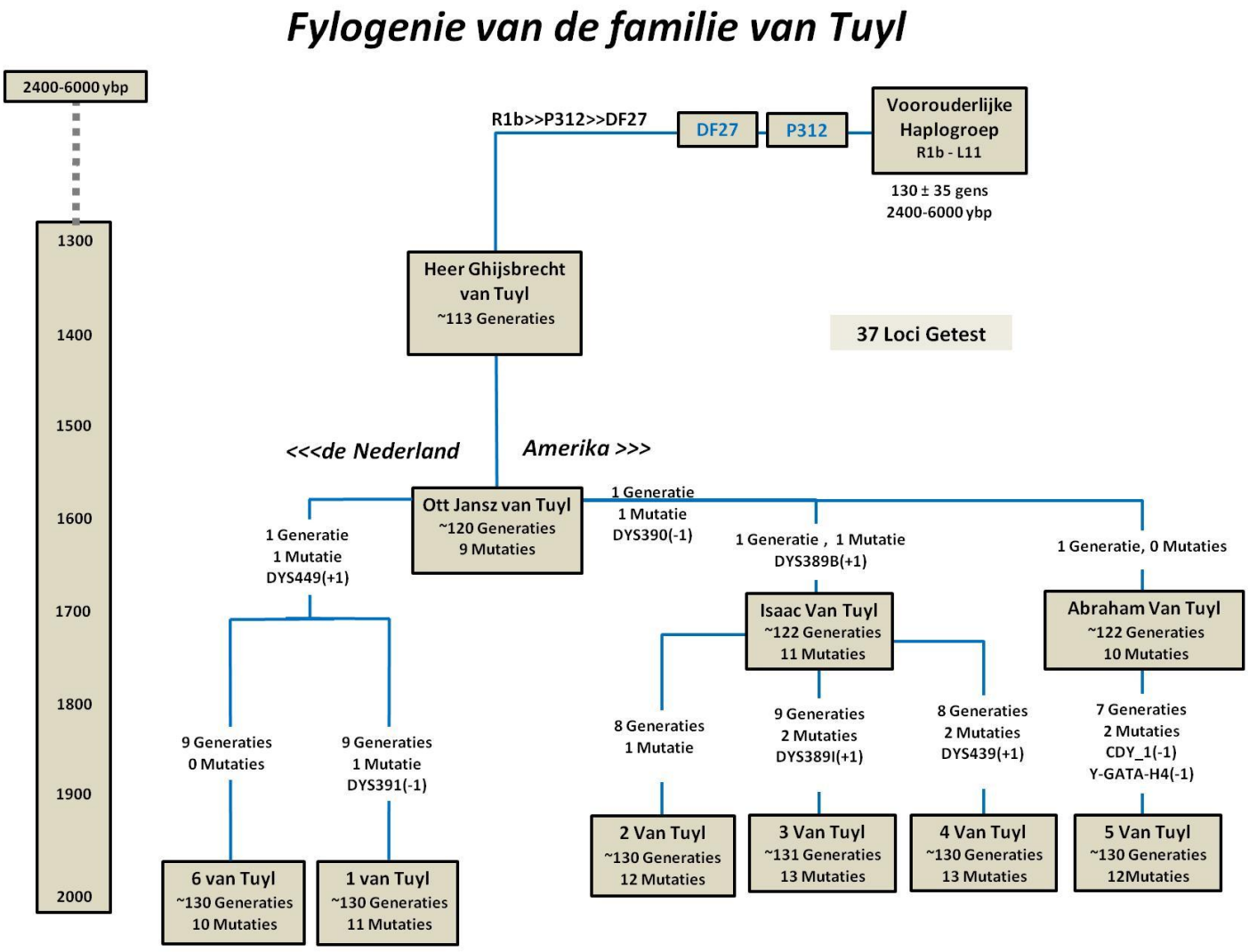


**Fig. 4 – Phylogeny of the family van Tuyl based on the six participants in the Van Tuyl DNA Project. About 130 generations have elapsed since the time of the ancestral haplogroup R1b – L11. During this time family members have accumulated two SNP mutations (P312 and DF27) and 10 to 13 Y-STR mutations. The precise pattern of Y-STR values shared by these participants is unique to the family van Tuyl and can be used to determine if a man is actually descended from Ott Jansz van Tuyl of Gameren (b. ~1606).**

## Conclusions

The Van Tuyl DNA project results were successful and informative on several counts:

1. We have verified the actual family relationship between 6 men named Van Tuyl. Their most recent common ancestor was born 400 years ago;
2. We demonstrated via SNP testing that one man named Van Tuyl is *not* a descendant of Ott Jansz van Tuyl, and using Y-STR haplotype analysis, we pinpointed a possible paternal connection for him in 19th century New York;
3. We established that - despite the confusion brought about by the similarity of names - there is in fact no genetic link between the families van Tuyl and van Tuyll van Serooskerken;
4. We linked the family van Tuyl to a particular clade of European descent, R1b-P312, and its subclade R1b-DF27 and showed that non-van Tuyls of this subclade inhabited the lower reaches of the Waal in former times;
5. We developed a Van Tuyl family haplotype, with variations of it indicating to which branch of the family a man belongs.

## Acknowledgements

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[1] http://www.familytreedna.com/public/R1b-DF27
[2] http://www.familytreedna.com/public/atlantic-r1b1c/
[3] This technique was similar to that used to prove that Thomas Jefferson was likely the father of children by his slave, Sally Hemmings. Paternity testing apparently knows no time limits.
[4] www.familytreedna.com