organism. DNA molecules allow this information to be passed from one generation to the next. Nearly every cell in a person's body has the same DNA.

DNA is made up of four building blocks called nucleotides: adenine (A), thymine (T), guanine (G), and cytosine (C). The nucleotides attach to each other (A with T, and G with C) to form chemical bonds called *base pairs*, which connect two DNA strands. The two DNA strands twist into the shape of a spiral ladder called a helix.

Human DNA consists of about 3 billion base pairs, and more than 99 percent of those bases are the same in all people on earth. The order, or sequence, of these bases determines the information available for building and maintaining an organism, like the way in which letters of the alphabet appear in a certain order to form words and sentences.

Genome - An organism's complete set of DNA is called its genome. Virtually every single cell in the body contains a complete copy of the approximately 3 billion DNA base pairs, or letters, that make up the human genome. Researchers have now finished sequencing the roughly 3 billion bases (or "letters") of DNA.

Gene - Genes are short pieces of DNA that carry specific genetic information, they are made up of sequences of DNA and are arranged, one after another, at specific locations on chromosomes. They are the basic unit of heredity passed from parent to child. They contain information for making specific proteins that lead to the expression of a particular physical characteristic or trait, such as hair color, or eye color, or to a particular function in a cell.

An international research effort called the Human Genome Project, which worked to determine the sequence of the human genome and identify the genes that it contains, estimated that humans have between 20,000 and 25,000 genes in almost every cell in our bodies. Most genes are the same in all people, but a small number of genes, less than 1%, are slightly different between people.

Genetic marker – A gene, or DNA sequence, with a known location on a chromosome. Genetic markers and genes that are close to each other on a chromosome tend to be inherited together. Examples of genetic markers are single polymorphism nucleotides (SNPs), and a variable number of tandem repeats (STRs). Genetic markers may or may not have a known function.

In short, chromosome, DNA, and gene work together to make you who you are. Chromosomes carry DNA in cells. DNA is responsible for building and maintaining your human structure. Genes are segments of your DNA, which give you physical characteristics that make you unique. Together, your body has a complete instruction manual that tells your cells how to behave.

1.2.2 Matching Haplotypes

STR test results define a person's haplotype. Haplotypes can be usefully compared to STR information of other persons. Such a comparison serves to detect possible recent genealogical relationships, essentially among living persons. However, the process requires a reliable number of STR markers and an existing database of confirmed haplotypes that is sufficient in size. Fortunately, the existing STR database at FTDNA[6] and its prediction program make it possible to carry out such a comparison. The prediction program delivers results in terms of exact and near matches.

Matching of Buursink STR values with existing haplotypes at FTDNA gives the following results:

> **Matching Haplotypes** - A comparison with existing haplotypes in the FTDNA database based on 12 markers results in 1 exact match with surname **Cremer**, paternal country of origin unknown.
>
> **Near Matches** - A near match is either one step or two steps genetic distance from our result and shows men that are distantly related. For 25 markers there is again a 1 step match with **Cremer**. There is a 2-step match with surname **Ewers**, paternal country of origin unknown.
>
> **Somewhat matching** – A comparison of my Y-DNA STR profile with that of other persons that are somewhat matching emerges from groupings that are genetically similar. Such groups appear on FTDNA website at the-Haplogroup H Y-DNA Project - Y-DNA Classic Chart. Here, the Buursink STR profile is listed in Group 6e[7]. Two other surnames appear in the same group – **Heida** and **Keuning**. Interestingly, all three are originally from the Netherlands (see also 2.5.). Only 12 markers are available for comparison in this case.

Haplotype information may reinforce or confirm historical genealogy information. In our case the above surnames with the above spellings do not appear in the Buursink genealogy since 1500.

Historical genealogy information on the Buursink family, since about 1500, is available in print format.[8] Prior to 1800 most Buursinks lived in Twente, in The Netherlands. There are four Buursink branches that descend from Welmer Buursink (1660-1748). Future STR analysis of individuals in the four branches would allow for a better understanding of recent genealogy and might confirm if all four branches indeed descend from the same Welmer, or not.

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[6] FTDNA = Family Tree DNA

[7] In 2024, Group 6e is marked as: H-L901 > H2-P96 > H2c-Z19080 > SK1180 > Z19072 > Z19049 > SK1182 > Y20839 > FT361585 > SK1177

[8] Buursink, John, 2003. *Buursink - Kroniek van een Twentse familie.* 626 p., Van Deinse Instituut, Enschede. ISBN 90-74064-205 and digitally at https://www.genealogieonline.nl/en/stamboom-buursink-een-twentse-familie/

Figure 38 Key mutations of Buursink Haplogroup H-P96 to modern times

Haplogroups & subclades	Haplogroup Age, BCE TMRCA	Prehistoric/Historic Period		
		Period	Subperiod	Approx. YBCE
H-P96	27 000	Stone Age	Upper Paleolithic	
H-SK1182 / Y21654	4 000	Stone Age	Neolithic	8 000 – 3 000
H-Y20839 / FT361585	1 900	Bronze Age / Iron Age		3 000 – 900/500
H-SK1177	100	Modern Historic Period		500 – date

In current genetic/genealogical research the level of mutations of H populations is usually limited to Haplogroup H2/P96. However, our Haplogroup mutations do not stop there. Haplogroup H2 did evolve after it was established and then mutated into its most recent terminal subclade H-SK1177.

Since 2021 our Haplogroup classification could be further refined because of Big Y-700 SNP testing. The Y-DNA Public Haplotree for Haplogroup H at FTDNA shows the position of the H2/H-P96 branch and its subclades seven levels down to H-SK1177 (Figure 39) [110].

Even the terminal subclade H-SK1177 has its uncertainties. In general, at least two testers from a descendant lineage are needed for a new branch to be named and added to the tree. In the case of H-SK1177, YFull reports 2 DNA tested descendants to support its classification. The two samples in the YFull Haplotree are labelled as YF05013 (Netherlands) and coded as YF84578) and YF09581 (France) identified as HGDP00528. FTDNA now also recognizes the same two descendants, one from the Netherlands and one from France.

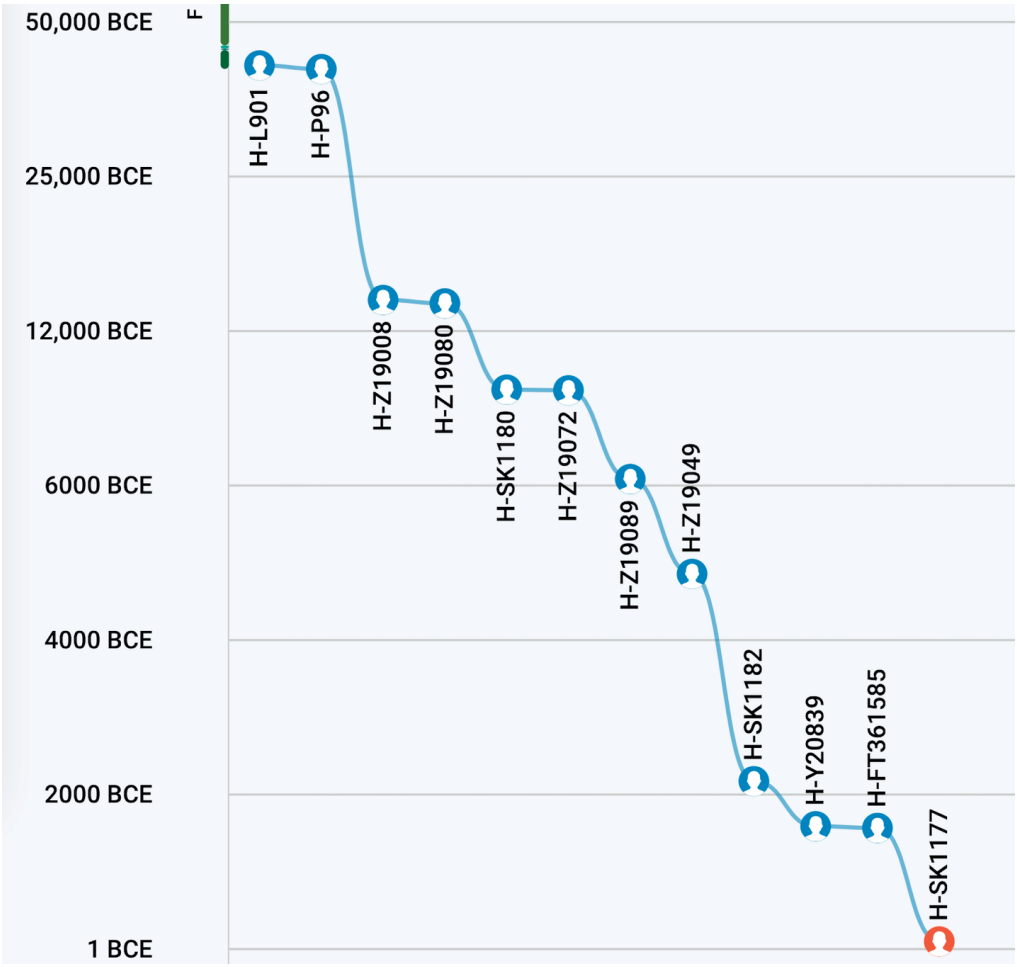
Further indication of the rapid research developments is the novel approach to the H2 classification that was proposed by Rohrlach, A.B. et al. (2021)[111]. As an alternative to the three H2/P96 "deep" classifications discussed above, Rohrlach et al. divide their H2 Haplogroup samples into two major clades depending on migration patterns, on how H2 ancestors moved across Europe, going from East to West. We will elaborate on the attractive Rohrlach proposals in Chapter 2.3.2. Rohrlach, et al. named the two clades as follows:

- H2d (green clade). All individuals are found along the so-called Inland/Danube route into central Europe,
- H2m (blue clade). All but one of the H2m individuals are found along the Mediterranean route into Western Europe, the Iberian Peninsula, and ultimately, Ireland.

[110] SK stands for Dr. Mark **S**tone**k**ing, M. Planck Inst. for E. Anthropology, Leipzig, Germany.

[111] Rohrlach, A.B. et al. *Using Y-chromosome capture enrichment to resolve haplogroup H2 shows new evidence for a two-path Neolithic expansion to Western Europe.* 2021; 11: 15005. Published online 2021 Jul 22. doi: 10.1038/s41598-021-94491-z : 34294811

Figure 39 Y DNA Haplotree from H2/P96 to terminal SK1177 level per FTDNA[112]



In 2023, FTDNA offered the following H-SK1177 Story with some further timeline detail:

- *"H-SK1177's paternal line was formed when it branched off from the ancestor H-FT361585 and the rest of mankind around 1550 BCE."*
- *"The man who is the most recent common ancestor of the H-SK1177's paternal line is estimated to have been born around 100 BCE. He is the most recent paternal line ancestor of all members of this group*".
- *"There are two DNA tested H-SK1177 descendants. Their earliest known origins are in France and in The Netherlands*".

[112] https://www.FTDNA.com/public/y-dna-haplotree/H (Dec 2021)

2.5.4 Some outstanding genealogical issues

Recent DNA research has greatly enriched our understanding of the origin and migration of our ancient ancestors. But, as usual, many questions remain, in particular in terms of unresolved genealogical relationships. Here, we mention a few of these unknown links that form a challenge to future DNA research.

The link between ancient and modern H2 persons
We lack reliable information and insight about the relationship between two groups of Y-DNA persons, between those living now and our ancient ancestors. Analysis of modern Y-DNA samples allows for detailed determination of Haplogroup subclades many levels deeper than the basic Haplogroup.

The FTDNA Y-DNA Public Haplotree for Haplogroup H shows the position of the H2/H-P96 branch and, in the Buursink case, its subclades some ten levels further down to the terminal SK1177 level. With regard to the living H2 Haplogroup men we have indications as to the number and geographic location of the persons sampled, which allows for some tracking of past migration trends. In ancient genomics generating 'high coverage', or high-quality genomes is a rarity. The publicly available SNP information on ancient H2 samples usually does not go deeper than H2 even as the persons sampled lived several levels more recent than the H2 "parent".

If the Y-DNA of ancient specimens could be identified past the H2 level, then relationships and location and eventual migration patterns of the H2 group as a whole might be better understood. We would like to see ancient samples placed into the phylogenetic tree to know how some of these H2 ancient persons are related to modern men.

Rohrlach, A.B. et al. (2021) [113] proposed an alternative approach, different from the phylogenetic tree, that is based on how certain groups of H2 people migrated along two routes. The authors were able to identify the ancient DNA characteristics of the two groups generally further to much deeper levels.

The link between terminal SNPs of modern H2 persons and their conventional family genealogy
The H2/P96 Haplogroup came into existence some 43 600 years BCE. Their descendants to Buursink DNA are in a specific section of the H2/P96 Haplogroup, which terminates at SK1177, and which originated only some 1 600 years BCE. The most recent common ancestor of the H-SK1177's paternal line is estimated to have been born around 100 BCE. Does this mean that since then no new SNPs have developed?
More importantly, how do DNA data link with what many people have established in their conventional genealogical research possibly since about 500 years ago? Often, there is a critical gap between 100 AD and !500 AD.

The link between H2 persons with identical terminal SNPs

[113] Rohrlach, A.B. et al. *Using Y-chromosome capture enrichment to resolve haplogroup H2 shows new evidence for a two-path Neolithic expansion to Western Europe.* 2021; 11: 15005. Published online 2021 Jul 22. doi: 10.1038/s41598-021-94491-z PMCID: PMC8298398. PMID: 34294811