Chapter Ten: The Origin and Evolution of the Rolnick Chromosomes

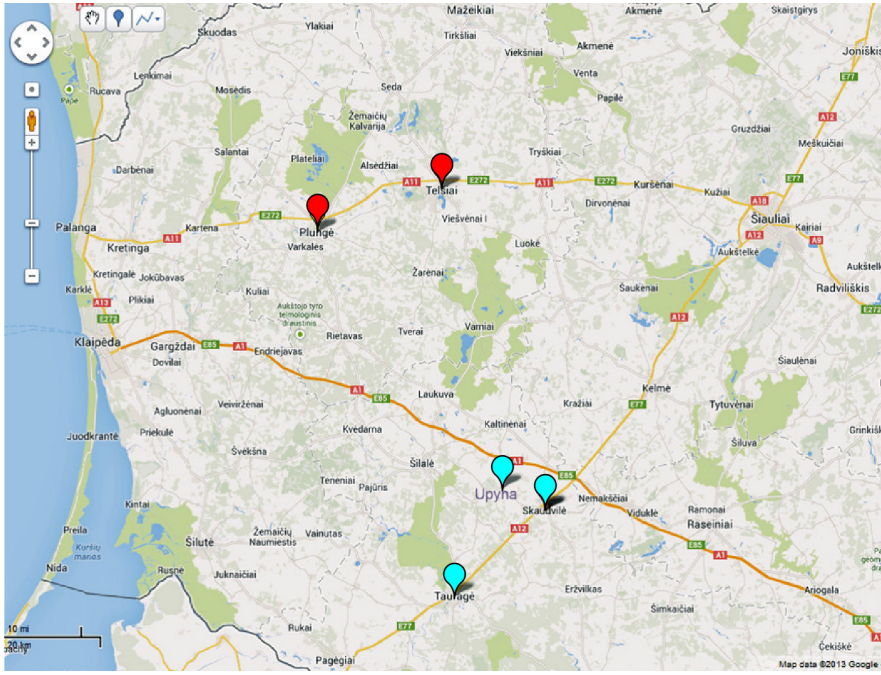
We all know how useful DNA testing has been in identifying people in criminal cases and in establishing parentage in disputed family origins. It was used, for instance, to track the children of Argentinian "disappeareds", by matching the DNA of children who had perhaps been seized by Argentinian security officers, with the DNA of their putative grandparents, the "Grandmothers of the Plaza de Mayo"[1]. DNA testing has now become part of genealogy. It can be used to confirm or deny the genealogical information found by searching family histories and official documents. I have used DNA studies in my research into the Lithuanian Rolnicks, and have managed both to confirm and to deny what I had found using the paper trails.

This is not going to be an easy chapter! There is much biology to become familiar with (or to recall if you know it already), and many names of people and places that we have read about in previous chapters but need to be reminded of. To help, let me put a map on the next page of our region of Lithuania with the names of the places I am discussing. We need to remind ourselves where Telsiai and Plunge are (in the Northern part of Lithuania, red peardrops) and where Upyna, Skaudvile, and Taurage are (in the Central part, blue peardrops).

As far as the people we will mention: from the Telsiai region, there will be Matthew Rolnick (of the New Jersey Rolnicks), Jerome Rolnick (of the Annapolis Rolnicks), and Gilad Ronnen (his name Hebraised from Rolnik, of the Plunge Rolniks). From the Upyna/Skaudvile/Taurage region there will be Stephen Rollnick (of the Wynberg Rollnicks), Anonymous Rolnick (of the Chicago Rolnicks), Robert Lewenson and Miriam Friedland (of the Wynberg Lewenson/Rollnicks) and the Silberstein/Silvertons (from Taurage and Upyna, with their story told in the Silberstein chapter). And now to the genetics:

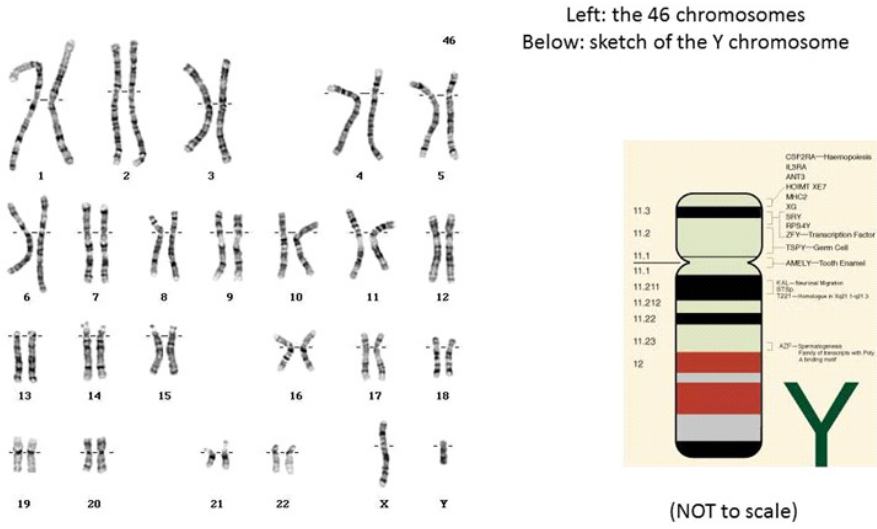
Each of us has 46 chromosomes in most of the cells of our bodies. These contain the long chains of genes that determined the embryological development of our bodies and continue to determine their maintenance. The genes themselves are the DNA, strings of the nucleotide bases which

[1] http://www.theguardian.com/world/2009/dec/30/argentina-dna-tests-babies-disappeared



The Northern (red) and Central (blue) Rolniks

we will write later as A, C, T, and G[2]. Look at the picture of the chromosomes on the left side of the following figure (the right side is a sketch of just the Y chromosome with some of the genes that it contains depicted on it):



[2] A for adenosine, C for cytosine, T for thymidine and G for guanosine
http://www.nyu.edu/pages/mathmol/library/dna/

44 of the chromosomes are found in pairs, one of each pair being contributed by our mother and the other by our father. In addition, men get a single chromosome, the Y chromosome, from their father and an X chromosome from their mother. Women get one X from their mother and another from their father. The 22 pairs that are neither X nor Y are called the autosomal chromosomes. The Y chromosome, the X chromosomes and the set of autosomal chromosomes together comprise the genome and contain our genetic information. Studies of all three are needed to give a full picture of one's heredity.

Let me give here the conclusions of this difficult chapter:

Analyzing DNA has become a valuable tool for researching family history. For the Lithuanian Rolnicks it showed that the Northern (Telsiai) Rolniks and the Central (Upyna/Skaudvile) Rolniks were not related, both tribes having independently taken on the occupational name of rolnik/farmer. This contradicted what had seemed clear on the documentary evidence. But for the Upyna/Skaudvile Rolniks, DNA analysis has shown that they are indeed a single tribe, fully confirming what had been only surmised based on family histories.

Studies on Y DNA

STR's: Short Tandem Repeats in Genealogy

Much data is accumulating on DNA-based markers that sit on the Y chromosome. Digging into the Y-DNA database in the case of the Rolniks of Lithuania, and other families close to them genetically, I have been able to track their wanderings across Europe before surnames came into use[3]. The trick is to use the STR's (Short Tandem Repeats) that are scattered along the chromosomes. But before we discuss STR's in detail, consider the following useful analogy:

Attached to most of the things that we pick up at the supermarket are these little bar-codes that, among other bits of information, tell you what the product is and from where it comes.

The DNA in the cells of our body is full of such bar-codes but these are not written in ink. Instead they are made of the long strings of the four bases, A, C, T and G that, as we saw, DNA is made from. In much of our DNA,

[3] Part of this material on the Y chromosome is taken from an essay that I wrote that was published in Avotaynu, a journal devoted to Jewish Genealogy (http://www.avotaynu.com/.) Avotaynu, Vol. 28, Summer 2012 p.21-49

these strings of DNA contain crucial genetic information that tells the cells what they must do, but some of the DNA seems to have no message and may be just "junk DNA". It is these bits of junk DNA that can be used to bar-code us. In this chapter, I will describe how these junk bar-codes can be used to work out the evolution of the human species and our dispersion all over the globe. The Rolnicks, being humans, can be studied in the same way and we can, to some extent, work out where the Rolnicks originated and how they are related to other folk. We do this by studying the "bar-codes" on the Y chromosome.

Just as we males inherit our surname from our father (fortunately for genealogists) and generally keep it throughout our life, so we inherit our Y chromosome. Thus the Y chromosome of the Northern Rolnicks has come down, together with their surname, all the way from Leyba Rolnik (who was born in 1760 in Telsiai, Lithuania). Scattered along the Y chromosome (and along the other chromosomes, too) are strings of junk DNA that are found as repeated patterns of A's, C's, T's and G's. It is these Short Tandem[4] Repeats (STR's) that are the bar-codes. The number of repeats is like the width of a line on the supermarket's bar-code and this carries the information. Here is one such STR, called DYS 385a[5]:

GAAAGAAAGAAAGAAAGAAAGAAA…. And this GAAA can repeat 12 to 17 times in different men (I myself have 13 repeats at marker DYS 385a).

Another STR, called this time YCAii (The STR's names are named conventionally and we can think of them as simply names) is :

CACACACACACACA…….. "CA" going on for between 11 and 22 repeats. (I have 19 repeats of CA at my YCAii marker).

These markers look like, and are, real junky messages but, since this DNA is handed down from father to son to grandson, the number of times that GAAA comes up at marker DYS 385a enables us to link up fathers and sons. Similarly for YCAii and for the other hundreds of such STR markers that have been identified. The chances are high that my sons and their sons will have the same 13 repeats at DYS 385a and 19 at YCAii as I have. But occasionally, when the Y chromosome is handed down, there is a copying error[6]. One of the repeated elements,

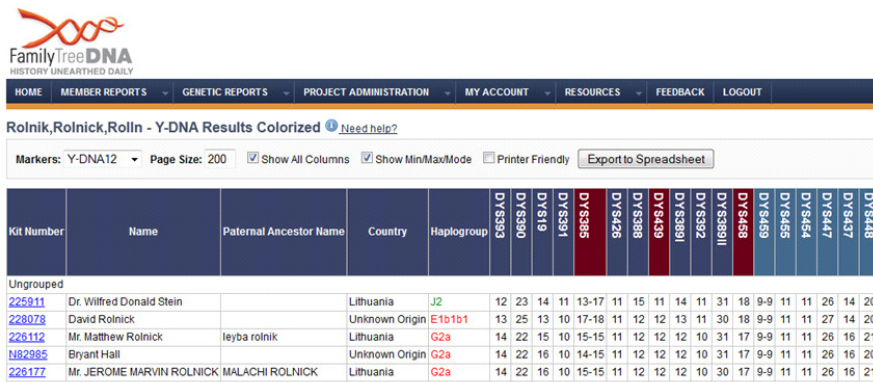
[4] Tandem, like on a tandem bicycle, one in front of the other.

[5] DYS stands for **D**iagnostic **Y**-chromosome **S**TR. I will sometimes refer to the STR's without the DYS prefix.

[6] Handing down the DNA requires the father's DNA to be copied when the sperm cells are made. Each time DNA is copied there is a chance that an error is made somewhere so that the copy will differ from the original. Similarly, when the mother's DNA is handed down a generation, errors can arise in the copying process. In the vast majority of cases such errors have no significance for the healthy functioning of the offspring.

perhaps the GAAA on DYS 385a, can be added or subtracted so that my greatgrandson might perhaps have 14 or 12 repeats at DYS385a instead of my 13 repeats or perhaps 20 or 18 at YCAii. This is known as a genetic step between two people in the same line of descent. A simple cheek swab can be used for the genetic testing[7]. Many people studied by these STR methods will have had 37 marker STR's looked at. This number makes a useful compromise between extracting the maximum possible genetic information and the increasing costs of looking at additional markers. In such a set of 37 markers a genetic step, a change in the number of repeats at one of the 37, will occur, on average, about once every four generations or as a round number, every 100 years, a useful number to remember.

I have listed, with the company FTDNA, the "Rolnik, Rolnick, Rollnick" surname group. A number of Rolnicks and people related to Rolnicks have contributed a cheek swab test to the group. The result of such a test comes as a report that looks like the picture below. (This shows just a section of the full report, 18 of the many STR's that people can be tested for).



Kit Number	Name	Paternal Ancestor Name	Country	Haplogroup	DYS393	DYS390	DYS19	DYS391	DYS385	DYS426	DYS388	DYS439	DYS389I	DYS392	DYS389II	DYS458	DYS459	DYS455	DYS454	DYS447	DYS437	DYS448
Ungrouped																						
225911	Dr. Wilfred Donald Stein		Lithuania	J2	12	23	14	11	13-17	11	15	11	14	11	31	18	9-9	11	11	26	14	20
228078	David Rolnick		Unknown Origin	E1b1b1	13	25	13	10	17-18	11	12	12	13	11	30	18	9-9	11	11	27	14	20
226112	Mr. Matthew Rolnick	leyba rolnik	Lithuania	G2a	14	22	15	10	15-15	11	12	12	12	10	31	17	9-9	11	11	26	16	21
N82985	Bryant Hall		Unknown Origin	G2a	14	22	16	10	14-15	11	12	12	12	10	31	17	9-9	11	11	26	16	20
226177	Mr. JEROME MARVIN ROLNICK	MALACHI ROLNICK	Lithuania	G2a	14	22	16	10	15-15	11	12	12	12	10	30	17	9-9	11	11	26	16	21

Here we see five current and analysed members of our Rolnik, Rolnick, Rollnick project group. The STR's are listed by name in the thick, dark row and the number of repeats at that STR is shown below the label. The Haplogroup column shows to which haplogroup a person belongs[8].

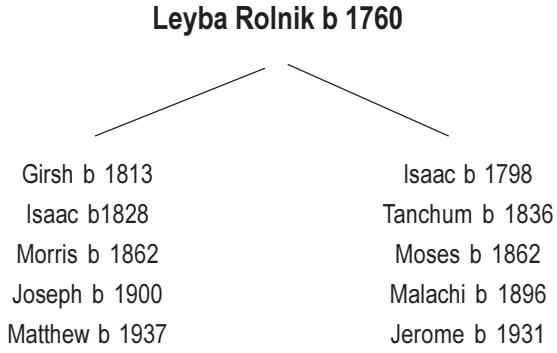
The first row shows the results for Dr. Wilfred Donald Stein (who

[7] The commercial firms that do this "recreational" genetic testing of cheek swabs offer various packages of marker tests. The widely-used FTDNA (https://my.familytreedna.com) offers the possibility of testing 12, 25, 37, 65 or 111 markers at an increasing price.

[8] A haplogroup is a line of people who share a common descent demonstrated by their sharing of rare mutations in DNA that appeared one after the other as copying errors in previous generations. The word **haplogroup** comes from the Greek *haploûs*, "onefold, single, simple" where this prefix *haplo* was originally used to refer to a single one of the two chromosomes in a pair. For a wonderful article on Y DNA haplogroups see Gabor Balogh at http://photos.geni.com/p13/8e/6d/a5/02/5344483a5c961516/260053_j2_ancestral_journey_eng_original.pdf

snuck into the group as its administrator, although it was really his maternal grandfather who carried a Rolnick chromosome). The results for three men with surname Rolnick are shown. One can see already on this small piece of the whole report that David Rolnick's pattern is distinctly different (in total it is more than thirty steps away) from that of Matthew and Jerome, whose patterns differ from each other by only two steps of the 37 for which they were tested[9]. Bryant Hall's pattern is close to that of the two Lithuanian origin Rolnicks, only 6 steps different. He must share a Most Recent Common Ancestor (MRCA) with the Lithuanian Rolnicks some 600 years back. (Hall joined the group after his connection to it was discovered). From the number of genetic step differences (or "mismatches") that were found, David Rolnick probably diverged from Hall and from Matthew and Jerome Rolnick more than three thousand years ago. Wilfred Stein is also thousands of years away in origin from them.

Now Matthew and Jerome have the following ancestry tree:



Their Most Recent Common Ancestor was Leyba Rolnik who was born in Telsiai, Lithuania, about 175 years before they were and was the first Lithuanian Rolnik to adopt that surname. This fits very well with the two genetic steps that they differ by, for which we expect a common ancestor back at *about* 200 years, not too far from the 175 years for which we have proper documentation.

We can move further along with this Y chromosome stuff. Over 100,000 men world-wide have had their STR markers analysed. The resulting data have been tabulated and there are dozens of people studying the results. A website called "**ysearch**" lets one search this database[10].

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[9] The two differ by one step each at STR markers DYS19 and DYS389/2, the latter being shown on the section of the report that is reproduced in the figure above.

For example, doing a search by using the name "Rolnick" gives:

User ID	Last	Ancestor	Origin	Haplogroup	Tested With
CHZVW	ROLNICK	rolnik	Telsiai,	G2a	Family Tree DNA
JQ2WA	Rolnick	Rolnick	Minsk,	E1b1b1	Family Tree DNA
Y27EP	Rolnick	Rolnik	Telsiai,	G2a*	Family Tree DNA

These are the three Rolnicks in the earlier picture of the YDNA report. Proceeding further, and using now the User ID's in this table, one can search for all the people in the **ysearch** database who are, at these 37 markers, 6 steps or less away from the queried person. For "CHZVW ROLNICK" of our Telsiai (Lithuanian) Rolnicks one gets the Table that follows, where the column headed "Steps" is the number of genetic steps or marker mismatches between the person listed and Rolnick J.

Searching with CHZVW, J. Rolnick's ID number, at 37 Markers

User ID	Last Name	Family Origin	Haplogroup	Markers Compared	Steps
CHZVW	Rolnick J	Telsiai, Lithuania	G2a (tested)	37	0
EEC6P	Drabkin	Mogilev, Belarus	Unknown	37	2
S7FKB	Hammer	Austro-Hungarian Empire	G2a (tested)	37	2
Y27EP	Rolnick M	Telsiai, Lithuania	G2a*	37	2
83TK3	Meyers	Yannisic, Lithuania	G2a1a (tested)	37	3
CCTR3	Sneirson	Vabalninkas and Panevezys, Lithuania	Unknown	37	3
GTTY9	Stearns	Unknown	Unknown	37	3
69GQ5	Weissman	Russia	Unknown	37	4
ZV2W5	Rothstein	Tolochin, Belarus	Unknown	37	4
JKU24	Hall	Unknown	Unknown	37	6

This is an amazing result. From amongst the 100,000 men in the **ysearch** database as at October 2013, it is only these ten men who are six steps or less away from each other[11]. They are a little family grouping (we can call them the Co-Rolnicks) whose Most Recent Common Ancestor (MRCA) lived some 600 years ago, and in whose ancestral line a series of mutations took place that separated them off genealogically from the rest of humanity. (Of course, as more people have their Y-chromosomes analysed, the number that are in the Co-Rolnick grouping will expand). Knowing the mutations that differ within this tight group one can build a tentative chart of how they relate to each other.

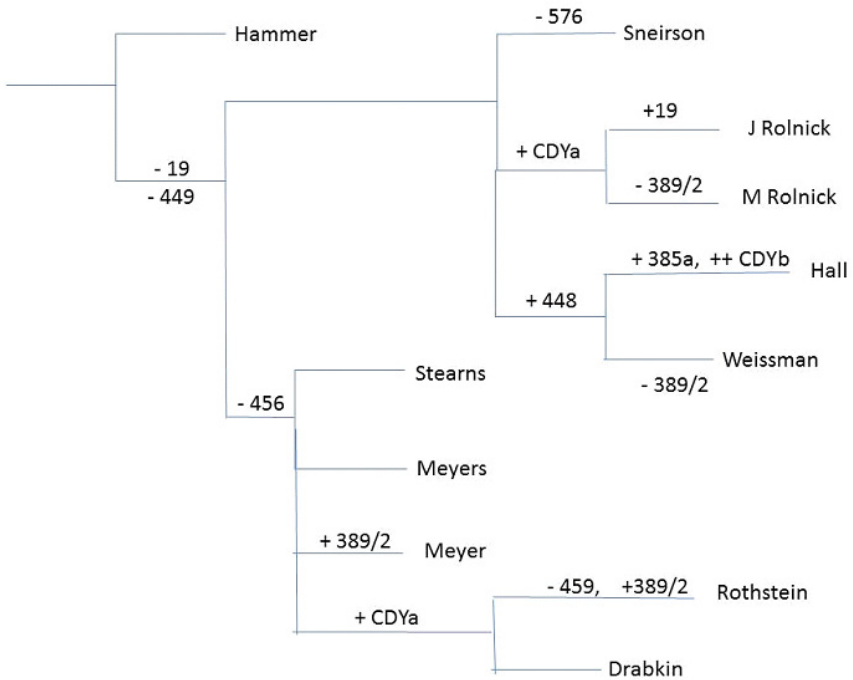
In the Family Tree of the Co-Rolnicks that follows, the numbers close to each horizontal line give the name of the STR marker (or

[10] Go to http://www.ysearch.org/lastname_start.asp?uid=S7FKB, put in a family name and see what comes up.

[11] One can choose any of these ten men. One always comes up with the same list...these ten individuals.

markers) that mutated and caused the descendant family lines to split up as a result. (For simplicity, I have left out the DYS's in the names). A plus indicates that the mutation was an increase in the number of repeats at this marker, a minus that there was a decrease. If two such markers are listed, there were two steps between a person and his next identified descendant. If no marker is listed, that line continued with no marker having mutated between the MRCA (the join point) and the next person depicted, or next join point):

Family Tree of the Co-Rolnicks

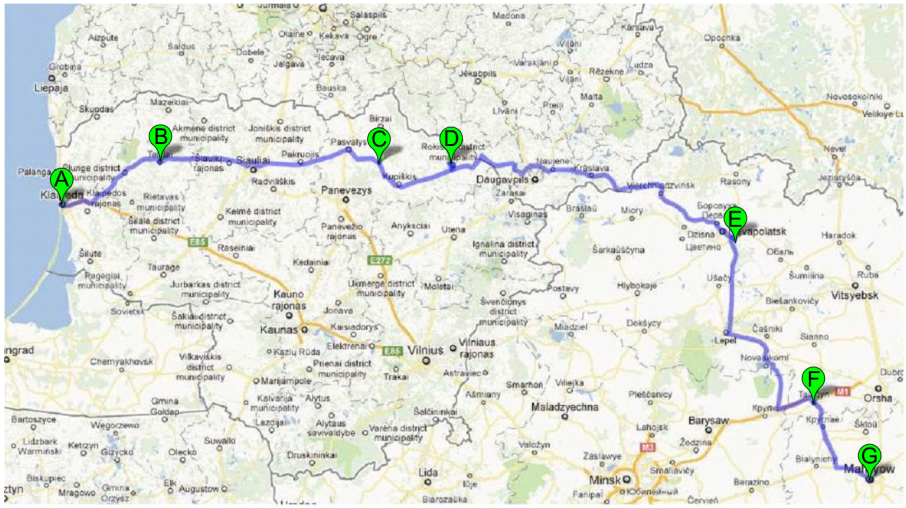


Meyers and Stearns do not differ even at one step in the 37 markers. They could be as close as 2 generations apart, second cousins, with the two lines splitting perhaps less than fifty years ago.

Many of these donors of cheek swabs listed the place of origin of their ancestors. The map at the top of the next page shows all who came from the Pale of Russia, from Lithuania or from Belarus[12].

Hammer, in the Family Tree above, whose line split off from the others two steps or some two hundred years ago, and who is not listed

[12] Two did not state their ancestral place of origin. For one of them, this study gave valuable information on his ancestry.



A Meyer, B Rolnick, C Sneirson, D Meyers, E Weissman, F Rothstein, G Drabkin

on the map, gives his ancestral origin as Austria-Hungary[13]. The men most closely related to him are towards the West on the map above; those further from him genetically are towards the East. I suggest this distribution is not a coincidence and that members of the family group actually migrated from West to East, mutating along the way, over the 500 years that separate Hammer's ancestor from the folk in Belarus. Only Meyer and Meyers (whose Most Recent Common Ancestor lived about a hundred years ago) have surnames that are similar. This is not surprising. Surnames came into common use in the Pale of Russia only after 1805, when the ancestors of these families had already moved far away from one another and chose very different surnames[14].

So where did our little group of Co-Rolnicks themselves originate? We can get help again from the **ysearch** database. We can, in our search, relax the constraint that a member of our little group must match an unknown person at all 37 markers by 6 genetic steps. Let's compare

[13] The ancestral group's living representative, Michael Hammer, is a well-known student of genetic origins, with his work on the Cohens being known to many. Conversations between him and a venture capitalist with an interest in genealogy, Bennet Greenspan, led to the founding of Family Tree DNA, the foremost such company (http://en.wikipedia.org/wiki/FamilyTreeDNA). Sherman Weissman , also in the little group, is a Professor of Genetics at Harvard University and hosted Francis Collins (later to become director of the Human Genome project) when Francis was a post-doctoral investigator.

[14] The earliest records I have found for the surnames in these families is our Leyba Rolnik in 1816 (http://data.jewishgen.org/wconnect/wc.dll?jg~jgsearch ~model2~ [NEWRL _REG]NEWRL_REGI3) and Essel Drabkin in 1827 (http://data.jewishgen.org/wconnect/wc.dll?jg~jgsys~sigsview~ 76121~ DRABKIN~904;7).

only 25 markers. What we find, for instance for the Rothstein of our group, is the following:

Searching with ZV2W5, Rothstein's ID number, at 25 Markers

User ID	Last Name	Origin	Haplogroup	Markers Compared	Steps
ZV2W5	Rothstein	Tolochin, Belarus	G2a (tested)	25	0
Y27EP	Rolnick M	Telsiai, Lithuania	G2a*	25	1
69GQ5	Weissman	Russia	Unknown	25	2
83TK3	Meyers	Yannisic, Lithuania	G2a1a (tested)	25	2
CCTR3	Sneirson	Vabalninkas , Lithuania	Unknown	25	2
EEC6P	Drabkin	Mogilev, Belarus	Unknown	25	2
GTTY9	Stearns	Unknown	Unknown	25	2
CHZVW	Rolnick J	Telsiai, Lithuania	G2a (tested)	25	3
VKTX9	Sor_Kashgar	Kashgar, China	Unknown	25	3
S7FKB	Hammer	Austro-Hungarian Empire	G2a (tested)	25	4
JKU24	Hall	Unknown	Unknown	25	4
CSJK6	Moody	Moulton, England	G2a1a (tested)	25	4
J5AYR	Moody	England	Unknown	25	5
CH3U6	Moody	Unknown	Unknown	25	5
9EMCY	Salinas	Mexico	Unknown	25	6
WFDB9	Linares	Ica, Peru	Unknown	25	6

The Co-Rolnicks are still present, of course, but the list has expanded since now we looked for "relatives" who match at only 25 markers, not the 37 that we considered before. It includes an obscure individual from Kashgar in China[15], three members of the Moody family with origins in England but also two men from South America, a Mr. Salinas from Mexico and a Mr. Linares from Peru. It turns out that our Michael Hammer and Linares from Peru, when compared at the 35 STR markers that they have in common, are only 9 mutations apart suggesting that their Most Recent Common Ancestor lived some 900 years ago, perhaps around 1200 AD. When one looks at all the available STR markers (and

[15] This "Sor-Kashgar" is an individual living in Kashgar, China. His ancestors separated from the Hammer founder line together with our little group, but then went in quite another genetic direction, some 500 years ago. "Sor-Kashgar" has no other genetic matches closer than with Meyers in our group at six steps or less over the 34 STR markers that he was tested for (he was tested by another company that tests with a slightly different STR marker set). It would be interesting to find out who he is. His Co-Rolnick ancestor could even have travelled to China as a companion to Marco Polo!

not just 25 as in the Table above), these Spanish speakers are the closest male persons to the Co-Rolnicks. (As a sort of "control", I did a similar analysis of my own Y chromosome DNA results. I found no links with Spain or the Mediterranean region. All my "relatives" and relatives of relatives were from Eastern and Central Europe.)

In the essay that I wrote for the journal Avotaynu, I argued on the basis of these and some further analyses that the original members of this tribe of Co-Rolnicks may have originated in Spain, Sephardi Jews who lived in Spain before the Expulsion of 1492. The full argument for this hypothesis will be found in my Avotaynu essay. There are, indeed,many cases of people with Ashkenazi surnames having Sephardi roots and a special Group at FTDNA is dedicated to researching this issue[16].

As far as our Rolnicks are concerned, what we had learned was that the Rolniks from Plunge (whose DNA was analysed from a cheek swab contributed by Gilad Ronnen[17], grandson of Meir Rolnik from Plunge), the Rolnicks from Annapolis (from a cheek swab contributed by Jerome Rolnick grandson of Moses Rolnick from Annapolis) and the Rolnicks from New Jersey (on the basis of Matthew Rolnick's cheek swab, Matthew being a grandson of Morris Rolnick of New Jersey), are all descendants of Leyba Rolnik of Telsiai. The paper trails and the Y-DNA analyses converge exactly.

I expected, therefore, when Stephen Rollnick (a great grandson of Wolf Rollnick of the shtetl Upyna and later Wynberg) sent in his cheek swab, the result would show that all the Lithuanian Rolnik/Rolnick/Rollnicks were also descended from Leyba of Telsiai, although I had been just a little doubtful. The paper trail in the Jewish Genealogy database had shown clearly that Yosel of Upyna, Wolf Rollnick's father, was the son of Leyba. There was indeed a Yosel living in Telsiai, son of a Leyba of Telsiai, and there was nothing to rule out his having relocated from Telsiai to Upyna. The records showed also that this Yosel of Telsiai had a son called Vulf. But this Vulf Rolnik was definitely still living when my grandfather Wolf was born. There could not be one Yosel with two sons, both called Vulf or Wolf. Were the two Yosels, each father of a Vulf, the same person…or not?

In the event, Stephen's Y DNA turned to be totally different from that of Gilad, Jerome and Matthew. He was in a different haplogroup (see the footnote 8 below the Table of STR's on page 389), the two family lines having separated from each other more than ten thousand years ago. The Telsiai Rolnicks (let's call them the Northern Rolnicks) are in

[16] http://www.jta.org/2009/08/14/life-religion/zeide-wasnt-meshuga-family-has-sephardic-genes

[17] The family name was Hebraised from Rolnik to Ronnen.

haplogroup G2a. Stephen (from the Central Rolnicks) is in J2. But Stephen was not alone with this YDNA profile. Robert Lewenson, a great grandson of Wolf Rollnick's brother James Lewenson, had his YDNA tested. It was just two markers away from Stephen's. Finally a greatgrandson of Berl Rolnik (brother to Wolf Rollnick and to James Lewenson) agreed to have his cheek swab tested, as long as his name was not listed. Anonymous Rolnick is just one step away from Stephen and three from Robert. It would seem, therefore, that when surnames were adopted after 1805, two separate households living in Lithuania took the name Rolnik. Both families might have been farmers and the Polish word rolnik, which translates as farmer, seemed to them to be appropriate. Return now to the map on page 386. The Rolniks and Rolnicks with origins in Telsiai and nearby Plunge are from the Northern Rolnicks. The Rollnicks, Rolnicks, and Lewensons with origins in Upyna are from the Central Rolnicks.

Below I show the latest version of the Table of STR's for the members of the Rolnik/Rolnick/Rollnick Surname project after Anonymous had joined us. You will see in this Table a number of men who have joined the project in order to find out more about their origins. One of them, David Richards, is just one step away from Stephen Rolnick and he had hoped that the Y DNA analysis would enable him to find the family of his Ashkenazi grandfather. So far his search has not yet been successful.

The Table of STR's for the Rolnik/Rolnick/Rollnick surname project looked like this after Anonymous's contribution was included:

Kit Number	Name	Paternal Ancestor Name	Country	Haplogroup	DYS393	DYS390	DYS19	DYS391	DYS385	DYS426	DYS388	DYS439	DYS389I	DYS392	DYS389II	DYS458	DYS459	DYS455
Rolnik,Rolnick,Rolln & me																		
225911	Dr. Wilfred Donald Stein		Lithuania	J2	12	23	14	11	13-17	11	15	11	14	11	31	18	9-9	11
228078	David Rolnick		Unknown Origin	E1b1b1	13	25	13	10	17-18	11	12	12	13	11	30	18	9-9	11
226112	Mr. Matthew Rolnick	leyba rolnik	Lithuania	G2a	14	22	15	10	15-15	11	12	12	12	10	31	17	9-9	11
N82985	Bryant Hall		Unknown Origin	G2a	14	22	16	10	14-15	11	12	12	12	10	31	17	9-9	11
226177	Mr. JEROME MARVIN ROLNICK	MALACHI ROLNICK	Lithuania	G2a	14	22	16	10	15-15	11	12	12	12	10	30	17	9-9	11
Ungrouped																		
226303	Jesse Rolnick	Abraham Abe Rolnik b. abt 1864 Russia d. 1928 NY	Unknown Origin	J2	12	22	14	10	14-15	11	15	12	14	11	31	15	9-9	11
156545	Mr. Sheldon Yusim		Unknown Origin	J1	12	23	14	10	13-15	11	16	12	13	11	30	18	8-9	11
96367	David J. Richards	Robert Richards b 1909 Philadelphia, PA	Unknown Origin	J2a4b	12	23	14	10	13-17	11	16	11	13	11	30	18	9-9	11
261862	Anonymous Rolnick		Unknown Origin	J2	12	23	14	10	13-17	11	16	11	13	11	30	18	9-9	11
230343	Dr. Stephen Rollnick		Lithuania	J2	12	23	14	10	13-17	11	16	11	13	11	30	18	9-9	11
230344	Mr. Stefan Rollnick		Unknown Origin	J2	12	23	14	10	13-17	11	16	11	13	11	30	18	9-9	11
245049	Mr. Robert Lewenson		Lithuania	J2	12	23	14	10	13-17	11	16	11	13	11	30	19	9-9	11
241562	Bart Rizzo	rizzo	Italy	E1b1b1	13	24	13	11	16-18	11	12	11	13	11	30	15	9-9	11
228508	Mr. gilad ronnen	Rolnik, eilenger, aptovizer	Lithuania	G2a	14	22	15	10	15-15	11	12	12	12	10	31	17	9-9	11
199857	Gerald Lynn Sneirson	Miche Louis Yehuda Sneierson, b. 1858, Vabalninkas	Lithuania	G2a	14	22	16	10	15-15	11	12	12	12	10	31	17	9-9	11

See now how Anonymous Rolnick, Stephen Rollnick and his son Stefan, and Robert Lewenson all have the STR's sequence 12 23 14 10 13-17 11 16 13 11 30 as only David Richards does in this Table, and then all, except Robert, continue with 18 9-9 and 11. These five are closely related, all a very few steps away from one another. All are very different from Matthew Rolnick, Jerome Rolnick and Gilad Ronnen with their defining sequence of 14 22 (15 or 16) 10 15-15 11 12 12 12 10 (30 or 31)

and 17 9-9 11. This latter sequence characterizes the Telsiai Rolnicks, while that shared by Anonymous and his relations characterizes the Upyna Rolnicks. I had originally intended to call this book "The Rolnick Chromosome". In the event, I have had to name it "The Rolnick Chromosomes". The two tribes are in different haplogroups, having separated tens of thousands of years ago and then having come together as members of the community of the Jews of Lithuania.

We saw earlier that the Telsiai Rolnicks were, in their Y DNA sequences, close (6 or fewer steps away) to only ten men in the **ysearch** database at 37 markers and to only a score when 25 markers were looked at. In great contrast, the Upyna Rolnicks are in a huge family of closely related individuals. Stephen Rollnick has 19 men who are 1 step away and 144 who are 4 steps or fewer distant. FTDNA doesn't even list the 5's and 6's! I have not been able to find any discussion of why there should be such great differences…a tiny group surrounding the Telsiai Rolnicks and an enormous one containing the Upyna namesakes. My own Stein group is again small, only one person as close as 2 steps away and only 18 in all at 4 steps distance. Of these 18, 11 are found in Stephen's close group so we Steins seem to be a sub-group of those around the Upyna Rolnicks. I myself am five steps away from Stephen.

There are two important points to make about the Upyna Rolnick Chromosome: First, Stephen Rollnick's haplogroup is a subgroup of the J's and is perhaps a haplogroup called J2a1b (M172)[18]. This group may have emerged in the Fertile Crescent containing present-day Palestine some time before Jericho was established[19], at the beginnings of the diffusion of domesticated cattle and goats.

Second, in the records of the Cape Town Jewish cemetery[20], the citations concerning Wolf Rollnick, his son Abraham Rollnick, and his daughter Sarah Rollnick Levy (Stephen's great grandfather, great uncle and great aunt, respectively) refer to their "tribe" as Cohen. I have not been able to establish whether the descendants of Wolf Rolnick's brothers also consider themselves to be of the Cohen tribe[21]. Many, especially Ashkenazi Cohanim, are in the J2 haplogroup.

Earlier I wrote that a genetic mutation that brings about a single step

[18] I write "perhaps" since Stephen himself has not had his haplogroup identified, although a man one step away from him has been identified as J2a1b (M67). M67 refers to a particular DNA mutation (a SNP, see later in this chapter) that has been found in this group.

[19] See as an appendix to this chapter two pages from the fine article by Gabor Balogh (J2a1b (M67) Y-DNA Genetic Ancestral Journey, 2012

http://photos.geni.com/p13/8e/6d/a5/02/5344483a5c961516/260053_j2_ancestral_journey_eng_original.pdf

[20] https://www.jewishcemetery.co.za/stones?deceased_id=16341

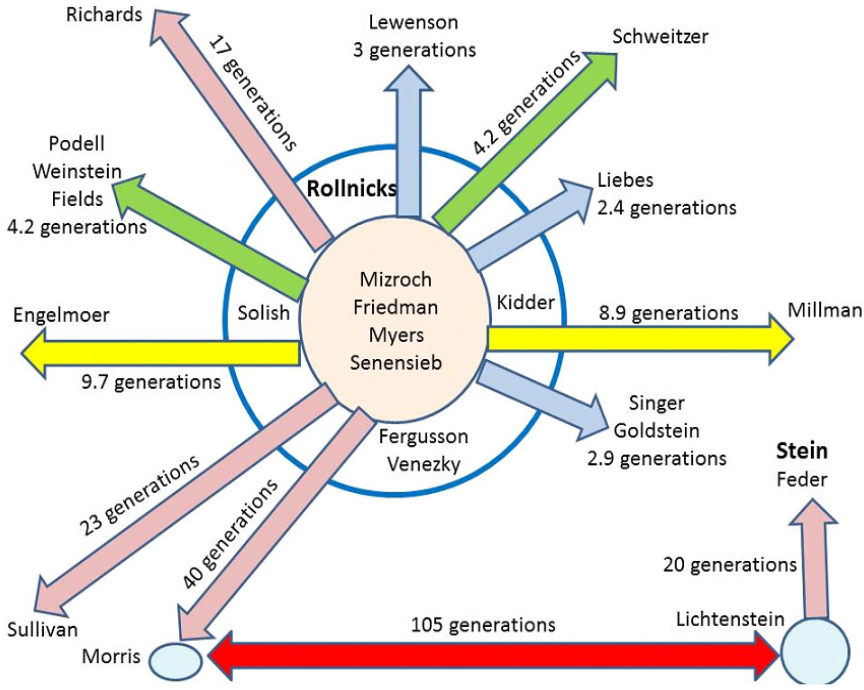
[21] Robert Lewenson, whose great grandfather was James Lewenson, Wolf Rollnick's brother, wrote " there has not been a priestly tradition on my father's side of the family. It has never been indicated to me that there ever was."

difference between two people can occur about once every hundred years. But this is only a rough average. Detailed studies have shown that the mutation rates at the different markers can vary greatly[22]. To take two extreme cases, a mutation at marker 448 (the single marker by which Stephen Rollnick and David Richards differ) occurs only about every seventeen generations or some 500 years while a mutation at CDYa (the marker at which Stephen differs from a group of four men with origins on the Polish/Belarus border) can occur once every generation. These four men have very close YDNA signatures and are separated from Stephen Rollnick by just this single step. The table that I reproduce below shows how the four (Messrs. Mizroch, Friedman, Myers and Senensieb) are separated from Stephen and other men close to these four. In the table, yellow shading indicates no difference from Mizroch, red represents a single positive step (gain of one repeat in a single STR marker) from him, while a green square represents a negative step (loss of one repeat). The columns with 0's and 1's are the 11 STR markers at which these men have different marker lengths. I have omitted all the markers at which they do not differ. (The first column gives their code names in the **ysearch** database, while the third gives the town or location where their oldest known ancestors are thought to have originated. The two Rollnicks on the list are Stephen and his son, both of whom had their cheek swabs analysed. Anonymous Rollnick is not in the table since his data have not yet been uploaded to the **ysearch** database.

3D4RK	Engelmoer	Hasselbach or Velmede, Germany	-1	0	0	0	-1	0	0	0	0	0	0
8DP6M	Goldstein	Poland	0	0	0	0	-1	0	0	0	0	1	0
YZEDK	Singer	Gonyu, Hungary	0	0	0	0	-1	0	0	0	0	0	0
KDK8P	Podell	Ukraine	0	0	0	0	-1	0	-1	0	0	0	0
FDYP2	Weinstein	Unknown	0	0	0	0	0	0	-1	0	0	-1	0
HJM7S	Fields	Tukum (sp?), Latvia	0	0	0	0	0	0	-1	1	0	0	0
EP8G3	Richards	Philadelphia, Pennsylvania, USA	0	0	0	-1	0	0	0	0	-1	0	0
WFPSY	Kidder (for	London, England	0	0	0	0	0	0	0	0	-1	-1	0
KEC2S	Rollnick	Telsiai, Lithuania	0	0	0	0	0	0	0	0	-1	0	0
MJEDR	Rollnick	Telsiai, Lithuania	0	0	0	0	0	0	0	0	-1	0	0
4XMNE	Mizroch	Svedasai, Lithuania	0	0	0	0	0	0	0	0	0	0	0
VWX75	Friedman	Makow Mazowicki, Poland	0	0	0	0	0	0	0	0	0	0	0
CQPJU	Senensieb	Kuty, Austro-Hungarian Empire	0	0	0	0	0	0	0	0	0	0	0
RSYJV	Myers	Yorkshire, England	0	0	0	0	0	0	0	0	0	0	0
BD6ER	Solish	Serock (near Warsaw), Poland	0	0	0	0	0	0	0	0	1	0	0
8PGV3	Schweitzer	Hungary	0	0	0	0	0	-1	0	0	0	0	0
GCT2E	Millman	Unknown	0	1	0	0	0	0	0	0	0	0	0
UF56M	Liebes	Rawitsch, Posen/Pozna'n, Germany	0	0	0	0	0	0	0	-1	0	0	0
VVWTD	Kohn	Tolcsva, Hungary	0	0	0	0	0	0	0	0	0	0	1
JTHZA	Fergusson	Connecticut, USA	0	0	0	0	0	0	0	0	1	-1	0
XNB7K	Venezky	Ukraine	0	0	0	0	0	0	0	0	1	-1	0
3T8D7	Sullivan	Unknown	0	0	-1	0	0	0	0	0	0	-1	0

On the basis of the genetic steps which separate Mizroch and his henchmen from others close to them, I have built the following relationship diagram:

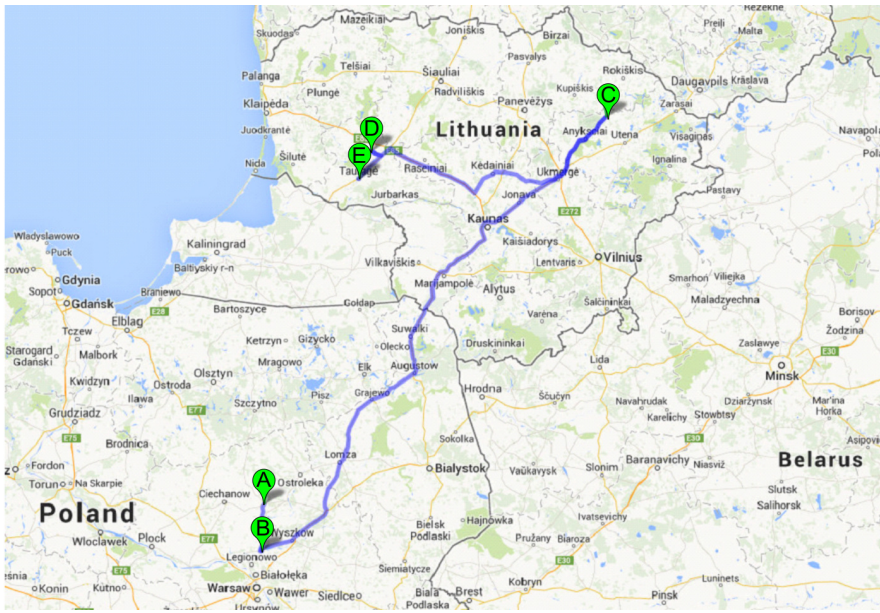
[22] For a useful table of these rates see: http://en.wikipedia.org/wiki/List_of_Y-STR_markers



In this "target" model, the central group contains the four men who differ not at all at the 37 markers at which most people test. The next surrounding circle contains men who are just one rapidly-mutating marker away from them. Here we find Stephen Rollnick and also Anonymous, (Berl Rolnik's great grandson), listed together as **Rollnicks**. David Richards is 17 generations away from the core group. Wilfred Stein, although only five steps away from Stephen Rollnick and the core group, differs from them by an extremely slowly mutating marker. His little group of people (from the Suwalki region of Lithuania - currently Poland) is over 100 generations, three thousand years, away from the J2a1b core. This was long before Jews came to Europe so the connection between the Stein group and the core group of our Rolnicks was not due to a recent geographical migration, although the migrations within the Rolnicks and their core group are probably recent.

In the map on following page, (A) is where Friedman, a member of the core group in the diagram above, has his family's origins, while Solish, in the ring with the Rollnicks one short step away, has his at (B). At (C) the family of John Mizroch originated, at (D), our Stephen Rollnick, and at (E), his father's cousin, Wilfred Stein... wandering Jews again, like the Telsiai Rolnicks, but this time in a more centripetal fashion.

David Richards, one slowly mutating step away from our Rolnicks,



has the M67 haplotype while they have the less-distinguished M172[23], which Balogh[24] describes as having originated somewhere in the Middle East towards the end of the last glaciation, between 15,000 and 22,000 year ago. I append Balogh's fuller description of these haplogroups at the end of this chapter.

Studies on the autosomal chromosomes

One can get much additional information, once again with the FTDNA company's aid, if one looks at the 22 pairs of autosomal chromosomes (those that are neither Y nor X). When the germ cells are being made (namely, the cells that end up in the sperm or the ovum – only a very small number of which will eventually be handed on to the next generation to contribute to one of one's children), an autosomal chromosome that one received from one's mother (red in the diagram on the next page) lines up against its match received from one's father (blue).[25]

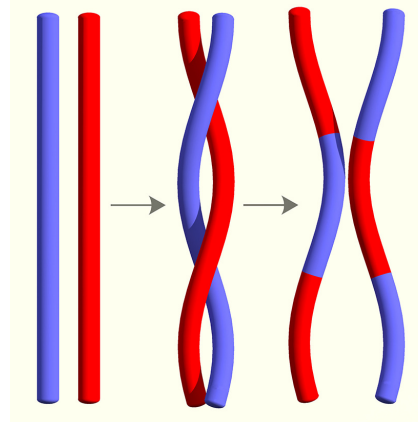
The two cross over each other and, between the two cross-over points, exchange between them parts of the genetic material by recombination, forming a new re-arrangement of the genes that lie along the chromosome. Each germ cell (sperm if one is a man, ovum if one is a woman) gets only one chromosome of the newly-rearranged pair. As

[23] carrying the DNA mutation designated M172

[24] See appendix B

[25] http://www.genomenewsnetwork.org/resources/whats_a_genome/Chp3_2.shtml

far as genealogy is concerned, this means that only some of the genes from one's father (or mother) will be passed on to the next generation. We said that the blue chromosome is the one that one received from one's father. Scattered along the length of the blue chromosome will be the genes that it holds. After crossing over and the formation of a new recombined chromosome, if it is the left-most chromosome that will go to one's germ cell, it will take with it only the middle blue section of one's father's genes. Only those genes in the blue middle section will be passed on to the child that this germ cell will form. That will be the longest unbroken length of one's father's genes that the to-be-formed child will receive. Similarly, for the red chromosome, the mother's. [26]



On average some 1.5 such cross-overs occur on each autosomal chromosome in the formation of a new germ-line cell. This crossing-over has important consequences for evolution (but these will not be discussed here). The extent of recombination is measured in centiMorgans (cM)[27], this being defined as the percentage of genetic material that is exchanged per generation. A long chromosome (one labeled with a smaller number: 1, 2, 3 etc.) will have a bigger chance of exchanging pieces with its fellow. So the frequency of exchange is the genetic measure of the "length" of a chromosome. The larger chromosomes are some 250 cM in length, so that on average there are about 2.5 (250/100) crossings-over along the chromosome in each generation. The smaller (numbers 20, 21, 22) are some 50 cM long…half a crossing over each generation. The total genetic length of our autosomal chromosomes is about 3,300 cM. On average, some 33 crossings-over occur across the whole genome, that is, taking into account all one's chromosomes, during the formation of a germ cell.

Single Nucleotide Polymorphisms: In addition to the rearrangements

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[26] In contrast to the autosomal chromosomes, the Y chromosome has no pair and hence is handed down, generation by generation, father to son, unchanged except for the occasional mutations of the length of the STR's and the rare mutations of the DNA bases themselves which, as we shall see, give rise to the SNP's that have been used to sort out our human haplogroups.

[27] Thomas Hunt Morgan was the geneticist who, working with mutations in fruit flies, discovered the process of crossing over and quantified recombination. http://en.wikipedia.org/wiki/Thomas_Hunt_Morgan#Morgan_and_Evolution

due to crossing over, some 60 mutations in the DNA itself occur at random along the chromosomes in each generation[28]. Thus only 60 A, C, T or G's will change, amongst the more than 3 billion of these bases, in each generation. These are the SNP's (the Single Nucleotide Polymorphisms) that are the basis of autosomal chromosome matching. So what is a SNP? It is just a mutation that has occurred here - at one position in the whole genome. A Single Nucleotide Polymorphism: a **s**ingle base (i.e.**n**ucleotide) that has mutated (changed) and thus formed a different DNA structure at this point in the genome - (a **p**olymorphism). Now in my family, each sibling received a different set of 60 or so SNP's when the germ cells that made us were formed. Each of Wolf Rollnick's seven children received a different set of 60 or so SNP's when their germ cells were formed. Each of Wolf Rollnick's five siblings … and so on. Thus, since the human race split off from their ancestors, zillions of different SNP patterns have accumulated in the current human population. These SNP's are spread out along the chromosomes. The bit of blue chromosome that recombined into the red chromosome, in the diagram on the previous page, carried with it its set of SNP's when this newly-rearranged chromosome was passed on to the new generation. Anyone whose SNP's match, SNP by SNP, with those in this blue section of the chromosone must be related to the person who donated the left hand blue chromosome.

The gene-testing company FTDNA has developed a resource that, using again DNA from cheek swabs, allows one to compare the SNP's on one's autosomal chromosomes with those of other people in their database[29]. The more SNP's that you have in common, the closer is your relationship. Two siblings will have half of their genome in common since they each received a random half of their mother's and a random half of their father's SNP's. The length of their overlap is half a genome's worth or some 1600 to 1700 cM. Cousins will have half of this again, 800 to 850, second cousins around 400, the content halving at each generation and so on. I made a Table in which I recorded all the data that I could find from my study of my own relatives and of people who had been in contact with me. First cousins had 900 +/- 55 cM in common, second cousins 340 +/- 60, thirds 170 +/-55 cM. The numbers show the spread that one expects from the random nature of the crossing-over process. FTDNA reports for each match, not only the total shared cM but also the Longest Block of continuous SNP's. This also halves each generation. I find 85 +/34 cM for first cousins, 56+/- 16 for seconds, 33 +/- 18 cM

[28] http://www.icr.org/article/6222/

[29] When I spoke to people at FTDNA last year, the database had over 40,000 entries. It may be some 60,000 at this time.

for thirds. My data for both Shared cM and Longest Block come from only a limited population (about fifty people) so the halving that I find is not the exact ½ that one would, in theory, expect.

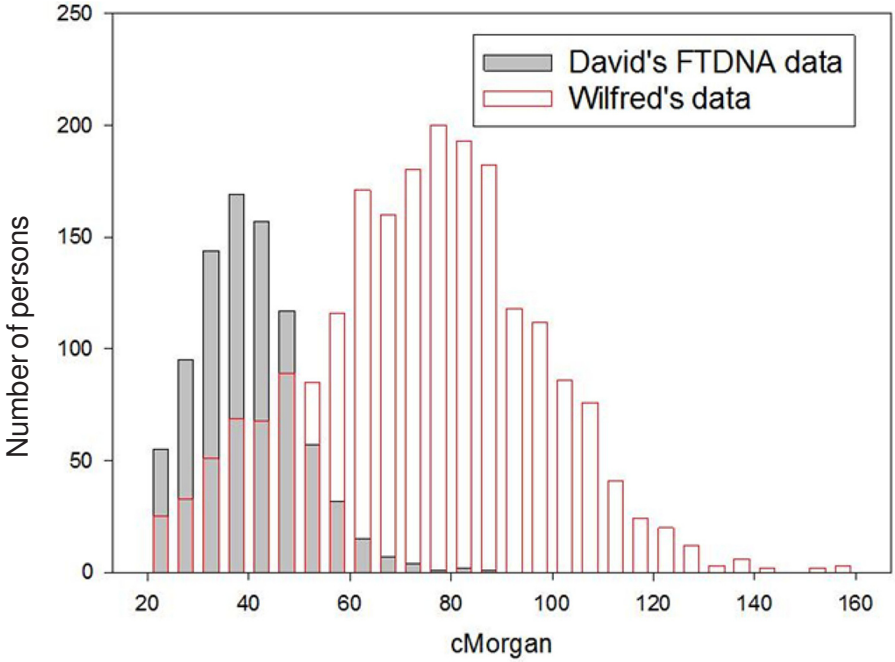
When, a year or so ago, I looked for Ashkenazi names in the FTDNA database, I found about 3,000. There are probably close to 5,000 today (2013). Most people with a 100% Ashkenazi background will find about 2,000 names of people who share more than 20 cMorgan (of the 3,400 cM possible) with them and these will display around 7.5 cM (of a possible 270 cM, the size in cM of the longest chromosome) in a continuous Longest Block. People, non-Ashkenazis, who have contacted me with questions about their possible Ashkenazi background often show up with far fewer matched names at this level, perhaps 600 or so for someone who is one-quarter Ashkenazi, rather than the 2,000 for a full Ashkenazi.

One can already see from this that we Ashkenazis are closely related to one another. Now look on the next page at the pattern of Shared cM that a non-Ashkenazi (David) displays as compared to my pattern. What you see in the diagram is a pair of histograms. On the x-axis is the total length of shared cM, the total across all the genome of the length of the segments along which SNP's match; on the y-axis the number of people with that amount of shared SNP's. (I have omitted the small number of known close relatives).

The peak for David's histogram is at 38 cM, that for my histogram 75. Going back to my predictions for cousinhood versus shared cM, this would put David's matches to be at 5th cousin-once-removed, mine would fit 4th cousin-once-removed. Since my matches[30] are about half of the total Ashkenazi pool, this would mean that half of the world's Ashkenazis (if the FTDNA pool is a fair sample) are my 4th cousins once-removed! This is clearly impossible. Even if each couple in each generation produces five children (so I would have five siblings, twenty five cousins and so on), I can expect to find only about 4,500 fourth cousins -once-removed. Since FTDNA's pool of cheek swabs has sampled only about half of one-thousandth of the world's Ashkenazis, I would expect to find, by random sampling, half of one-thousandth of these 4,500. That is, 2 matches – no more. Yet I have 2,000 matches which average out at this level. How can this be? The usual explanation for this paradox is that the Ashkenazi Jews originated from a small

[30] FTDNA counts only those people who match at above a total length of 20 cM

[31] Risch N, de Leon D, Ozelius L, Kramer P, Almasy L, Singer B, Fahn S, Breakefield X, Bressman S. Nat Genet. 1995;9:152-9. Genetic analysis of idiopathic torsion dystonia in Ashkenazi Jews and their recent descent from a small founder population.



cM shared with Ashkenazi pool - Wilfred and David compared.

population, perhaps as few as 4,000 persons, some 350 years ago[31] and has suffered bottlenecks of population destruction since then[32]. Added to this is the possibility that it was only a part of this population (the richer families and the rabbinical families – eagerly sought after as sons-in-law by these richer families) that had large families surviving to adulthood, and that within this small pool there was much intermarriage. It is easy to show, for instance, that the children of first cousins have a genetic similarity at the first cousin-once-removed level, half a generation closer than true second cousins. Thus intermarriage raises the genetic similarity between members of a group.

David's similarity average of fifth cousin once-removed is consistent with the possibility that it is the descendants of his grandfather's generation who are represented in the FTDNA database, not of his parent's generation, as in my own data. His list of matches is overwhelmingly Ashkenazi, almost certainly due to the fact that his Ashkenazi relatives have had a higher proportion of cheek swabs analysed than have his relatives amongst the general population.

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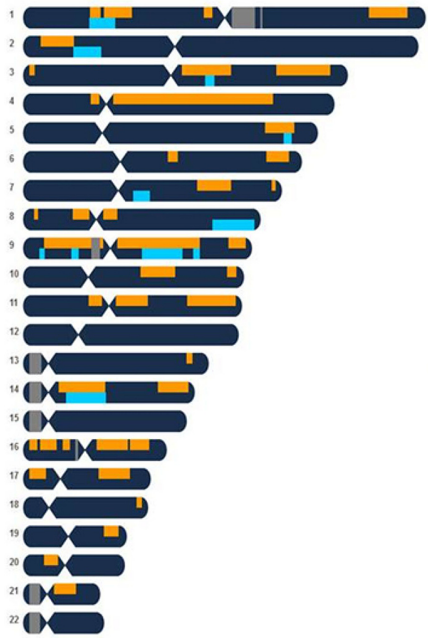
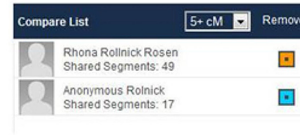
[32] A "bottleneck" occurs when the population is greatly reduced at a point in time, by disease or slaughter, so that only a small fraction of the pre-bottleneck population remains alive to re-establish the community. This has happened often in the history of the Ashkenazi Jews. It greatly reduces the gene pool.

The fact that an Ashkenazi's Family Finder (FF) data base is so heavily laden with people who are pseudo "fourth-cousins-once-removed" makes it almost impossible to identify anyone closer than third cousin-once-removed with any certainty. Even to make an identification at this level needs some further thinking which I leave as an appendix to this chapter, but which leaves me to conclude that only people with 25cM of Longest Block and 155 cM of shared cM can be considered as genetic close relations, third cousins-once-removed or closer.

The company FTDNA provides many useful tools for analyzing the Family Finder data. One of the most helpful is their "Chromosome Browser" which depicts in a colorful manner the overlaps of matching DNA segments between two or more persons. In the diagram below each chromosome, numbered and arranged in descending order of length, is shown with one person's genome as a background and the overlaps of SNP's between that person and other different people as



(A) The legend to the Chromosome Browser shown to the left



(B) persons "in common" between Rhona and Wilfred:

	Full Name	Suggested Relationship	Shared cM	Longest Block (cM)
2	Miriam Friedland	2nd Cousin	394	54
3	Harry Hurwitz	2nd Cousin once removed	366	45
4	Anonymous Rolnick	2nd Cousin once removed	320	53
5	Peter Silberstein	2nd Cousin once removed	265	34
6	Sandra Valerie Silberstein	2nd Cousin once removed	243	37
7	Sheldon Yusim	2nd Cousin once removed	179	75
8	Naomi Golde Silverton	2nd Cousin once removed	169	37
9	Ross Gallen	3rd Cousin	151	22
10	Samantha Straus	-	148	9

On the left is the Chromosome Browser picture with my own Family Finder (FF) data as a background.

Superimposed on this are the data of my cousin, Rhona Rollnick, in brown and those of my second cousin-once-removed, Anonymous Rolnick, in blue. Rhona shares some 949 cMorgans with me – a quarter of our genomes - and a Longest Block of 96 cM, as one would expect for a first cousin, and as you can get a feel for on the picture. The Longest

Block is there on Chromosome 4. (Most Longest Blocks will, of course, be on the longer chromosomes). See how random is the pattern of crossings-over. Anonymous shares 320 cM and a Longest Block of 53, much as would be expected for a second cousin (perhaps once-removed). Note how Rhona and Anonymous share large blocks with me on chromosomes 9 and 14, and also on 1. But note as well that there are many regions where Rhona and Anonymous do not overlap. This is to be expected since Rhona and I share only a quarter of our genes in common so three quarters of my genome will not show a match with Rhona's, while more than seven eighths of my genome will not show a match with Anonymous…although an eighth does, as we can see. In (B) in the little table on the right of the figure is a portion of the detailed "In common" match data that Family Finder presents, here for the persons who appear both on Rhona's list of matches and mine. The Table lists the shared cM between myself and the persons listed and also the Longest Block in cM.

One can see that some members of the Silberstein/Silverton family appear in the table with good matches. These are the descendants of Johanna Rolnik who married Tsvi Silberstein as was described in the chapter on the Silberstein branch of the Lithuanian Rolnicks. We would expect, and we do find, large amounts of shared cM and good Longest Blocks since these branches of the Upyna Rolnik family separated only three or four generations ago. Also on the list is Miriam Friedland, a granddaughter of James Lewenson, brother to my grandfather Wolf Rollnick and to Johanna Rolnik Silberstein and to Berl Rolnik, Anonymous Rolnick's great grandfather. All these are from the Upyna Rolniks branch. All of us appear with high match numbers, fully confirming the relationships that the paper trails and family histories had postulated. Harry Hurwitz appears on the list for the very good reason that Wolf Rollnick's wife, Chaya Hurwitz, (Rhona's and my grandmother) was sister to Harry's grandfather, Max Hurwitz. Although Miriam Friedland, top of the list in the table, is a granddaughter of James Lewenson, a Rolnik, she is also the greatgranddaughter of Frume Hurwitz (Chaya's eldest sister) so Miriam matches with the Silberstein/Silvertons and with Anonymous Rolnick and, as we will see, Sheldon Yusim, on the Rolnik side. She shares with Wilfred Stein and Rhona Rolnick on both the Rolnik and the Hurwitz sides, and with Harry Hurwitz on the Hurwitz side. It was lucky that the Rolnik/Rolnick/Rollnick surname project was able to recruit Miriam!

Also on this list is the match with Sheldon Yusim, grandson of the cousins Abraham Rolnick and Bessie Rolnick, of the Skaudvile Rolniks, confirming thie relationship between the Upyna and Skaudvile that the weak paper trail had suggested. How Sheldon's FF data were obtained

involves a sad story.

In the Chapter on the Skaudvile Rolnicks, I wrote that Mamie Rolnick, a daughter of the cousins Abraham Rolnick and Bessie Rolnick of Skaudvile, had married Samuel Yusim. They had two sons, Arnold and Sheldon. In the course of my researches, I contacted Arnold by email and we had a spirited correspondence on our family genealogy[33]. His wife said that she had not seen him so excited for years. In one of his last emails to me in June 2012, he wrote: "I will travel to wherever you are to meet you. I am 73 and time is important." And time was indeed important. I had last received an email from him in September of that year. I wrote emails to him a number of times at the beginning of 2013, asking if he would donate a cheek swab to have his Family Finder data tested. I received no answer. One day, I happened to come across a Social Security death notice. Arnold had died suddenly in November of 2012. His brother Sheldon had already had a cheek swab done to test his Y chromosome data. He gave permission for the FF data to be analysed and on the 14th April 2013, I made arrangements with FTDNA to have this done. Sheldon died suddenly on the 21st.

The FF results when they came in, months later, showed unequivocally that Sheldon Yusim and hence the Skaudvile Rolnicks were close relations of our Upyna Rolnicks. Indeed, as the table on the picture above shows, he shared a Longest Block of 75 cM with Rhona Rolnick. The actual relationship of Rhona and the late Sheldon is "third cousin-once-removed". The predicted length of the Longest Block that they might share is unlikely to be more than 55 cM. Some 40 cM or so would be an expected average value. So why do Rhona and Sheldon have so much DNA in common? Almost certainly this derives from, and confirms, the cousin/cousin marriage of Sheldon's grandparents. This close marriage resulted in the eye affliction that many of their children suffered but also meant that their grandchildren would have the genetic complement of "siblings-once-removed" and that they would thus count as genetic third cousins of Rhona and myself, rather than as thirds-once-removed. Really it was only that cousin/cousin marriage that enabled the link between the Upyna and Skaudvile Rolnicks to be so unequivocally established. (You might want to refer again to that section of Chapter 4 that refers to the Skaudvile Rolnicks and considers their link with their Upyna cousins, see page 177 *et seq*).

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33 "I will be very happy to work with you as best as I can. If I find any old pictures, you will get them. Please stay in touch. Arnie Yusim" and in another email:" I will see you when you come to the U.S. If you are able, I will arrange for all of us that are still in Chi. to meet with you. You will have to help me with their names and I will do my best to find them. please say that you will come. If not… " and this email continues in the text above.

So, analyzing DNA has become a valuable tool for researching family history.

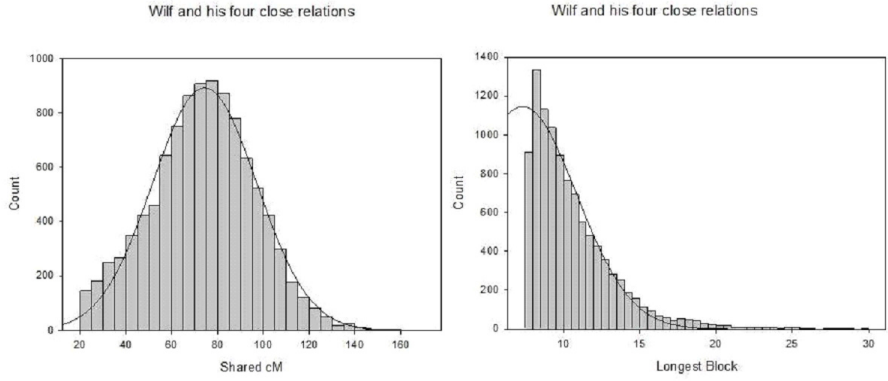
For the Lithuanian Rolnicks it showed that the Northern (Telsiai) Rolniks and the Central (Upyna/Skaudvile) Rolniks were not related, both tribes having independently taken on the occupational name of Rolnik/farmer. This contradicted what had seemed clear on the documentary evidence. But for the Upyna/Skaudvile Rolniks, DNA analysis has shown that they are indeed a single tribe, fully confirming what had been only surmised based on family histories.

We can look forward to further DNA-based genealogical discoveries as the databases expand.

APPENDICES:

A: The statistics of autosomal DNA data.

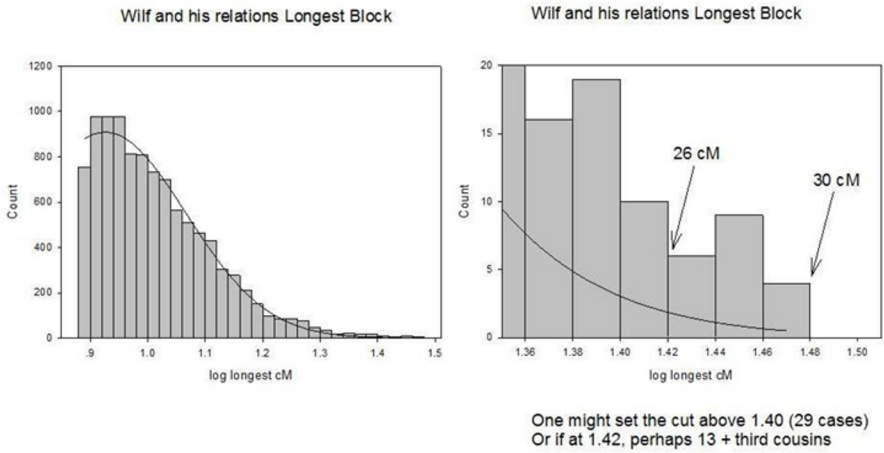
Take a look at the following histogram: Here, adding more data to provide better statistics, I have combined the data from my FF data set with the data from four of my close relatives (a cousin, two first cousins -once-removed, and a second cousin) to give a total of just over 10,000 data points. So as not to spread out the x-scale too much, I have omitted the data from very close relatives. I provide the data for the Shared cM and the Longest Block for this large data set. I have fitted the data by a Gaussian curve, a mathematical function that fits a population having a random distribution pattern.



You can easily see that the left hand graph (Shared cM) is well-fitted by the Gaussian curve, the bell-shaped line, but the Longest Block data deviate considerably from the Gaussian prediction. One can get a much better fit for the Longest Block data if one builds the histogram not using the data reported by FTDNA, but rather the logarithm of the

Longest Block data. Look first at the left hand figure on the next page, and compare it with the same data plotted on a linear scale, as the right hand graph above.

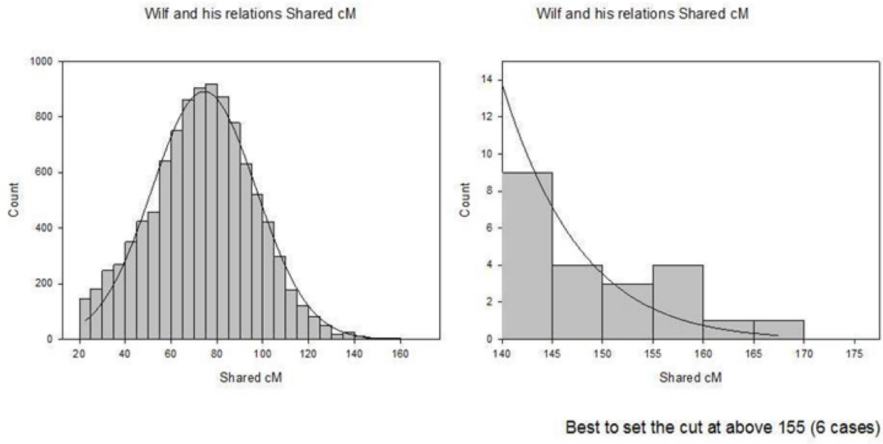
One can show by a statistical test (the F-test) that the log of the Longest Block data is the preferred measure to use. Indeed, there is a theoretical basis for this. Any data set in which the successive values are scattered around values that are halved set by set (as the Longest Blocks should be, halved in each generation) should fit what is called a log normal distribution…where the logs of the value are fitted by the random Gaussian curve.



But now look at the right hand half of the figure just above. Here, I have expanded the x and y axes so that one sees just the very highest (log) Longest Block data. Most of these highest values sit well above the prediction of the Gaussian curve. Statistically, it is unlikely that the individuals present in the three histogram blocks to the extreme right are part of the random distribution. It seems clear that one could safely set the cut-off point at a value of 1.40 in logs or 25 cM in absolute numbers. This would give, shared by my four close relations and myself, 34 third cousins and even one second once-removed as being very probably indicated by the data. Third cousins once-removed would be at about 1.24 in these log units and would be totally obscured by the weight of the random background.

The Shared cM data are not better fit by a logarithmic transformation. Indeed, the fit is worse for such a plot. (There is a good explanation for this. The huge number of fourth cousins-once-removed has arisen from marriages between closely-related persons, numbers of generations ago. These form a random distribution).

Therefore, in the histogram on page 408, I show the Shared cM data in a simple linear (not logarithmic) plot and, on the right, with the



expanded scale on the axes.

For these data, only the cases above 155 cM deviate from the random curve of the Gaussian distribution. This gives about six cases only that we can extract from the data with any confidence. These are third cousins or third cousins -once-removed. Any further cousinhood is obscured by the random nature of the Shared cM data. This makes much sense. Most of the Shared cM values are made up of lots of little pieces of segments containing matching SNP's, formed by intermarriage combinations and distant common ancestors, whereas the maintained Longest Block overlapping segments will have been formed in recent generations.

I have carried out these analyses for quite a few grouped and individual data sets. The conclusions that I have drawn using my own "close relatives" data apply also to those other data sets. The logarithm of the Longest Block numbers form a good overall random distribution but one can generally find some "outliers" that stand above, or even well above, the Gaussian prediction. For the Shared cM data, a Gaussian distribution gives a good fit, but only a few "outliers" can be found that might be considered to be identified as relatives. People with 25cM of Longest Block and 155 cM of shared cM can be considered as genetic close relations, third cousins once-removed or closer.

B: Two lineages within the J2 haplogroup

In a fine article on haplogroups by Gábor Balogh (J2a1b (M67) Y-DNA Genetic Ancestral Journey, 2012), he has:

X. Haplogroup J2 (M172): To the Mediterranean

Time of Emergence; 19,000 BP, 850 generations ago
Place of Origin: Fertile Crescent
Climate: Ice Age ending
Estimated Number of Homo sapiens: A few million
Tools and Skills: Neolithic

Haplogroup J2 is thought to have appeared somewhere in the Middle East towards the end of the last glaciation, between 15,000 and 22,000 years ago. Its present geographic distribution argue in favour of a Neolithic expansion from the Fertile Crescent. This expansion probably correlated with the diffusion of domesticated cattle and goats (starting c- 8000-9000 BCE) from the Zagros mountains and northem Mesopotamia, rather than with the development of agriculture in the Levant (which seems to have been linked to haplogroup G and perhaps also E1b1b). A second expansion of J2 could have occurred with the advent of metallurgy (also from Anatolia and Mesopotamia) and the rise of some of the oldest civilizations.

Quite a few ancient Meciterranean and Middle Eastem civilizations flourished in territories where J2 lineages were preponderant. This is the case of the Hattians, the Hurrians, the Etruscans, the Minoans, Greeks, Phoenicians, Carthaginians, Israelites, and to a lower extent also the Romans, the Assyrians and the Persians. All the great civilizations from the middle Bronze Age to the Iron Age were dominated by J2 men.

There is a distinct association of ancient J2 civilizations with bull worship. The oldest evidence of a cult of the bull can be traced back to Neolithic central Anatolia, notably at the sites of Qatalhoyuk and Alaca Hoyiik. Bull depictions are omnipresent in Minoan frescoes and ceramics in Crete. Bull-masked terracotta figurines and bull-horned stone altars have been found in Cyprus (dating back as far as the Neolithic, the first presumed expansion of J2 from West Asia). The Hattians, Sumerians, Babylonians, Canaanites, and Carthaginians all had bull deities (in contrast with Indo-European or East Asian religions). The sacred bull of Hinduism, Nandi, present in all temples dedicated to Shiva or Parvati, does not have an Indo-European origin, but can be

Human-headed winged bull

traced back to the Indus Valley civilization. Minoan Crete, Hittite Anatolia, the Levant, Bactria and the Indus Valley also shared a tradition of bull leaping, the ritual of dodging the charge of a bull. It survives today in the traditional bull-fighting of Andalusia in Spain and Provence in France, two regions with a high percentage of J2 lineages.

Haplogroup J2al b (M67)

Time of Emergence: 9,000 BP, 360 generations ago

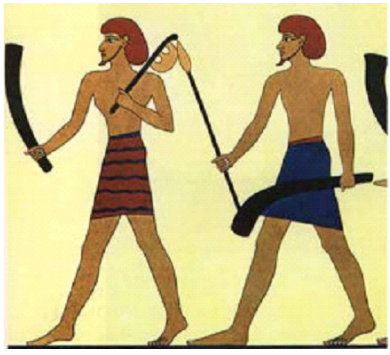
Place of Origin: Fertile Crescent, Canaan. Climate: End of the Ice Age

After a few centuries Jericho was abandoned for a second settlement, established in 8800 BCE perhaps by an invading people who absorbed the original inhabitants into their dominant culture.

Artifacts dating from this period include ten plastered human skulls, painted so as to reconstitute the individuals' features. These represent the first example of portraiture in art history, and it is thought that they were kept in people's homes while the bodies were buried. This was followed by a succession of settlements from 4500 BCE onward, the largest being constructed in 2600 BCE.

A range of sophisticated technologies appear. At Jericho, Catul Huyuk and Sabi-Abyad, craftsmanship skills are demonstrated both in creating objects and structures and in the careful selection of materials. Polished obsidian, copper smelting, metal working, electro-plating and the superb quality Halaf ceramics appear.

Ruins of Jericho



Canaanites