



# Lancaster Mennonite Historical Society

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September 23, 2011

Mr. Brackbill:

## **Human Migratory Path for the paternal ancestors of Mr. Brackbill, based on y-DNA analysis.**

### **Introduction**

Below I have articulated the path your ancestors took through ancient times to eventually link to your current genealogy. If you go back far enough, all humans descend from a common male ancestor, connecting us all to a world family tree. New research is being added to further specify the complexities surrounding our common human origins—the beginning of this tree. In addition, new research is uncovering more specific SNPs (specific mutations) related to your place in the world family tree. The information I have included here is what is currently available as of September 2011.

Single Nucleotide Polymorphisms (SNPs) are labeled according to their discovery in specific genetic laboratories with a letter followed by a set of numbers (for example, *V168*). A collection of individuals that exhibit the same SNPs is termed a “haplogroup,” which can be further defined into specific clades and subclades. Haplogroups are labeled according to their line of descent, alternating letters and numbers (for example, *R1b1a2*). SNP labels are permanent, while a haplogroup’s subclade labels may change slightly as new research further specifies a more exact line of descent. All SNPs within a parent clade are found in a descendant population. Nature exhibits new SNPs randomly throughout your past lineage, and initially each new SNP is carried by one male individual and passed on to his sons.

By following the line of descent through the various SNPs specific to your haplogroup, one can compare your SNPs to those of current populations around the globe and develop the specific migratory path of your ancestors, including where and when you diverge from other global populations. With each subsequent SNP, one defines a more specific population and moves closer to the present day, and closer to connecting your genealogy (paper records) with your deep ancestry as revealed through DNA.

Some haplogroups and their subclades are defined by more than one SNP. These have yet to be fractured into individual subsequent mutations that will further specify your line of descent. Your SNPs are indicated below followed by + signs. At the end of the line, there may be options for you to test additional SNPs to further specify your descent within your specific haplogroup’s subclade. This is termed “Deep Clade” testing. Please consult with me if you are interested in further “Deep Clade” testing.

The system used to give a specific time frame to the formation of successive SNPs is based on a combination of factors, including genetics, anthropology, archeology, cultural and social history, climatology and linguistics. Dates are approximate. Very recent research (2011) has rearranged haplogroup A by determining that some of the SNPs that previously defined subclade A1a are found within the whole population, therefore our common human descent flows through haplogroup A1a as defined below. Eventually the nomenclature for haplogroup A will be rearranged to match the current outline.

Before 140,000 years ago - All humans alive today share a common paternal ancestor who lived in East Africa. There were plenty of other humans alive at the time, but only one man represents the paternal decent of all of us. Others were also our ancestors, but not our direct paternal ancestor. A handful of Africans, particularly a small percentage of Bakola Pygmies of South Cameron and a few Berbers from Algeria split from the tree to form haplogroup A1b. All other humans descend through A1a-T below...

**A1a-T (V168+, V171+, V174+, V203+, V238+, V241+, V250+) Africa**

About 108,000 years ago - A1a-T split into A1a and A2-T. A1a is found in a small portion of samples in Guinea-Bissau, Mali and Morocco. All humans not part of A1b or A1a descend through A2-T below...

**A2-T (V221+) Africa**

About 105,000 years ago - A2-T further divides into A2, A3 and BT in Africa. A2 is typically found among Khoisan peoples of southern Africa and is divided into 3 subclades. A3 is more widely distributed in Eastern Africa and Southern Africa among many different tribes as a small minority haplogroup, and is divided into 7 subclades. All humans not part of A1b, A1a, A2, or A3 descend through haplogroup BT below...

**BT (M42+, M94+, M139+, M299+, M60+, M181/Page32+, P85+, P90+, P97+, Page65.1/SRY1532.1/SRY10831.1+, V21+, V29+, V31+, V64+, V102+, V187+, V202+, V216+, V235+) Africa**

About 75,000 years ago - BT forms and later splits into B and CT. Haplogroup B is found in approximately 30% of southern Sudanese males, and about 9% of males from Madagascar, and also distributed to a lesser extent throughout sub-Saharan Africa, particularly among pygmy populations. It is divided into 16 subclades. All other humans not part of the various A subclades (except A2-T) or B descend through haplogroup CT below...

**CT (P9.1+, M168+, M294+, V9+, V41+, V54+, V189+, V226+) East Africa**

About 68,500 years ago - CT forms and later splits into CF and DE. This is the first major paternal genetic differentiation among living populations today. DE includes up to 95% of the populations of Africa, and various subclades of E include up to 20% of the population of Europe and a large concentration of the Middle East. D by itself is found in India, Tibet and even Japan. CT forms in East Africa, DE splits off of CT in East Africa, and DE splits into D and E prior to the "out of Africa" migration of modern humans. Portions of CT and D (and

possibly E) migrate across the Straits of Mandab at the southern end of the Red Sea around 60,000 years ago during a time of lower sea level, probably in successive migrations over the course of thousands of years. Those belonging to CT are among your paternal ancestors, and the ancestors of most people who live outside Africa.

Among those who remain behind descend the majority of Africans, including those who later became the ancient Egyptians. While Egypt grew into a powerful kingdom 5,000+ years ago, it began to colonize modern Palestine, Turkey and Greece; bringing the E haplogroup into Europe. A few Swiss Mennonite families, (notably the Groff, Gingerich and some Witmer lines) fall into haplogroup E and trace their genetic descent through this “recent” migration from Africa via the Egyptians.

Your migratory path out of Africa is far older, following modern humans who later settled in Asia, Europe and the Americas, leaving Africa at the southern end of the Red Sea approximately 60,000 years ago. The portion of CT that migrates out of Africa to Arabia splits to form CF in Arabia, and it is from those populations you descend.

### **CF (P143+) Arabia**

55,000 – 60,000 years ago – CF forms and later splits into C and F either in Arabia or the Indian subcontinent. C goes on to have moderate distribution through Asia, including some of the later Mongol population, some Chinese, South-east Asians and the aborigines of Australia. Through the Mongol invasions of Europe in the 13<sup>th</sup> century, C finds a minority distribution in Europe, particularly Eastern Europe. Most Europeans, including your own paternal line, descend through F.

### **F (P14+, M89+, M213+, P133+, P134+, P135+, P136+, P138+, P139+, P140+, P141+, P142+, P145+, P146+, P148+, P149+, P151+, P157+, P158+, P159+, P160+, P161+, P163+, P166+, P187+) Arabia or the Indian subcontinent**

48,000 years ago – F forms and represents the ancestry of about 90% of the current world’s non-African population. F without additionally defined subclade SNPs is limited to India and the Caucasus. F is split numerous into F1 (Sri Lanka), F2 (Lahu People of China), F3 (South Iran, South India and Armenia), F4 (Sri Lanka), F5 (southeastern India), G (Caucasus and Near East), H (Indian subcontinent) and supergroup IJK (Eurasia) from which you descend.

On a side note, G is found in about 20% of the modern Swiss population and is represented among numerous Mennonite surnames including Beiler, Howery, Kurtz, and some within the Kreider, Souder and Stauffer families. These are all lines that trace their pre-European origins to the Caucasus Mountains.

### **IJK (L15/S137+, L16/S138+, L69.1/S163.1+) Southwest Asia/Arabia**

40,000 – 45,000 years ago – IJK forms from F, probably in the Middle East or modern Iran and later splits into IJ and K. IJ further splits into I and J, both of which have strong

representation in the Middle East and Europe, including many Mennonite families. However you descend through K.

**K (M9+, P128+, P131+, P132+) Southwest Asia or the Indian subcontinent**

40,000 – 45,000 years ago – K forms from IJK, and is distributed at low frequency throughout the coastal regions of southern Asia. Those within K that are not defined by further SNPs include peoples of East India, Timor, the Philippines and Oceania. K splits into LT which further splits into L and T, with the Swiss Mennonite Good family as part of L. You descend from the portion of K separate from LT, currently labeled as haplogroup K(xLT).

**K(xLT) (M526+) Central Asia or the Indian subcontinent**

35,000 – 45,000 years ago – LT splits from K, and the remaining portion of K later splits into M (New Guinea, Indonesia, Polynesia), NO (with N found in Northern Eurasia, and O found mainly in China and Southeast Asia and Oceania), P (Eurasia), and S (New Guinea and Indonesia). You descend through P.

**P (92R7+, M45+, M74/N12+, P27+, S25+) North of the Hindu Kush Mountain Range, Central Asia or southern Siberia**

27,000 – 41,000 years ago – P forms in Central Asia and later splits into Q and R. P without additionally defined SNPs is found among the Muslims of Manipur, India, the Madia Gond of India, and (ironically) the island of Hvar along the Croatian coast of the Adriatic Sea. Q is widely dispersed in low frequency in Asia with a minimal representation in Europe. Specific subclades of Q migrated across the Bering land bridge to the Americas about 18,000 years ago, and populated the entire Americas. R finds strong representation in Europe, the Caucasus, Central Asia and India. You descend through haplogroup R.

**R (M207/UTY2+, P224+, P227+, P229+, P232+, P280+, P285+, S4+, S8+, S9+, V45+) Central Asia or Northern India**

27,000 years ago – R forms from P and later splits into R1 and R2. R without any additionally defined SNPs is found in Iran, Pakistan and Gujarat, India. About 90% of the R2 subclade is found on the Indian subcontinent. You descend from R1 which is common in Europe, South Asia and Central Asia.

**R1 (M173/P241+, M306/S1+, P225+, P231+, P233+, P234+, P236+, P238+, P242+, P245+, P286+, P294+, L364+) Northern India**

25,000 years ago – R1 forms from R and later splits into R1a and R1b. R1a is found across the Eurasian steppe east into India, and is represented heavily in Russia and Eastern Europe. R1b is the most common haplogroup of Western Europe, comprising well over 50% of the Swiss population, and becomes an even greater percentage as one travels west

through Europe to the British Isles. Here you follow the most common western European haplogroup, R1b, and split from the common Eastern European haplogroup, R1a.

### **R1b (M343+) Iran/Caucasus Mountains or Central Asia**

18,500 years ago – R1b forms from R1 with the vast majority of R1b descendants later forming R1b1. R1b without a defined subgroup is extremely rare, but appears to have been found in Turkey, Jordan and Egypt. You follow the common line of descent through R1b1.

### **R1b1 (L278+, M415+, P25+) Turkey or Central Asia**

15,000 years ago – R1b1 forms from R1b and follows the warming climate after the Last Glacial Maximum to repopulate Europe along with many other haplogroups. The origins of the Indo-European Language groups may be represented in R1b1. Without any other defined subgroups, R1b1 is found in Turkey, Italy, Ukraine and Russia. R1b1a contains the majority of western European populations. R1b1b is also found throughout western Europe as a small minority, including the Amish Mast family. R1b1c is found in Turkey and deep Africa, including Chad and Cameroon, and may represent the spread of the Semetic Chadic languages in Africa. You descend through the most populous group, R1b1a.

### **R1b1a (P297+, L320+) Caucasus Mountains region or Central Asia**

12,000 years ago – R1b1a forms from R1b1 in the Caucasus Mountain region or Central Asia. R1b1a1 splits off with SNP M73+ and is found in Italy, Turkey, Kazakhstan, Pakistan, Siberia, France and Spain, indicating groups that migrated from Central Asia into Western Europe. R1b1a2 is your line of descent and is found heavily in the Caucasus and throughout western and central Europe.

### **R1b1a2 (L265+, M269+, M520+, S3+, S10+, S13+, S17+) Caucasus Mountains**

10,000 years ago – R1b1a2 forms from R1b1a and predominates in Western Europe, and is also found in lower concentrations throughout Eastern Europe, European Russia and the Caucasus region. Most within this clade belong to its main subgroup R1b1a2a, as do you...

### **R1b1a2a (L23/S141+, L49.1+) Caucasus Mountains**

7,000 B.C. – R1b1a2a forms from R1b1a2 and is found (without defined subgroups) scattered throughout western Europe excluding Scandinavia, Eastern Europe, Turkey and the Middle East. You descend through its main subgroup R1b1a2a1.

### **R1b1a2a1 (L150+) Turkey**

6,000 B.C. – R1b1a2a1 forms from R1b1a2a and is represented throughout Europe (especially western Europe) and found in lesser quantities in Turkey, Armenia and Iraq. The Swiss Burkholder family splits from your tree at this point and follows R1b1a2a1b as

defined by SNP L277.1. You and the majority of Swiss Emmental families follow R1b1a2a1a below.

**R1b1a2a1a (L51/M412/S167+) Eastern or Central Europe**

4,000 B.C. – R1b1a2a1a forms from R1b1a2a1 and is found almost exclusively in Europeans or those with confirmed European paternal descent. Without defined subgroups, R1b1a2a1a is found in Central Europe, the Balkans, Croatia, and Greece. You fall into the subgroup R1b1a2a1a1 below...

**R1b1a2a1a1 (L11/S127+, L52+, L151+, P310/S129+, P311/S128+) Central Europe**

2,000 B.C. – R1b1a2a1a1 forms from R1b1a2a1a and is found (when negative for subgroups) in south east France, Italy, Denmark, Germany, England, Ireland, Netherlands and Poland. None have tested negative for subgroups in Switzerland. This clade splits to form SNP U106+ (R1b1a2a1a1a) which is represented in the Frisian and Baltic populations of northern continental Europe and includes Swiss Mennonite families such as Hostettler and Leaman, and the German Mennonite Kulp/Kolb family. You likely fall under the subgroup defined by SNP P312+ (R1b1a2a1a1b) which represents the Celtic populations of Central Europe, particularly Switzerland, Austria, Eastern France and Southern Germany. Here is where your deep ancestry ends for now, because I cannot determine for certain whether you fall into the subclade R1b1a2a1a1a (U106+) or R1b1a2a1a1b (P312+). Here we would need to specifically test SNPs to determine your line further. If you want a “deep clade” test to confirm this line of descent, let me know. There are dozens of SNPs downstream from L11/S127+ that could be tested to further determine your deep ancestry from approx. 2,000 B.C. to the beginning of your genealogical paper trail. Let me know if you have any questions.

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