Grangeburgh German-Swiss Genealogical Society

Oktoberfest 2014

October 10th and 11th, 2014

Program Schedule

FRIDAY, OCTOBER 10, 2014

A. S. Salley Archives open for research ..... 9:00 AM – 2:00 PM

Registration – Family Life Center ..... 4:00 – 6:15 PM

Exhibit Area open – Family Tables, Vendors, Other Societies ..... 4:00 – 6:15 PM

President's Dinner (advance purchase required) ..... 6:30 PM
Speaker: Dr. Michael Byrd, *White Poverty and Poor Relief in St. Philips and St. Matthews Parishes, 1725-1775*

SATURDAY, OCTOBER 11, 2014

Exhibit Area open – Family Tables, Vendors, Other Societies ..... 8:30 AM – 3:00 PM

Registration (coffee, juice, pastries, and fruit available) ..... 8:30 AM

Annual Business Meeting .....9:00 AM

Ya'll Come: Early Marketing of South Carolina in Europe, William Delk.....9:30 AM

Westward Ho: Outmigration via the Federal Road, video by Larry Holman .....10:00 AM

Break .....10:45 AM

DNA Basics: yDNA and Beyond, Lynn Teague .....11:00 AM

Lunch (advance purchase required) ..... 12:00 – 1:00 PM

Progress at the Salley Archives, Eric Powell ..... 1:00 PM

Working with Your Autosomal DNA Test Results ..... 1:15 – 2:00 PM

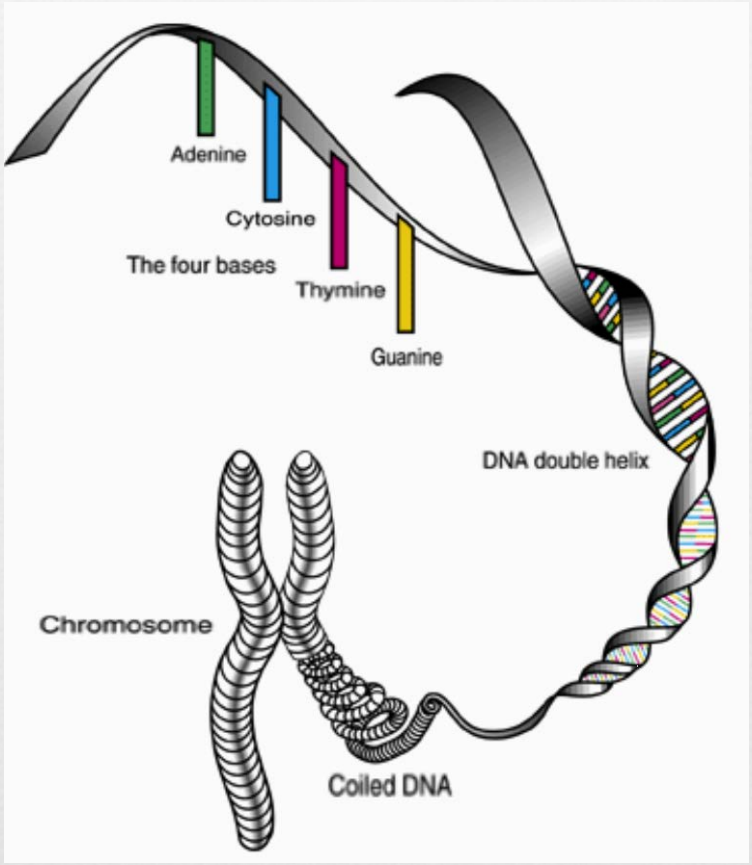
Individual DNA Consultations* ..... 2:00 – 3:00 PM
Lynn Teague, Margaret Waters
(*or small group discussions as participants desire)

Some family tables, vendors, and other societies may not be available the entire time.
Meal purchase deadline is October 3, 2014. Revised 11 October 2014

DNA in 2014

An Overview of Progress

The History We Carry With US



The Bases in DNA

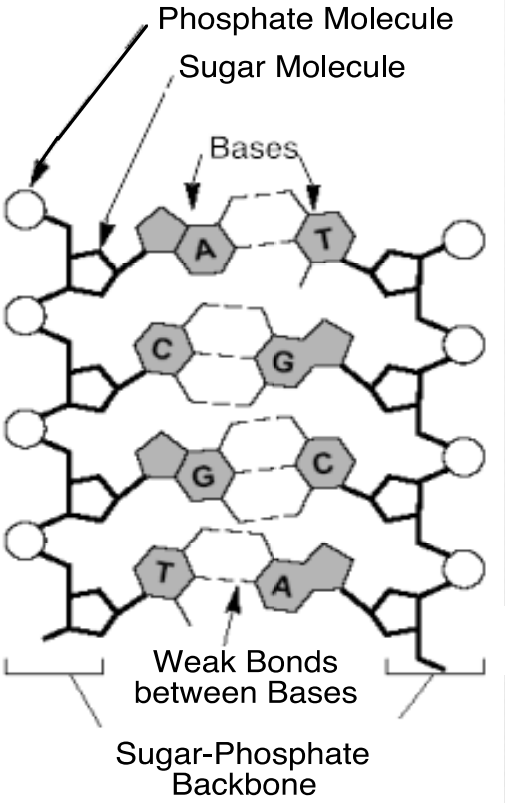


Figure 1. DNA Structure

Adenine always pairs with thymine, and cytosine with guanine. If one changes, the other also changes.

Varieties of DNA

- yDNA: paternal lines
- Mitochondrial DNA: maternal lines
- Autosomal or Recombinant DNA: reflects all ancestral lineages; can't be associated with a particular line of descent without comparison of matches having common ancestry. 22 chromosomes plus the X chromosome

Transmitting DNA

- yDNA is transmitted only to men by their fathers, while mtDNA is transmitted to all children by their mothers

Subject

Mutations: SNPs and STRs

STR

STR test results reveal haplotypes

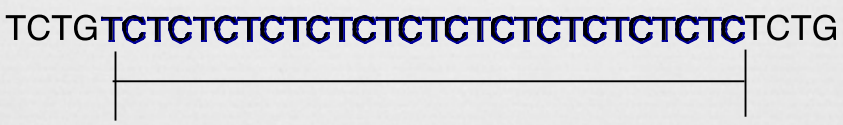
7 repeats of TCTA

The value of this marker is 7, for 7 repeats of the sequence TCTA.

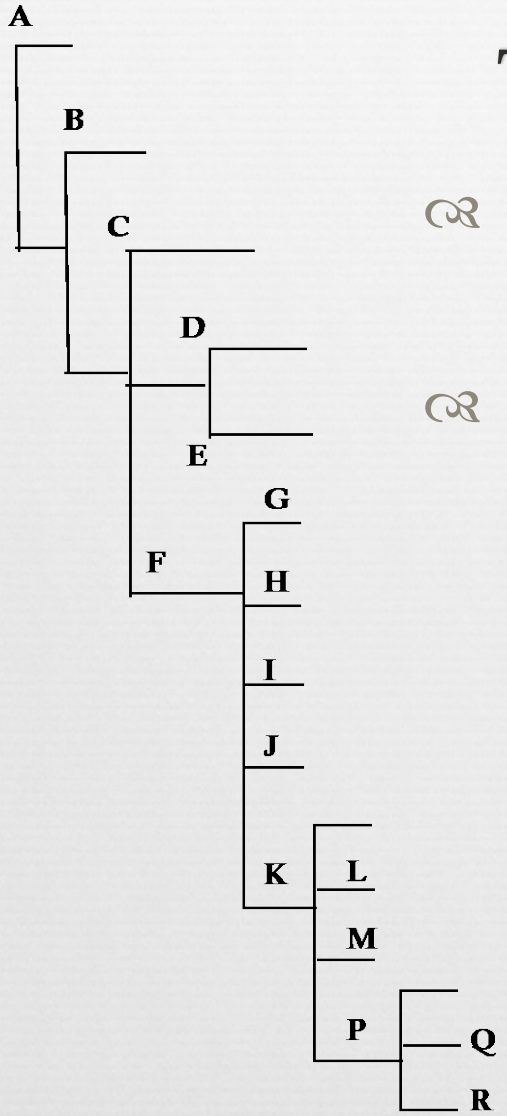
If the marker is, for example, DYS 19, then DYS 19 = 7.

SNP

SNP test results reveal haplogroups



A is replaced with C, so sequence is TATA, repeated 7 times.



The yDNA Haplogroup Tree

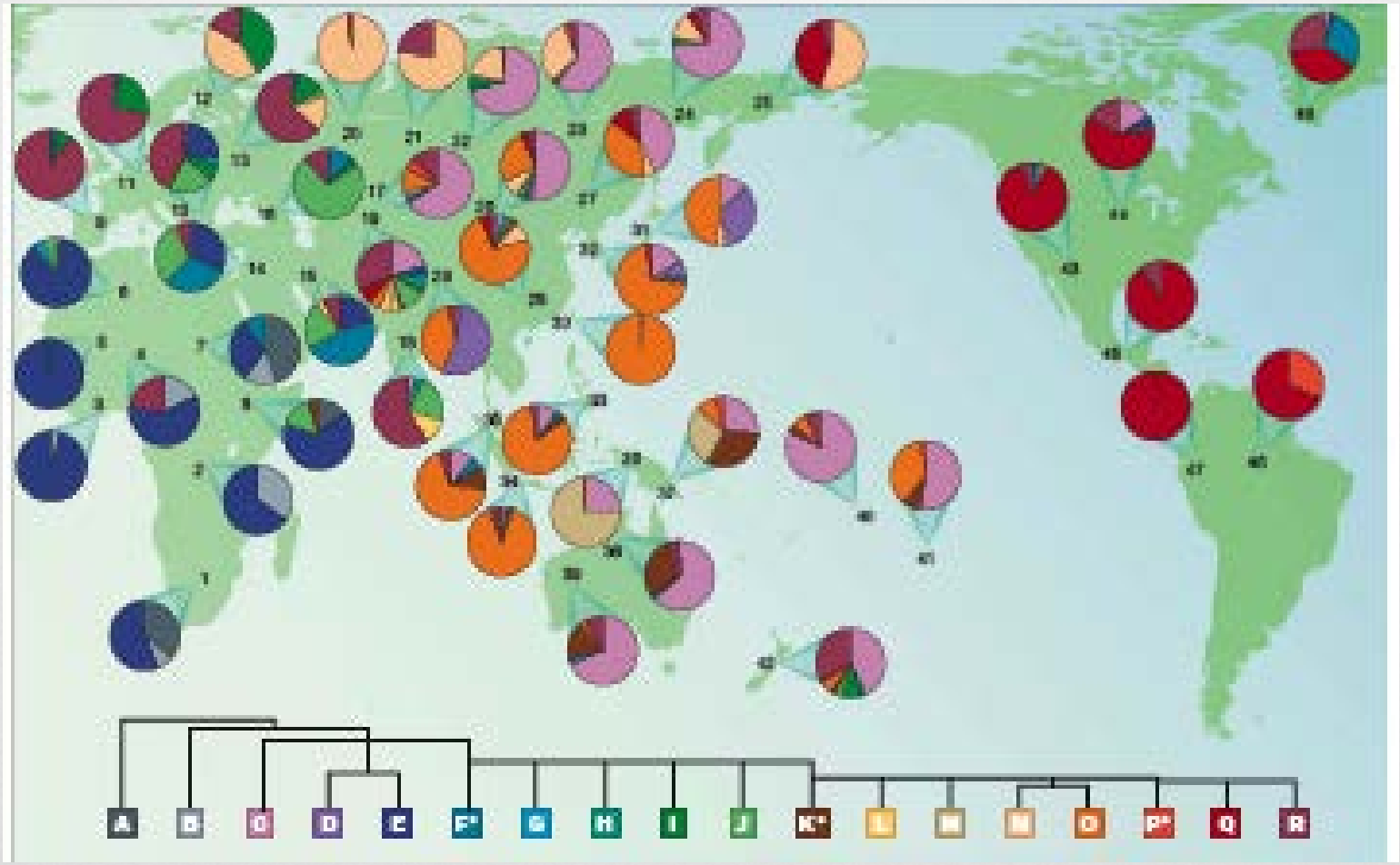
- As mutations happened, haplogroups split off from earlier haplogroups
- For a more detailed tree, see
  - http://www.isogg.org/tree/
  - http://https://www.familytreedna.com/y-dna-haplotree.aspx

Years before Present

2,500	Greco-Roman Expansion into Europe, often by sea
5,000	
	Neolithic farmers enter Europe, haplogroups J, G, E
10,000	
20,000	LGM (Last Glacial Maximum) R1b in Iberian Peninsula; I in Balkans Gravettian Tradition, Upper Paleolithic; Venus Figurines, shell jewelry
40,000	Paleolithic, Aurignacian Tradition, Lascaux
50,000	modern humans migrate out of Africa in significant numbers
	modern humans in Yemen
100,000	modern humans at Skhul Cave
200,000	Neanderthals at Tabun Cave

Haplogroups identify lines of descent that embody large-scale aspects of human history. All of the people who share a haplogroup share a common ancestor. These ancestral lines can be traced through the migrations that humans made to populate the earth.

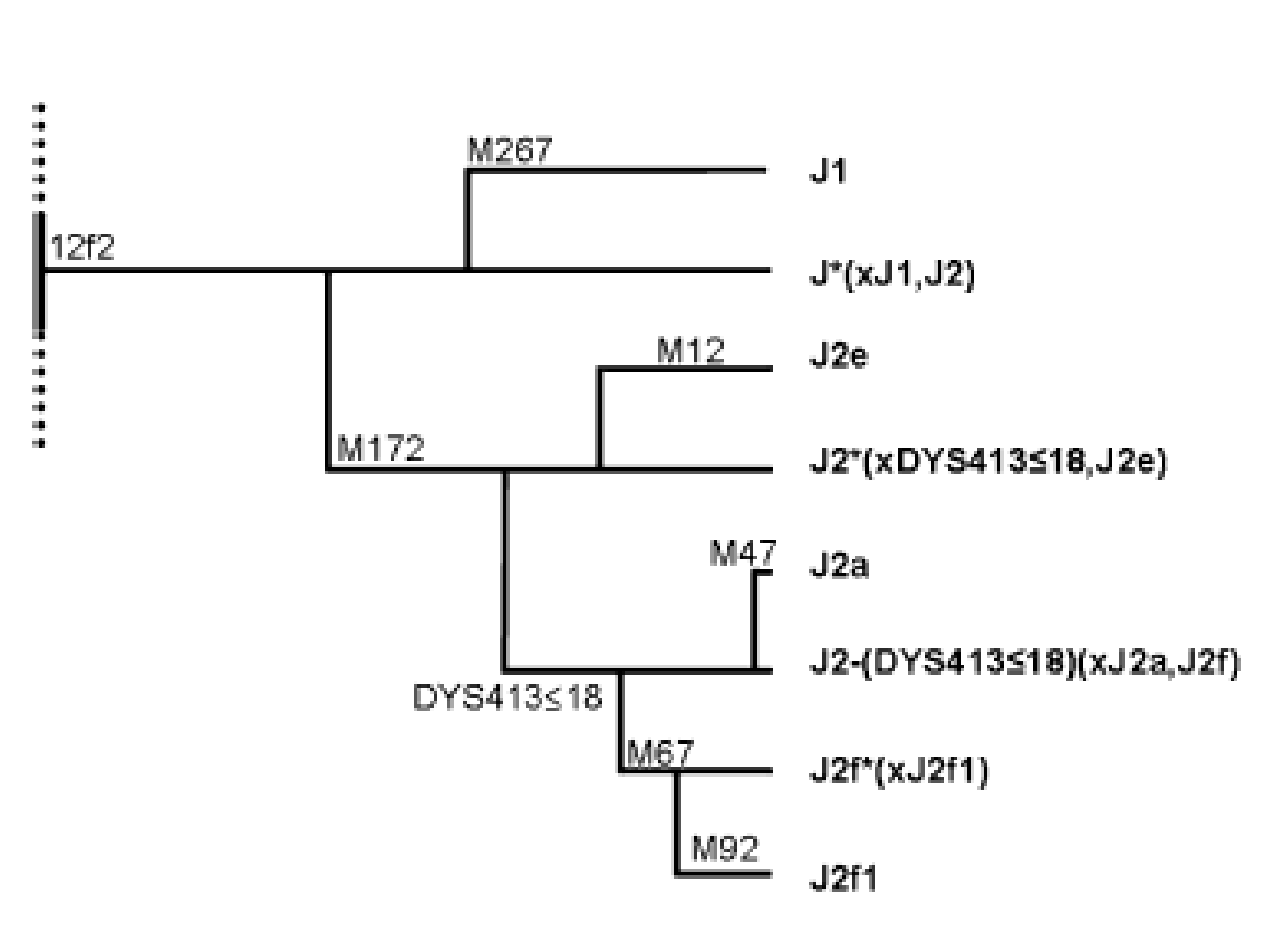
yDNA Haplogroup Distributions



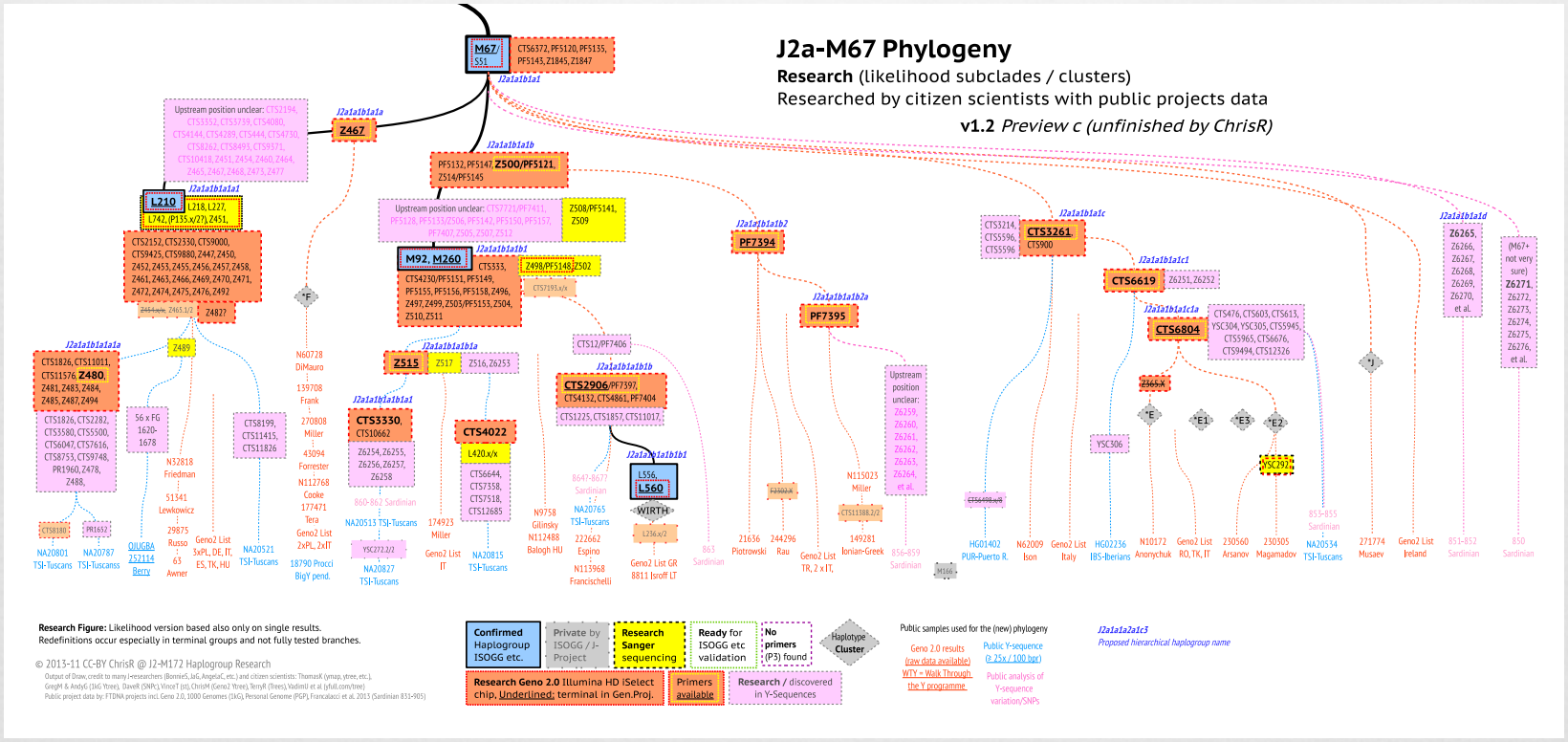
Advances in Interpreting yDNA

- Today, it is possible to create increasing levels of refinement in our understanding of the progressive mutations in human yDNA and the implications for genealogy. In the past, we've just looked at major subdivisions (subclades) of haplogroups, and the STR mutations within those subclades. Now, tests like "The Big Y" test hundreds of SNPs in yDNA, so that within the previously defined subclades we are seeing finer and finer subdivisions. Since SNP mutations occur much less often than STR mutations, we are able to identify many more "matches" in the far distant past as "accidental"or of genealogical interest..

Subgroups of J, as identified in 2010



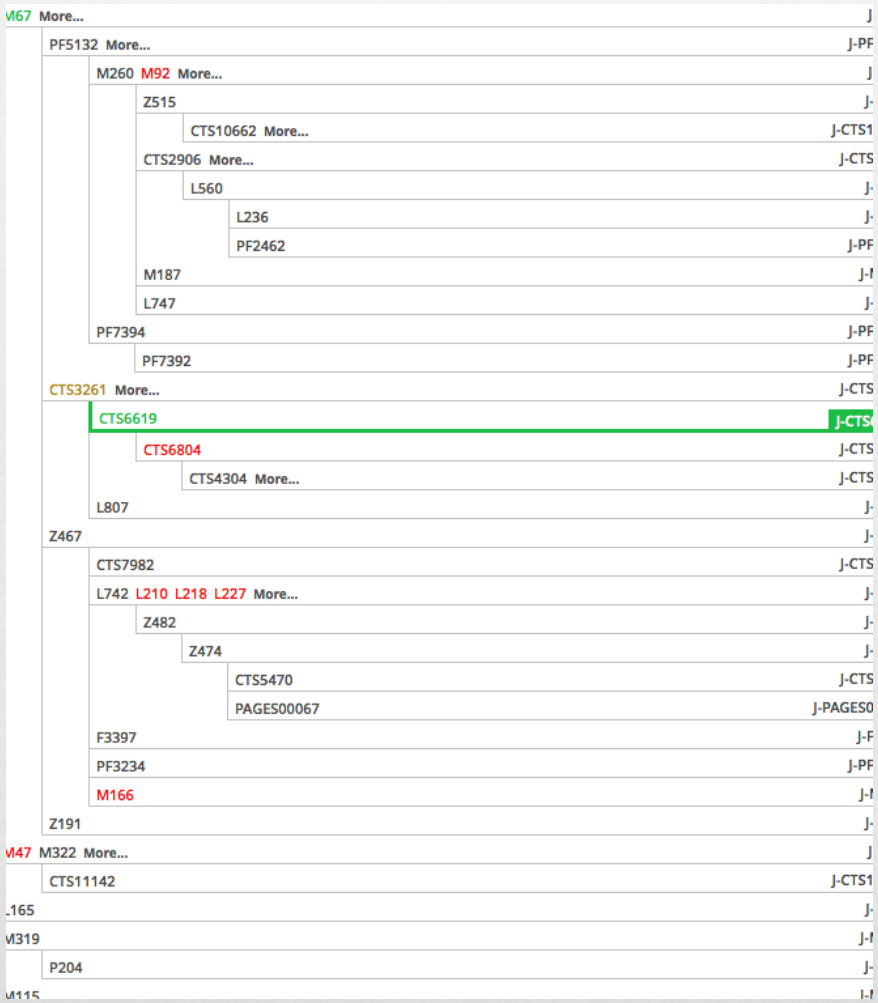
Subgroups of J, 2014



Current yDNA Classification

- Because significant mutations are being discovered on a regular basis, the old system of classifying yDNA subclades is on the way out. No more J2a2b1 type designations. Instead, the trend is to use the major haplogroup designation (R1, J1, and so forth) followed by the last significant mutation that has been identified for the sample. The Dukes family yDNA, for example, is now J2a-CTS6619.

The Dukes Family in J2a



Dukes Origins

- J2 mutation: 27,000 years ago, northern Fertile Crescent
- J2a mutation: 19,000 years ago in eastern Anatolia
- J2a-L26 mutation: 15,000 years ago, major expansion
- J2a-M67 11,000 years ago, eastern Anatolia
- CTS3261/CTS900 8,000 years ago, northern Caucasus Mountains
- CTS 6619 about 4,000 years ago, northern Caucasus
- *CTS 6804 Heavily concentrated in northern Caucasus, Dukes negative for this SNP*

Seafaring Dukes Ancestors

- Within J2a-M67 there are three major groups marked by new mutations. Those having the Z467 and Z500 mutation are heavily distributed through the Balkans and eastern Europe, pointing toward overland migrations into Europe.
- Those who are CTS3261/CTS900 positive, like the Dukes lineage, are found in the Caucasus and adjacent regions (Armenia, eastern Anatolia) and in coastal Italy, Spain and eastern Britain.

Tests for Additional SNPs

- There are two ways to test for additional SNPs:
- The Big Y and similar tests: A comprehensive yDNA SNP test that costs around $600
- Buying a SNP at a time, which costs only $35/SNP.
- Joining an active study group on your haplogroup helps you keep up with the relevant SNPs that you might want to have tested.

Ordinary yDNA STRs Still Most Important for Recent Genealogy

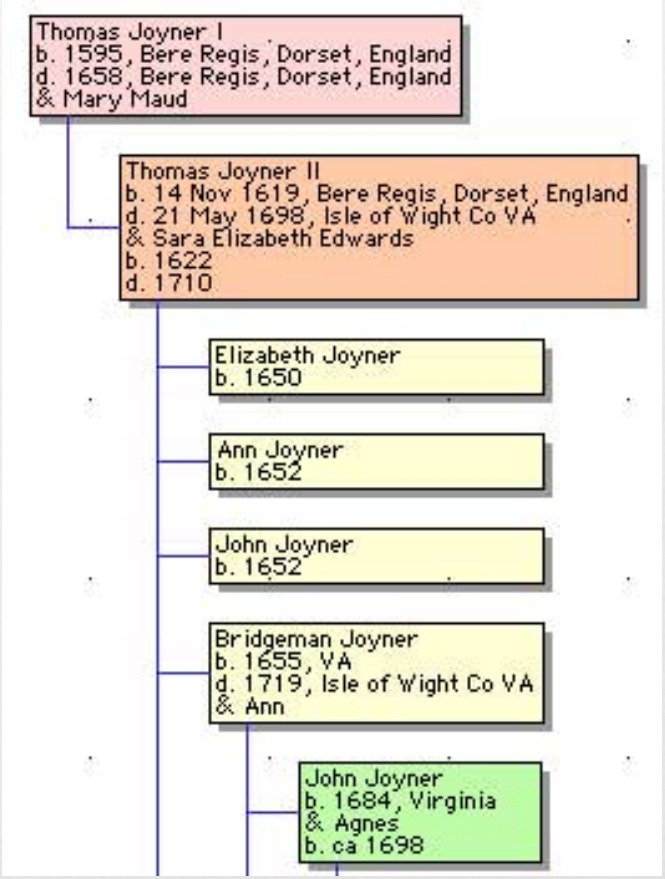
Joyner Family

Several years ago we identified a member (Kit No. 145557) who is an Orangeburgh Joyner, and is a perfect match of STR markers for descendants of the Joyner family of Isle of Wight County, VA, which is descended from an emigrant from Bere Regis, Dorset, England.

	Haplogroup I - Lineage I		14	22	14	10	12	14	11	14	11	12	11	28	15	8	9	8	11	24	16	20	29	12	14	15	16
38286	Needham Joiner, 1870-1941, Dodge Co. Georgia	I1	14	22	14	10	12	14	11	14	11	12	11	28	15	8	9	8	11	24	16	20	29	12	14	15	16
100604	Amos Joyner, b c1786-1796, d 1853 NC, m Lottie	I1	14	22	14	10	12	14	11	14	11	12	11	28	15	8	9	8	11	24	16	20	29	12	14	15	16
145557	Thomas Joyner of SC m c1740 Faithful Carse	I1	14	22	14	10	12	14	11	14	11	12	11	28	15	8	9	8	11	24	16	20	29	12	14	15	16
110655	Nathan Gilbert Joyner, b. August 1825, Alabama	I1	14	22	14	10	12	14	11	14	11	12	11	28	15	8	9	8	11	24	16	20	29	12	14	15	16
109115	S Joyner	I1	14	22	14	10	12	14	11	14	11	12	11	28	15	8	9	8	11	24	16	20	29	12	14	15	16
153472	Not Provided	I1	14	22	14	10	12	14	11	14	11	12	11	28	15	8	9	8	11	24	16	20	29	12	14	15	16
122121	MK Joyner (Amos Joyner)	I1	14	22	14	10	12	14	11	14	11	12	11	28	15	8	9	8	11	24	16	20	29	12	14	15	16

yDNA and Documents

John Joyner acquired an early Orangeburgh land grant, and Agnes, presumed to be his wife, appears in the Giessendanner *Book of Record*. John Joyner, son of Bridgeman Joyner of Isle of Wight County, VA, is lost to Virginia records and, given the combination of DNA and documents, is surely the John Joyner of Orangeburgh.



mtDNA Haplogroup Origins

A: an ancient haplogroup most common among American Indians, and also among some Asian groups

H: SW Asian haplogroup that arrived in Europe about 25,000 years ago; most common mtDNA group in Europe

I: an early haplogroup in Europe, greatly reduced in frequency after medieval period

J: probably a Neolithic introduction into Europe from SW Asia

U: widely distributed, ancient group; U5 probably oldest mtDNA in Europe, Sykes says originated near Delphi, Greece 50,000 years ago (this seems awfully specific!).

mtDNA Results

- Mitochondrial DNA or mtDNA is the least sensitive form of DNA testing, although it has the virtue of reflecting only the direct maternal line. It is most useful for identifying the broad ethnic origins of the maternal lineage, and is useful in a genealogical time frame – the past several centuries – only when the most comprehensive test (HVR1 and HVR2, Coding Region) produces perfect matches.

mtDNA Matches

My mtDNA report shows two perfect matches in the most complete form of the test. The first of these lists the same brick wall that I have been working with, Nancy Stevens Cauthen of Lancaster County, SC

HVR1, HVR2, CODING REGION - 50 MATCHES

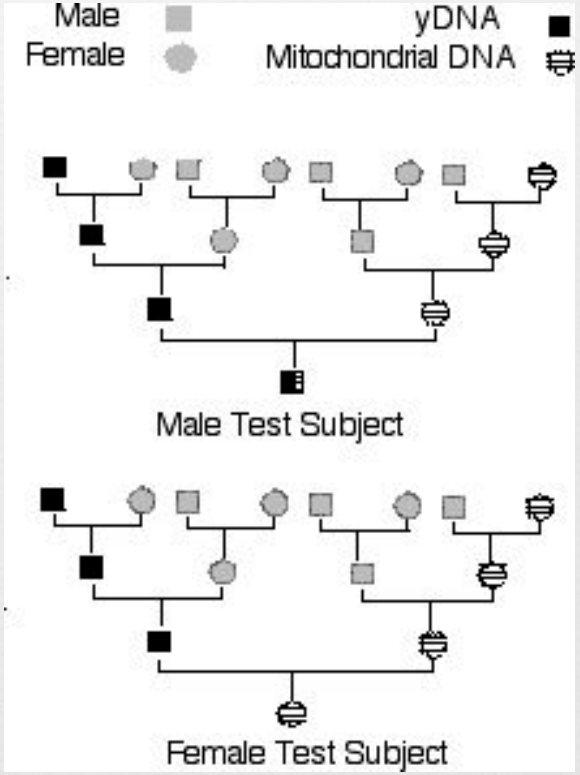
Genetic Distance	Name		Most Distant Ancestor	mtDNA Haplogroup
0	Ms. Ameta Ridgeway Macaluso	FMS FF	Nancy Stevens, b. 1800 and d. 1849	U5b2c2
0	Mr. Bruce Milton Deterding	FMS FF	Elizabeth Robertson, 1882-1977	U5b2c2
1	Steven Kensil	FMS	Eliza Whitney, b. 1789 and d. 1870	U5b2c2
1	Carolyn Harrison	FMS		U5b2c2
1	Jennifer Leigh Connolly	FMS FF		U5b2c2
1	Mark Arvid Krubsack	FMS FF	Mary Anderson, b. 1895 and died ?	U5b2c2
1	S L Mawyer	FMS FF	unknown	U5b2c2
1	Dr. Margie Burns	FMS FF	Obedience Whitney, d. 1803	U5b2c2

Autosomal DNA

- Autosomal DNA comes from both of our parents. It is also called recombinant DNA because it "recombines" with each new generation. DNA segments inherited from our ancestors is usually broken up into smaller segments as the generations continue, so that eventually segments from distant ancestors are no longer identifiable. There are exceptions, which we will talk more about later.

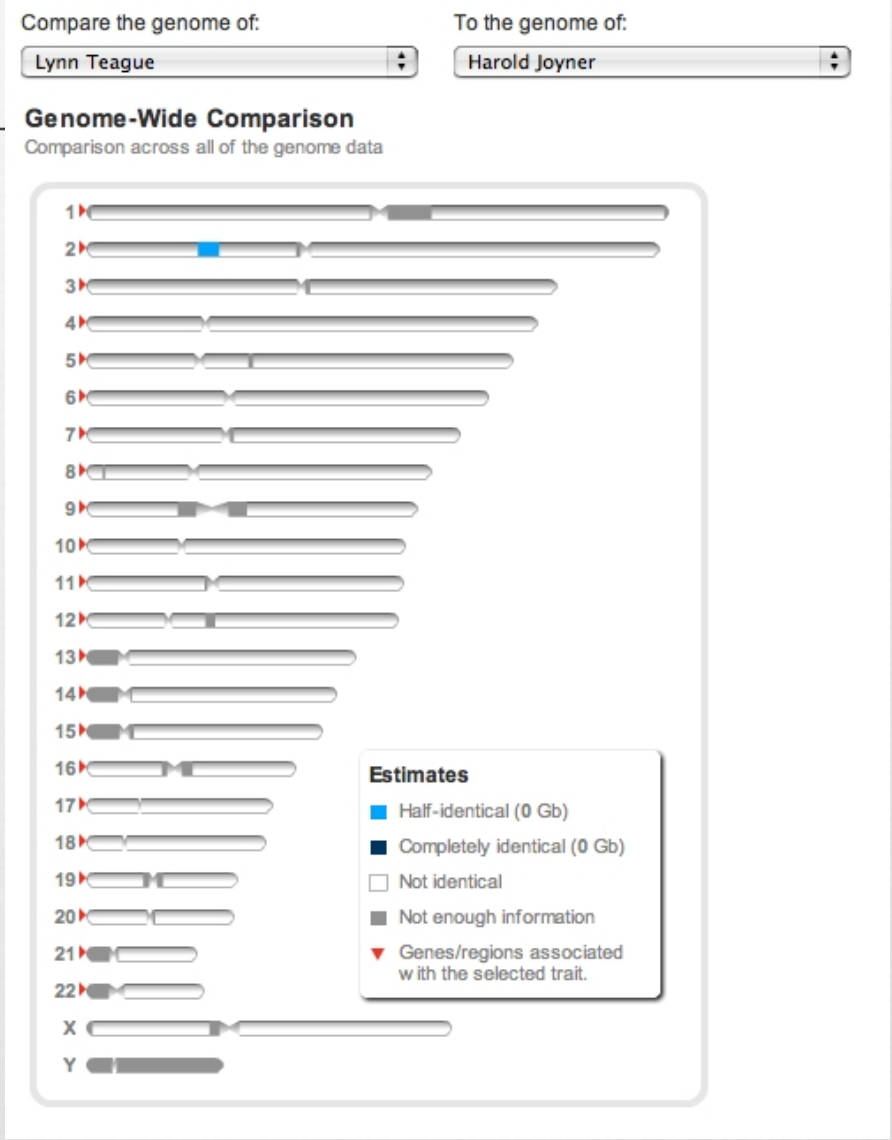
Autosomal DNA: Combining the SNPs

yDNA and mtDNA only reflect direct male and direct female lines of descent. Now, testing through the ftDNA Family Finder program, through 23andMe, and through Ancestry.com identify large numbers of SNPs (around 500,000) to identify overlapping segments of autosomal DNA, allowing identification of relatives through both these and other lines of descent. Documentary information is needed to identify the likely source of shared autosomal DNA.

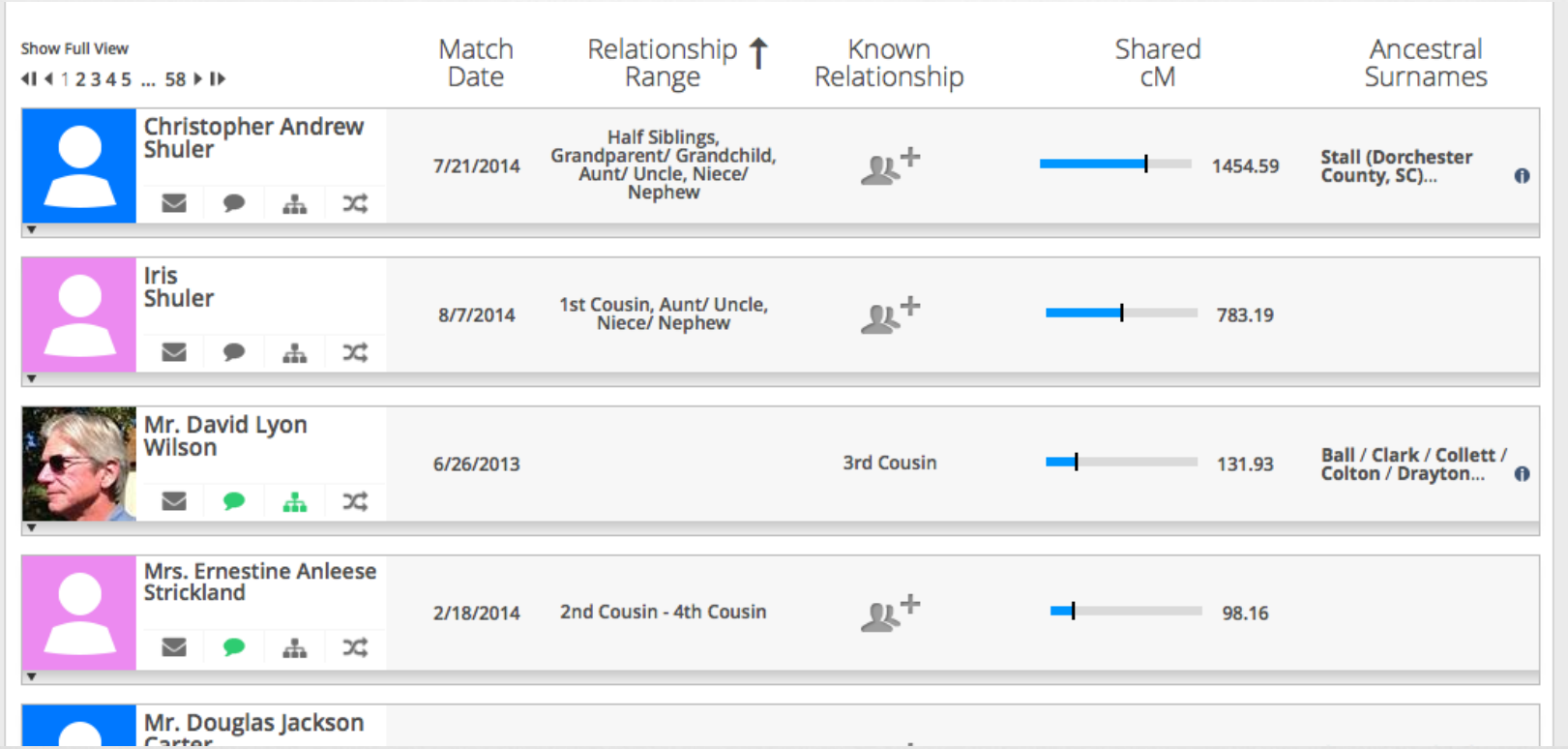


The Joyners Again

- Even before the Joyner yDNA match was known, an overlapping sequence in my 23andMe results with Harold Joyner pointed towards a match with the Isle of Wight County, VA, Joyner family. This shows the DNA segment that matches. The closely associated Orangeburg Jacksons (Miles Jackson II married Joseph Joyner) were probably also from Isle of Wight County, VA.



ftDNA Family Finder Report

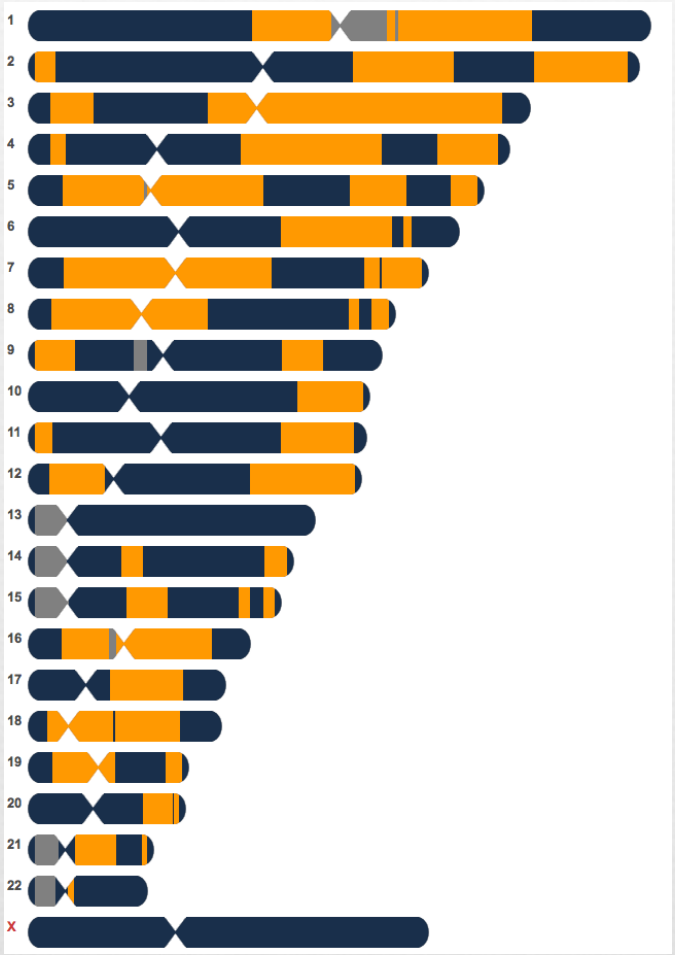


Show Full View

1 2 3 4 5 ... 58

	Match Date	Relationship Range	Known Relationship	Shared cM	Ancestral Surnames
Christopher Andrew Shuler	7/21/2014	Half Siblings, Grandparent/ Grandchild, Aunt/ Uncle, Niece/ Nephew		1454.59	Stall (Dorchester County, SC)...
Iris Shuler	8/7/2014	1st Cousin, Aunt/ Uncle, Niece/ Nephew		783.19	
Mr. David Lyon Wilson	6/26/2013		3rd Cousin	131.93	Ball / Clark / Collett / Colton / Drayton...
Mrs. Ernestine Anleese Strickland	2/18/2014	2nd Cousin - 4th Cousin		98.16	
Mr. Douglas Jackson Carter					

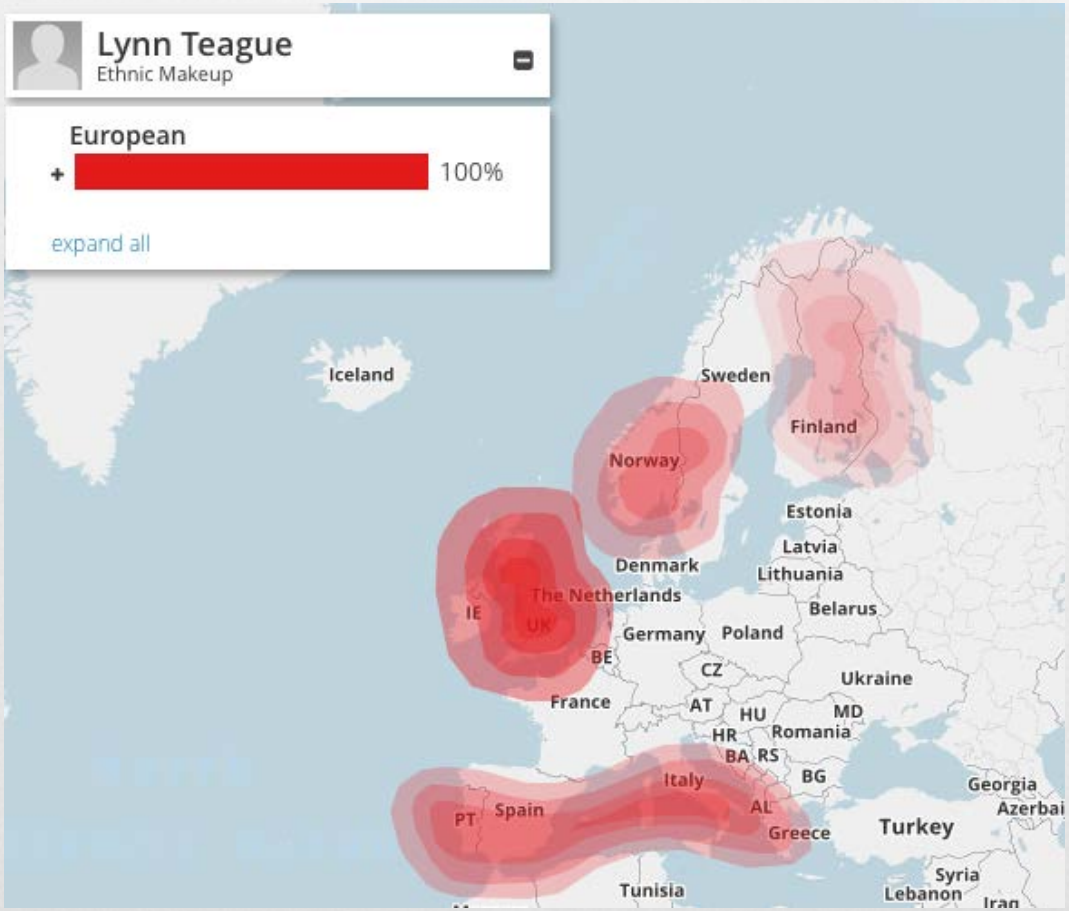
Chromosome Browser



Autosomal DNA and Origins

- One of the very popular interpretive uses of autosomal DNA is to look at the ethnic or geographic origins of one's ancestors by comparison to samples from all over the world. Each version of this kind of test produces different results, often dependent on the samples used in the database to which individual results are compared. Both FamilyFinder and 23andMe provide very general maps of origins. Transfer of results to GedMatch, a free service, permits comparison through a variety of different models.

My Origins at ftDNA



Ancestry at 23andMe

99.7%	European
	Northern European
33.5%	British & Irish
20.2%	French & German
6.3%	Scandinavian
33.4%	Broadly Northern European
	Southern European
2.9%	Iberian
1.3%	Broadly Southern European
2.2%	Broadly European
0.1%	Middle Eastern & North African
0.1%	North African
< 0.1%	Broadly Middle Eastern & North Afric…
0.1%	Sub-Saharan African
0.1%	Broadly Sub-Saharan African
0.1%	Unassigned
100%	**Lynn Teague**

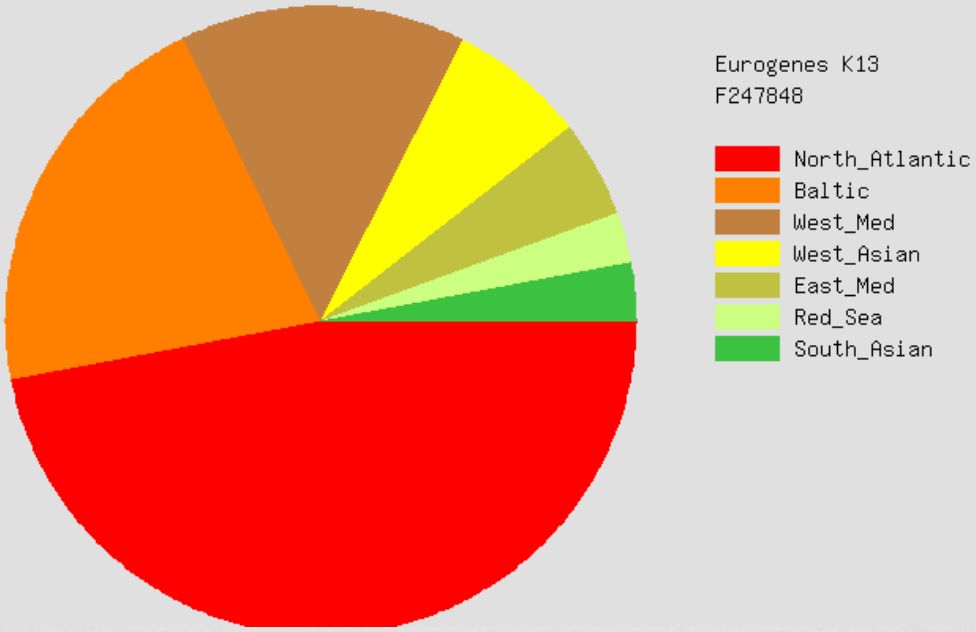
The Eurogenes K13 Model

Eurogenes K13 Admixture Proportions

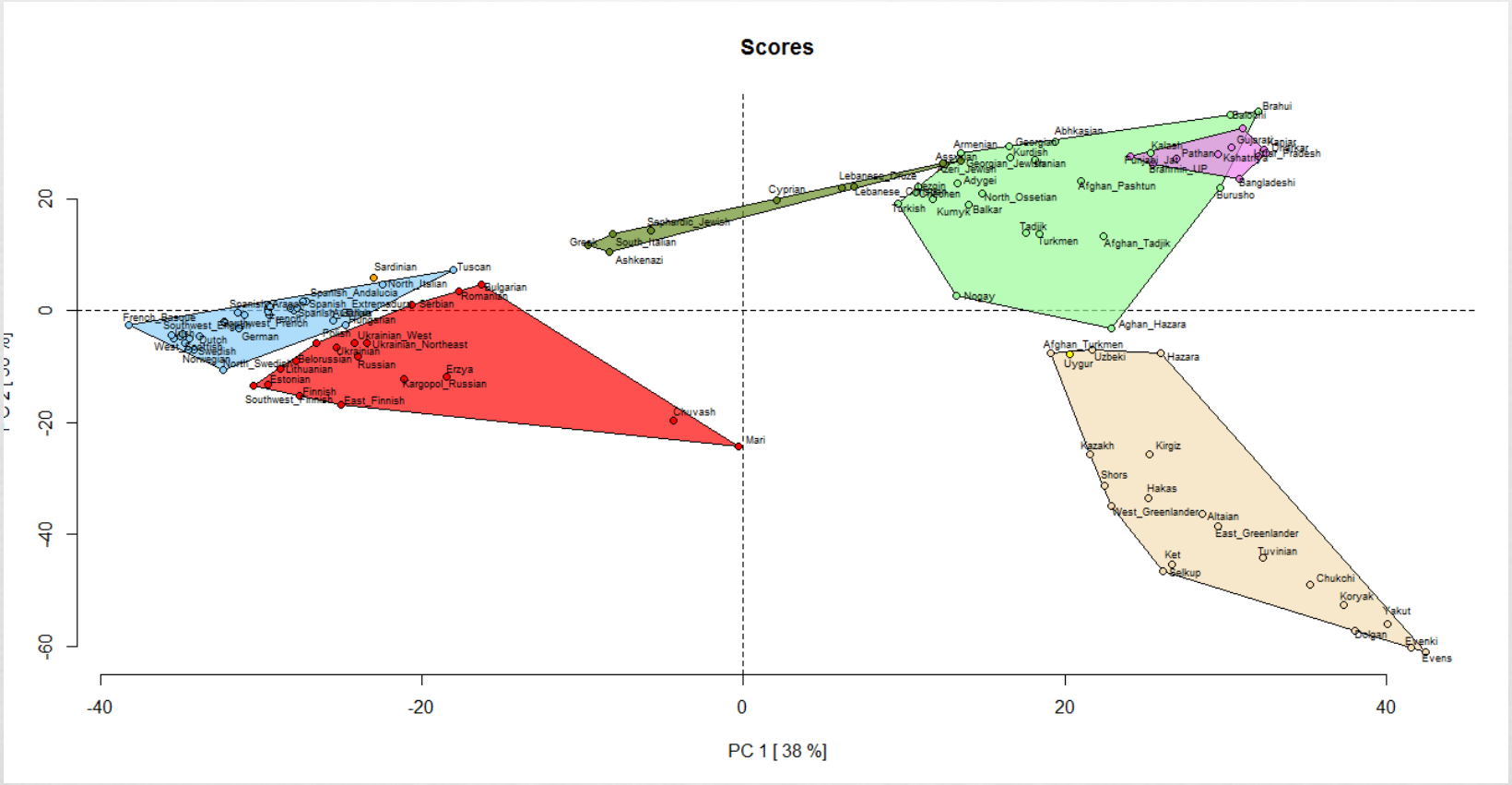
This utility uses the Eurogenes K13 model (rev 21 Nov 2013), created by Davidski (Polako). Questions and comments about this model should be directed to him at his Project Blog.

Kit Number: F247848 Iteration: 1000 Delta-Q: 8.674710e-03 Elapsed Time: 75.35 seconds

Population	
North_Atlantic	47.05%
Baltic	20.82%
West_Med	14.70%
West_Asian	6.75%
East_Med	5.14%
Red_Sea	2.59%
South_Asian	1.29%
East_Asian	0.45%
Siberian	-
Amerindian	0.65%
Oceanian	0.56%
Northeast_African	-
Sub-Saharan	-

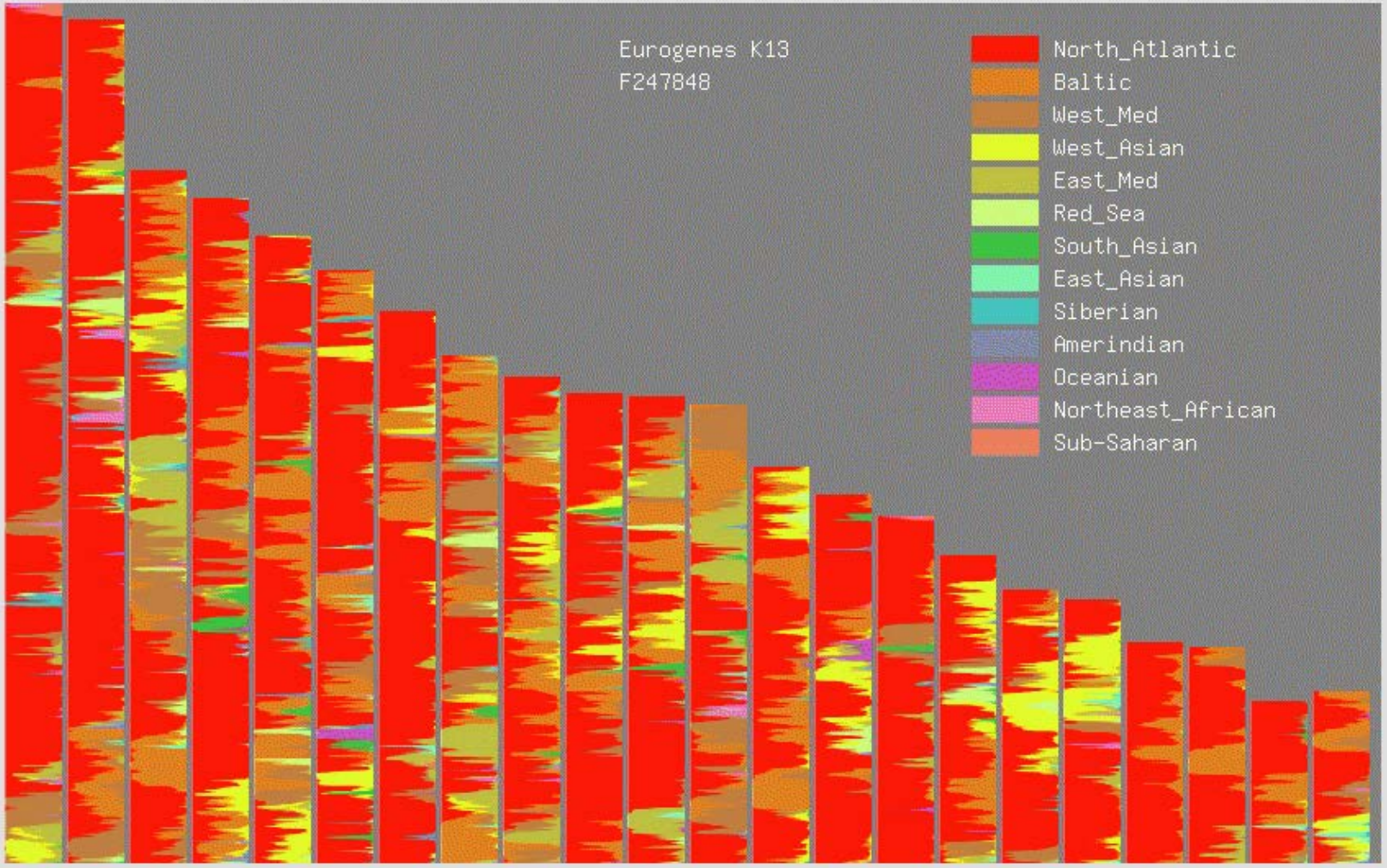


The K13 Model Principal Components



Chromosome Painting

This utility uses the Eurogenes K13 model (rev 21 Nov 2013), created by Davidski (Polako). Questions and comments about this model should be directed to him at his Project Blog.



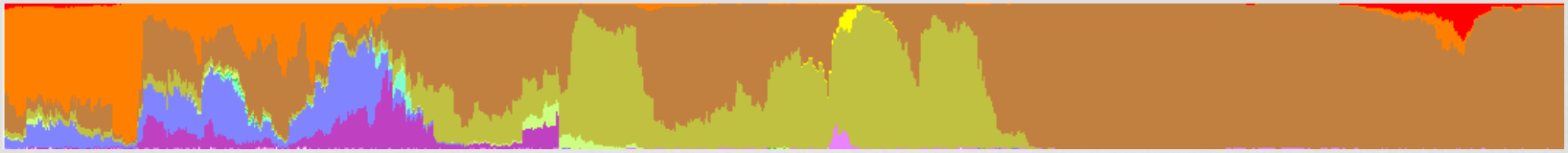
High Resolution Chromosome Painting

The Dodecad V3 (dv3) admixture calculator is courtesy of Dienekes Pontikos and was developed as part of the Dodecad Ancestry Project; more information here.

- East_European
- West_European
- Mediterranean
- Neo_African
- West_Asian
- South_Asian
- Northeast_Asian
- Southeast_Asian
- East_African
- Southwest_Asian
- Northwest_African
- Palaeo_African

Kit Number: F247848

Chr 1



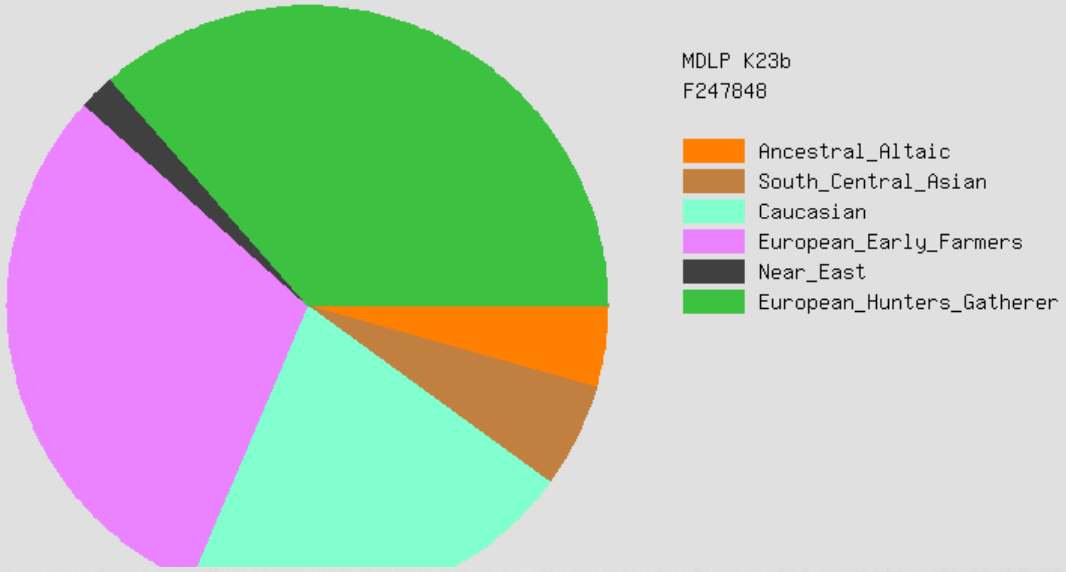
MDLPK23b Origins

MDLP K23b Admixture Proportions

This utility uses the MDLP K23b calculator, created by Vadim Verenich. Questions and comments about this calculator should be directed to him at vadimverenich@gmail.com or visit his Project Blog.

Kit Number: F247848 Iteration: 1000 Delta-Q: 2.019514e-02 Elapsed Time: 59.73 seconds

Population	
Amerindian	-
Ancestral_Altaic	4.36%
South_Central_Asian	5.72%
Arctic	-
South_Indian	0.11%
Australoid	-
Austronesian	-
Caucasian	21.35%
Archaic_Human	-
East_African	-
East_Siberian	-
European_Early_Farmers	30.36%
Khoisan	0.53%
Melano_Polynesian	-
Archaic_African	0.14%
Near_East	1.85%
North_African	0.68%
Paleo_Siberian	0.46%
African_Pygmy	-
South_East_Asian	-
Subsaharian	0.11%
Tungus-Altaic	-
European_Hunters_Gatherers	34.29%



Limitations of Autosomal Testing

- Autosomal testing is subject to a few major restrictions:
  - Documentary evidence is essential to identify the ancestral source of shared DNA.
  - Shared DNA is defined in terms of intact sequences that match. After about five generations, sequences tends to be so scrambled by recombination in each generation that matches often cannot be identified.
  - There are also matching segments that are so "sticky" – resistant to being split in the recombining process – that they represent very ancient DNA origins, preserved generation after generation. Very large numbers of matches tend to pile up in these locations.

Sticky Segments

My autosomal DNA includes a segment on chromosome 12 in which all matches are Scandinavian. It falls within a larger segment in which the ancestry is through my maternal grandmother, whose heritage was predominantly northern English and lowland Scottish. My mtDNA is very Scandinavian, reflecting the strong connections between Scandinavia and those areas. The "sticky" segment of deep ancestry DNA that is found on chromosome 12 reflects that heritage.

Chester Melin	12	118354477	123534302	7.78	500		all Swedish
Eleanor Louise Robertson	12	118354477	123534302	**7.78**	1094		no info
Lisbeth Corvinius KjÃ¦rsgaard	12	118354477	123534302	**7.78**	1094		all Danish; in common with Ecklund, Robertson
Mark Christopher Ecklund	12	118354477	123691027	**8.75**	1094		all Swedish
Oddmund Filseth c/o Amund Nedland	12	118354477	123691027	**8.75**	1173		all Danish
Olle Anders Erik Ringaby	12	118354477	123534302	**7.78**	1173		Danish or Swedish
Patrik Hallberg	12	118354477	123534302	**7.78**	1094		all Swedish
Sandra Ruth Bartman	12	118354477	123691027	**8.75**	1094		Canadian
Scott Nystrom	12	118354477	123534302	**7.78**	1173		Norwegian

Interpreting Autosomal DNA in a Genealogical Time Frame

- Margaret Waters will be talking about this in detail.
- Just a few thoughts at this point:
  - Ancestry does not provide the data needed for chromosome mapping.
  - 23andMe provides opportunities to ask matches for their data. Most do not respond.
  - Only Family Finder at Family Tree DNA is easy to work with for genealogical purposes.