

Help! I Just Got My DNA Results and I'm Confused -- UPDATED 2023

Prioritize your match lists, get organized, and thus reduce the stress and confusion

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- TAKE A DEEP BREATH. Try and relax as the goal at the end of this presentation is for you to be able to say, "Now I get it. I understand what to do. I can do this."
- The primary goal of working with DNA matches and ethnicity is to assist you in your genealogical research. To fill out the branches and leaves of your Family Tree.
- I have tested at the four major companies and have over 200,000 matches. Stress, confusion, what do you do next...these are the things we are all confronting. Let's take it step by step to slow the process down and deliver results by managing expectations and prioritizing your matches
- Managing Expectations and the 7 rules: [SEE PAGE 5 SLIDE 4](#)
- You are doing data analysis and interpretation – FOLLOW THE EVIDENCE!
 1. Do not draw conclusions based on what we want the results to be
 2. DNA doesn't lie, but results can be misinterpreted
- If you are new to this, be prepared that you may learn secrets that you and/or others may not want to know about
- Genetic Genealogy (DNA) is a tool in your Genealogical Tool Belt
 1. ***It is not stand alone!***
 2. **It provides CLUES**
 3. ***Ethnic Origins you receive are just estimates and will change every 18-24 months***
 4. ***DNA is a key to confirming or denying family relationships***
 5. ***It is BETTER TO BE LUCKY THAN GOOD***
 6. ***HAVE PATIENCE – your relatives may not have tested yet***
 7. Chart showing generations, shared ancestor, max # of possible ancestors, matches to look for and average % of DNA each generation. Autosomal DNA dilutes by about 50% each generation you go back in time
 8. Chart showing history timeline of the Jewish people and where DNA fits www.odyeda.com. Autosomal DNA is reasonably accurate back to about 350 years ago +/- 100 years. So, you won't see your ancient Israel origins.
- Discussion and review of Ethnicity ***Estimates*** and match results
 1. My Heritage
 2. Ancestry

3. 23andme
 4. Family Tree DNA
- Chart on How Much DNA in cM you can expect based upon a relationship
<https://larasgenealogy.blogspot.com/>
 1. Lara Diamond survey data compared to Shared cM Project (all people)
 2. Shows a range of total shared DNA ranges min/max and average
 3. Segment length of Longest Segment -- **KEY**
 4. Explanation of Endogamy effect on amount of DNA shared
 5. Possible (up to 10%) for known 3C or earlier to share zero (0) or significantly less DNA than the avg amount of any chart
 - Perhaps a Few Caveats
 1. *Always check with your doctor first before performing any exercises...*
 2. Formulas are a prioritizing method that I use to narrow my focus to stop feeling overwhelmed. They are not meant to be all encompassing. You are related to your DNA match list
 3. Formulas are not definitive and not set-in concrete
 4. Expect exceptions; perhaps a lot of them especially known relatives > 3C
 5. But you can always go back and work on the exceptions
 6. These formulas work best in the 3rd Cousin Range +/- (2C1R – 4C1R)

TAKE ADVANTAGE OF NOTES SECTIONS AT EACH COMPANY ON MATCH PAGES SO YOU DON'T "CHECK" THE SAME PEOPLE OVER AND OVER AGAIN!

- **WHAT IS THE GOAL OF THIS PRESENTATION?**
 1. **Prioritizing unknown matches to a reasonable number that you can contact who could be related to you to in the timeframe of your Genealogy Family Tree.**
 2. *IGNORE THE "COUSIN" ESTIMATES by the company in all cases*
 3. For each one there will be a formula* that I utilize (subject to Rules 1 & 2).

Family Tree DNA- Process (ignore pre-July 1 matches and start over with new matches)

- (1) Examine match list– download list and segment data list in csv format if you can work with spreadsheets. Otherwise use your own system for dealing with lists.
- (2) Focus first on Longest Block (same as longest segment, largest segment) then,
- (3) Those with DNA shared of 100cM minimum – less than this amount can mean still related but probably further back than your genealogy tree – **see Rule 5**
- (4) Select those that meet the criteria of the Longest Block >= (greater than or equal to) 20cM (30cM would be better yet)
- (5) Write them down or enter them in your own spreadsheet
- (6) Utilize Chromosome Browser

- (7) Move your mouse cursor over the segments and read the size
- **Do not estimate length by visual size of segment (chromosomes are not the same length)**
 - Basic formula = [SEE PAGE 5 SLIDE 18](#)
 - 1 segment (**greater than or equal to**) $\geq 20\text{cM} + 2 \text{ segments } \geq 10 \text{ cM}$
 $(20+10+10) + \text{total } \geq 100\text{cM shared DNA}$
 - Then triangulate (does your match, match your known matches in a Chromosome Browser (not your siblings on the same segments) – Use MATRIX.
 - In all cases more and larger segments are better
 - Chart as a test, which ones are prioritized matches and why
 - Chart of my prioritization numbers and then REPEAT WITH YOUR SIBLINGS' MATCHES! They will be different!

23andme- Process

- a. On the dashboard click on Family & Friends on Nav Bar
- b. What a match list looks like screenshot
- c. Unique first step of two (2) step formulas
 - i. Re-sort match list by Segments (upper right corner)
 - ii. Then go to last, most distant match at end and work BACKWARDS
 - iii. Then list those who match the formula for further processing (takes less than 30 minutes). Really it will go fast.
 - iv. Number of Segments < 10 (less is better) and % of DNA Shared of $> 1.30\%$
[SEE PAGE 6 SLIDE 27](#)
 - v. Write their information down or enter a spreadsheet (amazing how few there are compared to your total match quantity)
- d. Go to Advanced DNA Comparison then enter those names and compare them (up to 5 at a time) to you in the Chromosome Browser (go to bottom of that page for the data in table format)
 - i. Do they qualify at [SEE PAGE 6 SLIDE 30](#)
 - ii. $\geq 100\text{cM Shared DNA} + \text{segments with genetic distance (lengths) of } \geq 20\text{cM} + \geq 10\text{cM} + \geq 10\text{cM} + \text{triangulation using the Chromosome Browser on the same segment?}$

23andme calls longest segment, Genetic Distance

- e. Charts and test showing a real prioritized matches and those that does not qualify
- f. Examples of Priority Matches and not priority matches (you could still be related but further back in time perhaps beyond your family tree)

My Heritage - Process

- (1) Review match list and note down on spreadsheet or paper the matches that meet the qualifications
- (2) Do they qualify at [SEE PAGE 6 SLIDE 37](#)
 - a $\geq 100\text{cM}$ Shared DNA + Segment lengths of $\geq 20\text{cM}$ + $\geq 10\text{cM}$ + $\geq 10\text{cM}$ + triangulation?
- (3) Chart shows your matches & prospect's matches & symbol shown if triangulate
 - a Click on triangulate icon to reach chromosome browser
- (4) Write these people down or enter a spreadsheet (amazing how few there are compared to your total match quantity)

Ancestry – Process has different formula as they do not have chromosome browser

- (1) [SEE PAGE 7 SLIDE 46](#)
- (2) $\geq 90\text{cM}$ Total Amount of DNA (more is better) + Longest Segment $\geq 20\text{cM}$ → Number of Segments (less is better as it can mean longer segments)
- (3) Examples of the math formula
- (4) Example/test of matches that may qualify on your priority list
- (5) An option would be to download raw data and upload it to Gedmatch to utilize that chromosome browser

Gedmatch - Process

- (1) Upload any of your other testing site raw data (follow instructions carefully)
- (2) One to Many Beta free Tool -- Sort match lists by longest segment
- (3) Write down the ones that qualify by the standard formula
- (4) [SEE PAGE 7 SLIDE 51](#)
- (5) $\geq 100\text{cM}$ + $\geq 20\text{cM}$ + $\geq 10\text{cM}$ + $\geq 10\text{cM}$
- (6) Triangulate


*Note that the formulas provided have not been empirically tested/verified. They are the ones that I have used to effectively prioritize my matches (and finding real relatives) to a reasonably sized list to start search and manage my own expectations. Formulas are not definitive and not set-in concrete. Expect exceptions; perhaps a lot of them. But you can always go back and work on the exceptions. They work best in the 3rd Cousin Range +/- (2C1R – 4C1R)

After you complete these exercises and prioritize/contact your matches you will find many new questions, exceptions and what are the next steps.


REMEMBER -- The key to success will be your family tree – Can you find where your matches fit on your tree and document that information?

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I'm Confused!

2023
Part 1



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Manage Expectations

- Rule 1: **New science and things are changing rapidly!**
- Rule 2: **"Based upon what we know now..."**
- Rule 3: ***Family Tree – wide & tall***
- Rule 4: **Autosomal DNA is Random**
- Rule 5: **Expect Exceptions**
- Rule 6: **Segment Length first...**
- Rule 7: **Shared/in-Common with ...**



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Prioritize Unknown Matches
Family Tree DNA

Ignore "Cousins" estimates instead use the following Criteria 20 + 10 +10 +100

1
Segment
Block
≥ 20 cM

+

2
Segments
Blocks
≥ 10 cM

+

Shared
cM
≥ 100 cM

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Prioritize Unknown Matches - Step 1
23andme

Ignore "Cousins" estimates, instead use the following criteria to prioritize

Number of Segments
3 to 10
Smaller is better

&

% of DNA Shared
> 1.30%
More is better



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Prioritize Unknown Matches - Step 2
23andme

Ignore "Cousins" estimates instead use the following Criteria 20 + 10 +10 +100

1 Segment ≥ 20 cM

+

2 Segments ≥ 10 cM

+

Total Amount of DNA ≥ 100 cM*

*Exclude X Chr Amount

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Prioritize Unknown Matches
MyHeritage

Ignore "Cousins" estimates instead use the following Criteria 20 + 10 +10 +100

1 Segment ≥ 20 cM

+

2 Segments ≥ 10 cM

+

Shared cM ≥ 100 cM

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Prioritize Unknown Matches
Ancestry

Ignore "Cousins" estimates instead use the following Criteria 90 + 20 + <11

Shared DNA
≥ 90 cM
More is better

+

Longest Segment
≥ 20 cM

→

Number of Segments
11*
Less is Better

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Prioritize Unknown Matches
GEDmatch

Ignore "Cousins" estimates instead use the following Criteria 20 + 10 + 10 + 100

1 Segment
≥ 20 cM

+

2 Segments
≥ 10 cM

+

Shared cM
≥ 100 cM

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