Interpreting DNA Test Results

Presented by

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Overview

- What DNA Testing Can Not Do
- What DNA Testing Can Do
- Exact Science Combined with Probability
- One Method of Grouping Participants

DNA Testing

A <u>TOOL</u>

to be used along with conventional genealogical research

DNA Testing Can Not

- Tell you who your ancestors are
- Tell you who your common ancestor is
- Tell you when your common ancestor lived
- Provide positive proof of a suspected connection

DNA Testing Can

- Indicate that you and another participant share a common ancestor
- Give you **ROUGH** idea of how far back your common ancestor lived
- Provide evidence that suspected lines are connected
- Provide proof that suspected lines are **NOT** connected

Exact Science
Combined with Probability

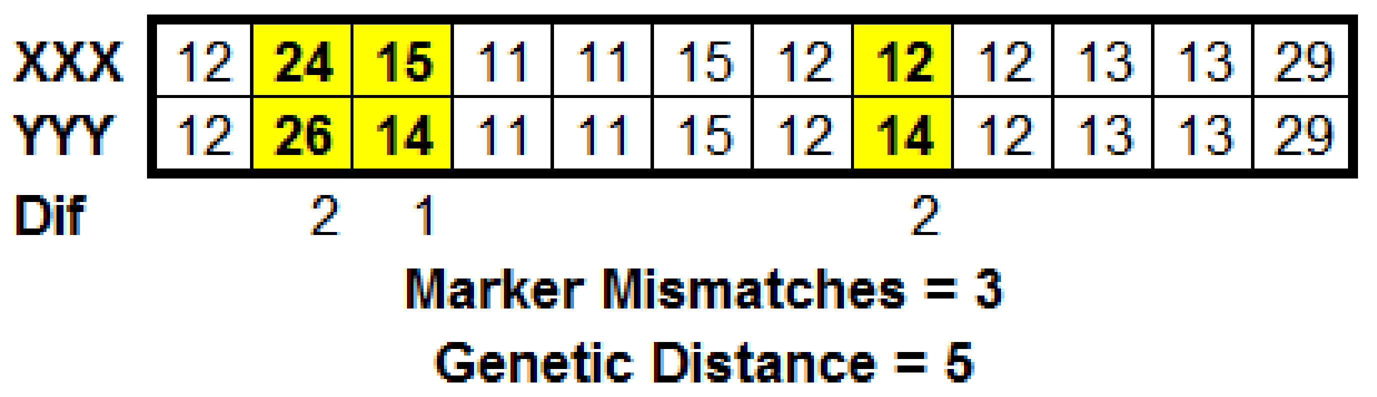
- The actual DNA testing procedure is an extremely accurate and precise science
- Using the test result involves applying probability and inexact estimates of mutation rates

Exact Science
Combined with Probability

- Must use statistics and probability to **estimate** the Time to the Most Recent Common Ancestor (TMRCA)
- The actual calculations of TMRCA are mathematically complex and depend on knowing the number of mutations and the rate of mutation

Number of Mutations

- Number of Mismatches: Each marker is either a match or a non-match
- Genetic Distance: Sums the difference of mismatched markers
- Example



XXX	12	**24**	**15**	11	11	15	12	**12**	12	13	13	29
YYY	12	**26**	**14**	11	11	15	12	**14**	12	13	13	29
Dif		2	1					2				

Marker Mismatches = 3

Genetic Distance = 5

Mutation Rate

- Has a marked effect on the TMRCA
- Doubling mutation rate cut the TMRCA in half
- If you have a match on 36 of 37 markers
  - Rate = 0.002 –> 50% within 12 generations
  - Rate = 0.004 –> 50% within 6 generations

Mutation Rates

- Mutations occur at random
- Can’t be predicted
- Mutation rates must be estimated based on past observations

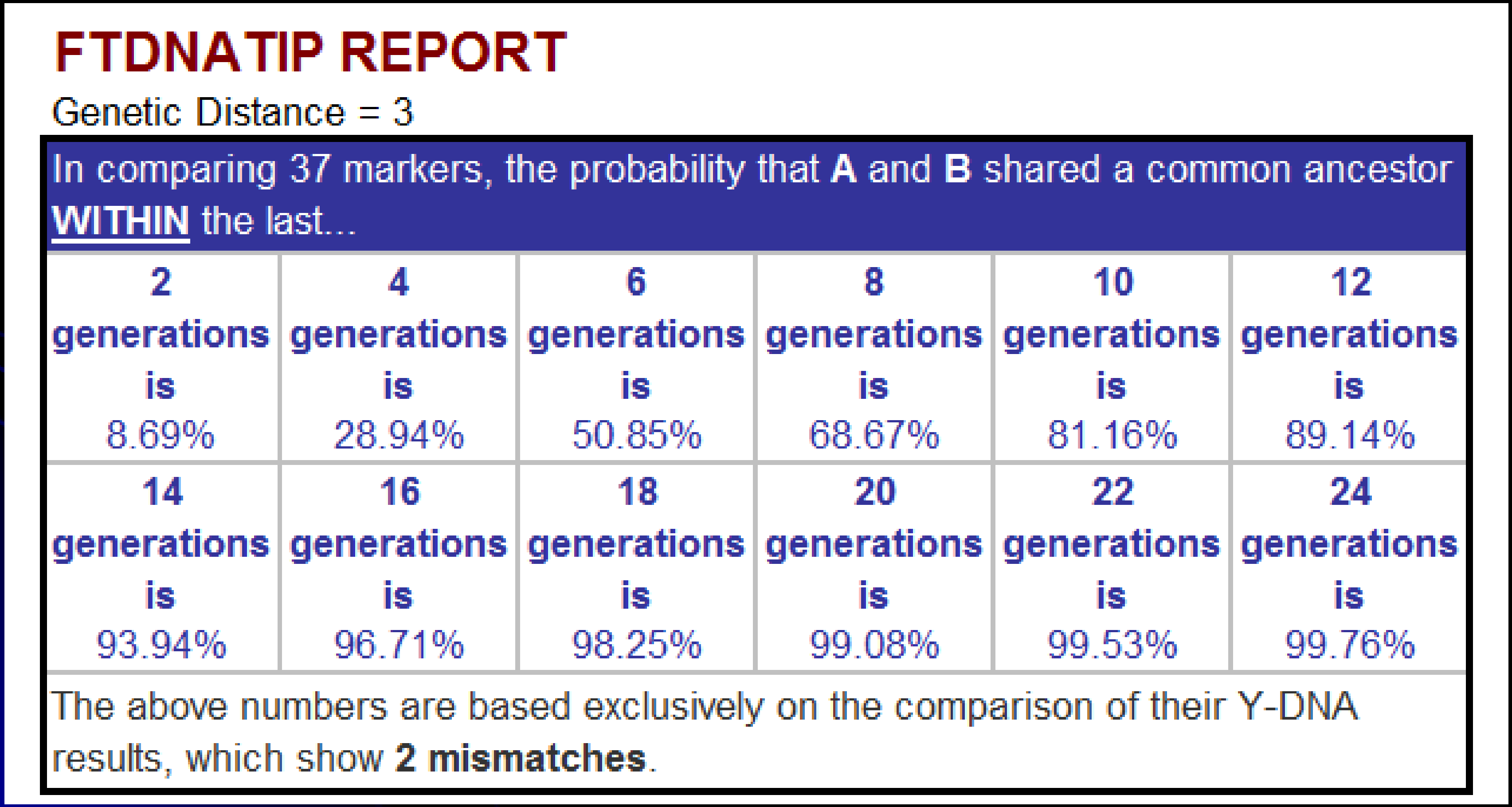
Mutation Rates

- No real consensus on Individual Marker or Average Mutation Rates
- Different studies have come up with different rates
- Still not enough data available
- I use FTDNATip to calculate TMRCA

See handout for other mutation rate sources

Time to the Most Recent Common Ancestor

- Typical FTDNATip Report



FTDNATIP REPORT

Genetic Distance = 3

In comparing 37 markers, the probability that **A** and **B** shared a common ancestor **WITHIN** the last...

2 generations is 8.69%	**4 generations is** 28.94%	**6 generations is** 50.85%	**8 generations is** 68.67%	**10 generations is** 81.16%	**12 generations is** 89.14%
14 generations is 93.94%	**16 generations is** 96.71%	**18 generations is** 98.25%	**20 generations is** 99.08%	**22 generations is** 99.53%	**24 generations is** 99.76%

The above numbers are based exclusively on the comparison of their Y-DNA results, which show **2 mismatches**.

Time to the Most Recent Common Ancestor

- **A VERY BROAD ESTIMATE**
- Results are **WITHIN** X generations
- Based exclusively on the comparison of the Y-DNA results
- Assumes no prior knowledge of genealogies

TMRCA Alternative

- **FTDNA - Interpreting Genetic Distance within Surname Projects**
- 37 Markers
  - Distance: 0 - Very Tightly Related
  - Distance: 1 - Tightly Related
  - Distance: 2 or 3 - Related
  - Distance: 4 - Probably Related
  - Distance: 5 - Only Possibly Related
  - Distance: 6 or more - Not Related

Grouping Participants
Things I Consider

- The Strength of the DNA Match
  - The Number of Markers Tested
  - The Number of Marker Matches
  - Unusual Marker Values
- Conventional Research

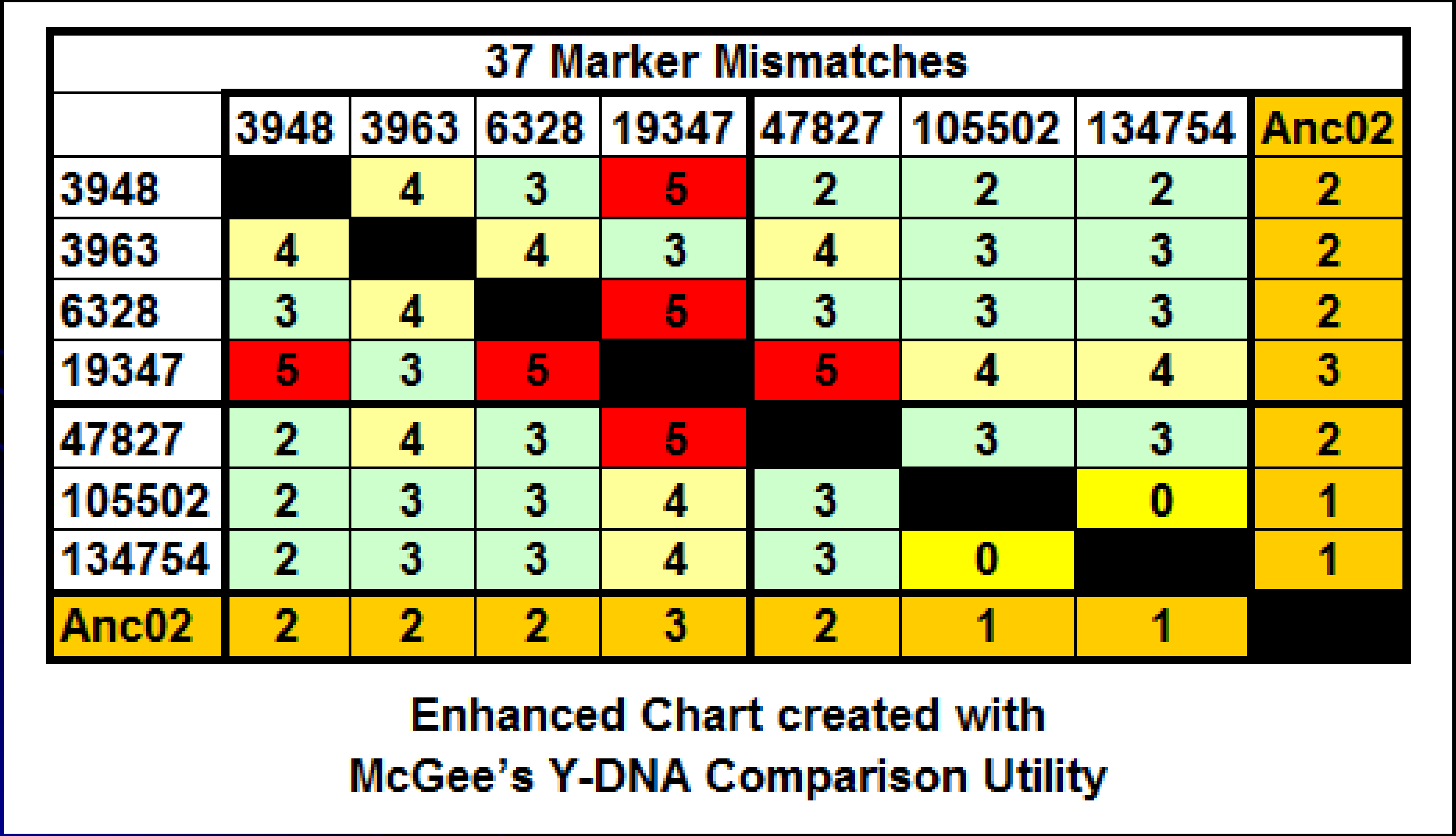
Markers Tested - Markers Matched

- Minimum of 25 Markers Tested
- ~50% Probability of sharing a common ancestor within 12 generations
    - 23 of 25 markers = 48.6 – 54.2%
    - 33 of 37 markers = 53.6 – 59.2%
    - 61 of 67 markers = 44.2 – 48.5%

FTDNATip

Marker Mismatches

- McGee’s Y-DNA Comparison Utility



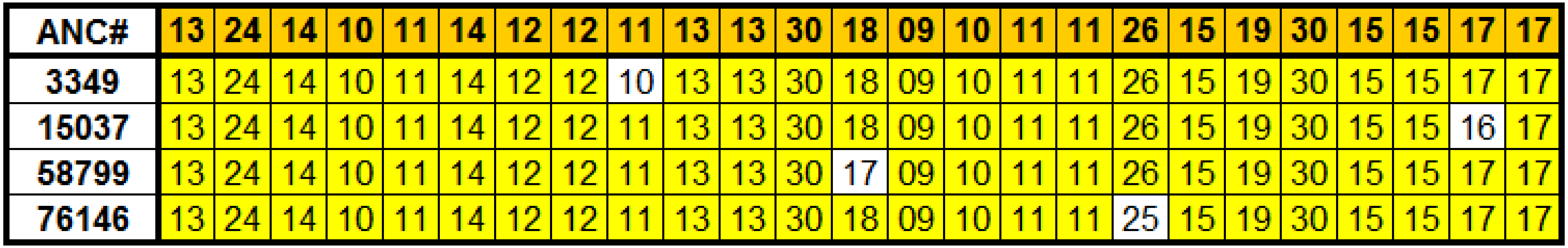
37 Marker Mismatches

	3948	3963	6328	19347	47827	105502	134754	Anc02
3948		4	3	5	2	2	2	2
3963	4		4	3	4	3	3	2
6328	3	4		5	3	3	3	2
19347	5	3	5		5	4	4	3
47827	2	4	3	5		3	3	2
105502	2	3	3	4	3		0	1
134754	2	3	3	4	3	0		1
Anc02	2	2	2	3	2	1	1	

Enhanced Chart created with
McGee’s Y-DNA Comparison Utility

Ancestral Haplotype

- **Anc##** is the hypothetical "common ancestor" of the participants in Group #
- Impossible to actually know his DNA test results
- Possible to derive his most likely test results based on the results of his descendants
- Results may change as more participants fall into Group # and more test results are available



ANC#	13	24	14	10	11	14	12	12	11	13	13	30	18	09	10	11	11	26	15	19	30	15	15	17	17
3349	13	24	14	10	11	14	12	12	10	13	13	30	18	09	10	11	11	26	15	19	30	15	15	17	17
15037	13	24	14	10	11	14	12	12	11	13	13	30	18	09	10	11	11	26	15	19	30	15	15	16	17
58799	13	24	14	10	11	14	12	12	11	13	13	30	17	09	10	11	11	26	15	19	30	15	15	17	17
76146	13	24	14	10	11	14	12	12	11	13	13	30	18	09	10	11	11	25	15	19	30	15	15	17	17

Unusual Marker Values

- Do any of the participants share a rare value on any of their markers?
- Example from Blair DNA Project - Group 3
  - Value of 26 on DYS#390 = 1.095 % *
  - Values of 12/14 on DYS#385a/b = 3.655% *
- Sorenson Molecular Genealogy Foundation Website *
- Y-Base Statistics
- Leo Little data from FTDNA data and Y-search

Conventional Research

- Do the participants in question share a common ancestor?

- How complete are their paper trails?

- Are there any inconsistencies in their paper trails?

Putting It All Together

- DNA testing can be a valuable tool in genealogical research when combined with conventional research
- Test results can be used to support a suspected connection between two families or disprove a connection
- Although it is impossible to pinpoint a common ancestor from the test results alone, with a proper paper trail you may be able to do so

Time for Tea and Biscuits

15:15 Questions and Answers