

# CLAN CRAWFORD Y-DNA LINEAGE UPDATE PROCEDURES

By

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Y-DNA updates are continually arriving from Family Tree DNA and being posted to the Clan Crawford website. These consist of results from current Crawford surname participants who have purchased additional STR or SNP testing and new individuals who have just joined the Crawford Surname Project. It is not time efficient to post each one as they arrive so usually about every 2-3 months it is necessary to update the entire site by checking the status of every participant and noting changes in information.

The lineages are determined by the two Crawford Co-Administrators with discussion with the clan genealogists when questions arise concerning conflicts between DNA results and known or perceived genealogical family information. A master list is kept with the lineage group, individual participant's name, Family Tree kit number, number of STR markers tested and the predicted on known end SNP for each person.

In order to place individuals into specific lineages, the administrators complete an analysis using the Family Tree Y-DNA Comparison Utility FTDNA 111 Mode Beta at <http://www.mymcgee.com/tools/yutility.html> .

The following protocol is followed:

1. The Y-DNA markers for each person being compared are entered in the entry window with the first 10 spaces being used for their name or coded alphanumeric number.
2. The Genetic Distance is set to "infinite allele mutation model".
3. A PHILIP TMRCA file is generated
4. Confidence level is set at 95%
5. Mutation rate is set to reflect FTDNA calculated levels for each loci (.004-.0075).
6. A generation is set to 30 years.
7. Upon executing the computer program, tables are generated for:
  - a. Mutation distances for all of the individuals entered into the program;
  - b. Estimated TMRCA between individuals tested.
  - c. A PHILIP table

8. The PHYLIP software is activated using the Philip file and the Kitch least squares analysis is generated. The Kitch program is set as follows:
  - a. Option D Kitsch-Margoliash
  - b. Select **L** for Lower triangular data matrix
  - c. Select option **J** for randomized input order of species.
  - d. When prompted for random number seed enter **9**
  - e. When prompted for number of jumbles enter **99** .
9. The out file chooses the best fit of all the jumbles as the basis for creating a lineage tree.
10. The MEGA software is then used to generate a formal lineage tree

Table 1. Example of a Genetic Distance table between individuals (mutations)

ID	Genetic Distance																																																
	Ab3 -520477	Ab3 -B10746	Ab6 -151365	Ab9 -136902	Ab9 -519372	Ab6 -413080	Ab9 -127457	Ab6 -76403	Ab9 -636875	Ab9 -87507	Ab9 -37564	Ab9 -38087	Ac6 -87590	Ac6 -112747	Ac3 -183276	Ac6 -555331	Ad9 -229314	Ad3 -138442	Ad9 -134368	Ad6 -48160	Ad9 -357293	Af9 -413803	Af9 -203412	Af9 -447476	Af6 -84633	Af6 -276787	UG3 -155890	UG2 -84615	UG6 -523855	UG6 -121071	UG3 -504012	UG6 -239351																	
Ab3-520477	37	1	1	1	2	2	2	2	2	2	3	3	5	5	5	5	5	5	4	2	2	4	4	3	3	3	3	3	3	4	4	6	3	7	6	6	7												
Ab3-B10746	1	37	0	1	1	1	1	1	2	2	4	4	4	4	4	3	1	1	3	3	2	2	2	2	2	3	3	5	2	6	5	5	5	6	5	6													
Ab6-151365	1	0	67	1	2	2	2	2	2	3	3	5	6	6	6	4	6	4	1	3	3	4	3	3	3	3	4	4	5	2	7	7	5	8	5	6													
Ab9-136902	1	0	1	111	6	1	2	1	5	7	7	7	5	5	4	5	7	1	7	4	6	5	7	9	3	3	5	2	6	6	5	7	6	5	7	6													
Ab9-519372	2	1	2	6	111	2	6	2	6	5	7	7	6	6	4	6	6	2	5	4	9	7	9	8	4	4	6	2	6	7	6	8	5	7	6	8													
Ab6-413080	2	1	2	1	2	67	0	0	0	1	2	3	6	6	5	6	4	2	3	3	4	3	3	3	2	4	6	2	7	7	6	8	5	7	6	8													
Ab9-127457	2	1	2	2	6	0	111	0	3	5	6	5	6	6	5	6	7	2	7	3	6	5	7	9	2	4	6	2	7	7	6	8	5	7	6	8													
Ab6-76403	2	1	2	1	2	0	0	67	0	1	2	3	6	6	5	6	4	2	3	3	4	3	3	3	2	4	6	2	7	7	6	8	5	7	6	8													
Ab9-636875	2	1	2	5	6	0	3	0	111	3	4	5	6	6	5	6	8	2	7	3	8	6	7	9	2	4	6	2	7	7	6	8	5	7	6	8													
Ab9-87507	3	2	3	7	5	1	5	1	3	111	5	6	7	7	6	7	8	3	6	4	10	8	9	11	3	5	6	2	8	8	7	9	5	7	6	8													
Ab9-37564	3	2	3	7	7	2	6	2	4	5	111	7	7	7	8	7	10	3	8	5	8	8	9	11	4	5	7	2	7	8	5	9	5	7	6	8													
Ab9-38087	5	4	5	7	7	3	5	3	5	6	7	111	7	7	6	7	10	4	8	4	10	5	8	9	3	5	4	4	8	8	7	10	5	3	8	7													
Ac6-87590	5	4	6	5	6	6	6	6	6	7	7	7	67	2	2	3	8	4	5	9	4	5	3	3	4	4	5	2	11	5	3	8	5	3	8														
Ac6-112747	5	4	6	5	6	6	6	6	6	7	7	7	2	67	2	3	8	4	5	9	4	5	3	3	4	4	5	2	11	5	3	8	5	3	8														
Ac3-183276	5	4	4	4	4	5	5	5	5	6	6	6	2	2	37	2	5	4	3	5	3	4	2	2	3	3	5	3	8	3	3	6	5	3	6														
Ac6-555331	5	4	6	5	6	6	6	6	6	7	7	7	3	3	2	67	8	4	5	9	4	5	3	3	4	4	5	3	11	3	3	8	5	3	8														
Ad9-229314	4	3	4	7	6	4	7	4	8	10	10	8	8	5	8	111	4	8	5	10	8	10	12	6	6	8	3	6	8	7	10	5	6	7	10														
Ad3-138442	2	1	1	1	2	2	2	2	2	3	3	4	4	4	4	37	2	4	4	2	2	2	2	2	3	3	5	2	7	5	6	5	6	5	6														
Ad9-134368	2	1	3	7	5	3	7	3	7	6	8	8	5	5	3	5	8	2	111	6	8	6	6	7	3	3	4	2	8	6	4	7	6	4	7														
Ad6-48160	4	3	3	4	4	3	3	3	3	4	5	4	8	9	5	9	5	4	6	67	7	5	6	6	5	7	6	3	6	10	8	11	5	6	11														
Ad9-357293	4	3	4	6	9	4	6	4	8	10	8	10	4	4	3	4	10	4	8	7	111	8	8	10	4	4	6	3	8	5	2	7	6	5	8														
Af9-413803	3	2	3	5	7	3	5	3	6	8	8	5	5	4	5	8	2	6	5	8	111	4	6	3	3	4	3	7	6	5	8	5	8	5	8														
Af9-203412	3	2	3	7	9	3	7	3	7	9	9	8	3	3	2	3	10	2	6	6	8	4	111	6	1	1	3	2	8	4	3	6	5	6	6														
Af9-447476	3	2	3	9	8	3	9	3	9	11	11	9	3	3	2	3	12	2	7	6	10	6	6	111	1	1	3	2	8	4	3	6	5	6	6														
Af6-84633	4	3	4	3	4	2	2	2	2	3	4	3	4	4	3	4	6	3	3	5	4	3	1	1	67	2	4	2	9	5	4	7	6	5	4														
Af6-276787	4	3	4	3	4	4	4	4	4	5	5	5	4	4	3	4	6	3	3	7	4	3	1	1	2	67	4	3	9	5	4	7	6	5	4														
UG3-155890	6	5	5	5	6	6	6	6	6	6	7	4	5	5	5	5	8	5	4	6	6	4	3	3	4	4	37	4	9	6	6	8	5	6	8														
UG2-84615	3	2	2	2	2	2	2	2	2	2	4	2	2	3	3	3	2	2	3	3	3	2	2	2	2	2	3	4	25	5	3	3	5	6	8														
UG6-523855	7	6	7	6	6	7	7	7	7	8	7	8	11	11	8	11	6	7	8	6	8	7	8	8	9	9	9	5	67	10	8	13	5	6	10														
UG6-121071	6	5	7	6	7	7	7	7	7	8	8	8	5	5	3	3	8	5	6	10	5	6	4	4	5	5	6	3	10	67	2	9	5	6	10														
UG3-504012	6	5	5	5	6	6	6	6	6	7	5	7	3	3	3	3	7	5	4	8	2	5	3	3	4	4	6	3	8	2	37	7	6	7	10														
UG6-239351	7	6	8	7	8	8	8	8	8	9	9	10	8	8	6	8	10	6	7	11	7	8	6	6	7	7	8	5	13	9	7	67	5	6	10														

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- Infinite allele mutation model is used

- Values on the diagonal indicate number of markers tested

