

Cheshire Group TMRCA Calculations

TMRCA Criteria																					
1 Mutation Rates based on Marco Heinila - the only complete set.																					
2 Date range is 1 standard deviation (16% - 84% probability).																					
3 Rates averaged for each combination of matched markers:																					
FTDNA - 37 Markers										0.36%											
DNAH - 43 Markers										0.25%											
Common - 32/34 Markers										0.24%											
4 McGee used for calculations, but not for calculating average mutation rates as multiple markers have to be pre-averaged.																					
5 Genetic Distances are hand calculated as all but one 2 step differences are due to two results being one step from the mode.																					
The two step difference from the mode is counted as one mutation, all other 2 step differences are counted as 2.																					
Also the Phylogenetic tree indicates one mutation (DYS444 from 12 to 11 must have occurred twice so an apparent match is two cancelling mutations).																					
6 No allowance is made for unknown counteracting mutations.																					
7 A start date of 1945, and 35 years per generation are used to convert generations to dates. The formula is therefore 1945 - (35 * No of generations).																					
8 Profiles are identified by their Family Tree DNA Kit Numbers																					
9 Phylogenetic Tree profile reference shown in brackets after the kit number																					
																		Years per generation:		35	
Warburtons																					
H1564 (A)										H1112 (Me)											
Markers tested										43											
Distance from Warburton mode										0											
										1 @ 43 markers, 3 @ 37 markers											
					16%					50%					84%						
Kit Number	Markers tested	Known date	Markers compared	Genetic Distance	TMRCA (gens)	Date	TMRCA (gens)	Date	TMRCA (gens)	Date	Known date	Markers compared	Genetic Distance	TMRCA (gens)	Date	TMRCA (gens)	Date	TMRCA (gens)	Date		
H1564 (A)	43										1608	43	1	3	1840	8	1665	16	1385		
H1112 (Me)	111	1608	43	1	3	1840	8	1665	16	1385											
224096 (F)	37	1230-1500	32	2	9	1630	18	1315	31	860	1230-1500	37	6	18	1315	27	1000	39	580		
H1572 (B)	43	1230-1700	43	1	3	1840	8	1665	16	1385	1230-1700	43	2	7	1700	13	1490	22	1175		
H1579 (B)	43	1230-1700	43	1	3	1840	8	1665	16	1385	1230-1700	43	2	7	1700	13	1490	22	1175		
H1580 (E)	43	1230-1500	43	2	7	1700	13	1490	22	1175	1230-1500	43	3	10	1595	18	1315	28	965		
H1574 (C)	43	1230-1500	43	3	10	1595	18	1315	28	965	1230-1500	43	4	14	1455	23	1140	35	720		
H1578 (D)	43	1230-1500	43	4	14	1455	23	1140	35	720	1230-1500	43	5	14	1455	23	1140	35	720		
224421 (G)	37	1230-1500	32	3	14	1455	25	1070	40	545	1230-1500	37	7	22	1175	32	825	45	370		
306676 (H)	37	1672	32	2	9	1630	18	1315	31	860	1608	37	5	15	1420	23	1140	34	755		

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224096 (F)												H1572 (B)																			
Markers tested												Markers tested																			
Distance from Warburton mode												Distance from Warburton mode																			
				16%				50%				84%								16%				50%				84%			
Kit Number	Markers tested	Known date	Markers compared	Genetic Distance	TMRCA (gens)	Date	TMRCA (gens)	Date	TMRCA (gens)	Date	Known date	Markers compared	Genetic Distance	TMRCA (gens)	Date	TMRCA (gens)	Date	TMRCA (gens)	Date												
H1564 (A)	43	1230-1500	32	2	9	1630	18	1315	31	860	1230-1700	43	1	3	1840	8	1665	16	1385												
H1112 (Me)	111	1230-1500	37	6	18	1315	27	1000	39	580	1230-1700	43	2	7	1700	13	1490	22	1175												
224096 (F)	37										1230-1650	32	2	9	1630	18	1315	31	860												
H1572 (B)	43	1230-1650	32	2	9	1630	18	1315	31	860																					
H1579 (B)	43	1230-1650	32	2	9	1630	18	1315	31	860	1734	43	0	1	1910	3	1840	9	1630												
H1580 (E)	43	1230-1650	32	3	14	1455	25	1070	40	545	1230-1650	43	3	10	1595	18	1315	28	965												
H1574 (C)	43	1230-1650	32	4	20	1245	32	825	50	195	1230-1650	43	4	14	1455	23	1140	35	720												
H1578 (D)	43	1400-1750	32	3	14	1455	25	1070	40	545	1230-1650	43	5	18	1315	28	965	41	510												
224421 (G)	37	1230-1650	37	7	22	1175	32	825	45	370	1230-1650	32	3	14	1455	25	1070	40	545												
306676 (H)	37	1230-1500	37	5	15	1420	23	1140	34	755	1230-1608	32	2	9	1630	18	1315	31	860												
H1579 (B)												H1580 (E)																			
Markers tested												Markers tested																			
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				16%				50%				84%								16%				50%				84%			
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H1574 (C)	43	1230-1650	43	4	14	1455	23	1140	35	720	1400-1750	43	3	10	1595	18	1315	28	965												
H1578 (D)	43	1230-1650	43	5	18	1315	28	965	41	510	1230-1650	43	6	22	1175	33	790	48	265												
224421 (G)	37	1230-1650	32	3	14	1455	25	1070	40	545	1400-1750	32	2	9	1630	18	1315	31	860												
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Markers tested												Markers tested																			
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				16%				50%				84%								16%				50%				84%			
Kit Number	Markers tested	Known date	Markers compared	Genetic Distance	TMRCA (gens)	Date	TMRCA (gens)	Date	TMRCA (gens)	Date	Known date	Markers compared	Genetic Distance	TMRCA (gens)	Date	TMRCA (gens)	Date	TMRCA (gens)	Date												
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224421 (G)	37	1400-1750	32	3	14	1455	25	1070	40	545	1230-1650	32	6	32	825	48	265	69	-470												
306676 (H)	37	1230-1500	32	4	20	1245	32	825	50	195	1230-1500	32	5	26	1035	40	545	59	-120												
224421 (G)												306676 (H)																			
Markers tested												Markers tested																			
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Calculations									
Probability of x mutations in 20 generations, i.e. since circa 1250, using Ann Taylor's calculator:									
37 markers @ average mutation rate of 0.36%					43 markers @ average mutation rate of 0.26%				
	Mutations	Probability	Cumulative probability			Mutations	Probability	Cumulative probability	
	0	7.0%	7.0%			0	10.7%	10.7%	
	1	18.6%	25.6%			1	23.9%	34.6%	
	2	24.9%	50.5%			2	26.7%	61.3%	
	3	22.0%	72.5%			3	19.2%	80.5%	
	4	14.6%	87.1%			4	11.1%	91.6%	
	5	7.8%	94.9%			5	5.0%	96.6%	
	Mean = 2.7 mutations		Average of 4 Warburton profiles = 3.0 mutations			Mean = 2.2 mutations		Average of 7 Warburton profiles = 1.7 mutations	
Weighted average TMRCA:									
Excluding pairs of profiles where the common ancestor is known, or is shown through shared mutations to be more recent than the first Warburton, there are 32 pairs where the common ancestor could be the first Warburton.									
						16%	50%	84%	
	Weighted average of 32 pairs:					837	1177	1643	
	Weighted average of 20 pairs with a minimum of 37 shared markers:					933	1232	1635	
	Weighted average of 15 pairs with 43 shared markers:					1016	1308	1701	
	Weighted average of 5 pairs with 37 shared markers:					644	967	1394	