

Lichtenstein Cave Data Analysis

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This document is a summary in English of the Ph.D. Thesis of Felix Schilz. He obtained his Ph.D. degree in May of 2006 from the Georg-August-University of Göttingen in Germany. This summary will focus on the data of his thesis which is relevant to Genetic Genealogy. To this end, the 5 unique Y-DNA haplotypes reported in his thesis were assigned to a haplogroup by the author of this document.

His Ph.D. Thesis is available online at:

<http://webdoc.sub.gwdg.de/diss/2006/schilz/schilz.pdf>

Wikipedia has as of now only a German-language entry about the Lichtenstein cave:

<http://de.wikipedia.org/wiki/Lichtensteinh%C3%B6hle>

1.) Location of the Lichtenstein Cave, Number of Identified Individuals, and Time Period of Cave Occupation:

The Lichtenstein cave [51° 43 '28" North & 10° 10' 27" East, <http://www.alder-digital.de/earth.php?long=10.174167&lat=51.724444> (Google Earth needs to be installed.)] is situated on the northwestern side of a hill located just to the west (< 10 miles) of the Harz mountains in central Germany. The skeletons of 21 females and 19 males were identified in the cave. The items, see figure 4 on p. 12, found in the cave are typical for the regional time period of 1000 to 700 B.C.E. (Jungbronzezeit, Spätbronzezeit, Urnenfelderbronzezeit, Urnenfelderkultur, Urnfield culture) (p. 12). Figure 4 is reproduced here.



A ¹⁴C analysis to determine the age of the bones was not reported in his dissertation!

2.) Investigation of Autosomal Markers:

The following 11 autosomal markers were investigated in all 40 individuals: D3S1358, D5S818, D7S820, D8S1179, D13S317, D18S51, D21S11, CSF1PO, FGA, VWA, and Amelogenin. The autosomal results of the 21 females are reported in table 14 on p. 75, while the autosomal results of the 19 males are reported in table 15 on p. 76.

3.) Investigation of Mitochondrial DNA:

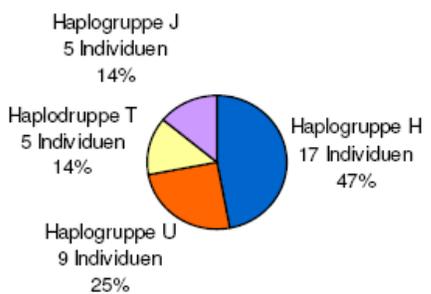
20 unique mt-DNA haplotypes could be identified in the individuals found in the cave. These 20 unique mt-DNA haplotypes are reported in table 16 on p. 84. Table 16 is reproduced here.

№	HVR II										HVR I										mt-Haplotype													
	71G	73A	89A	150C	152T	185G	195T	217A	228G	239T	242C	263A	295C	309C	315C	16051A	16069C	16074A	16126T	16129G		16134T	16145G	16172T	16189T	16192C	16222C	16249T	16261C	16270C	16294C	16296C	16299A	16304T
1	*	*	*	*	C	*	*	*	*	*	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	H#1
2	*	*	*	*	*	*	*	*	*	*	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	G	*	H#2
3	*	*	G	*	C	*	*	*	*	*	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	H#3
4	*	*	*	*	*	*	*	*	*	*	G	*	*	*	.2C	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	C	H#4
5	*	*	*	*	*	*	*	*	*	*	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	H#5
6	*	*	*	*	*	*	*	*	*	*	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	T	*	*	*	*	*	H#6
7	*	*	*	*	*	*	*	*	*	*	G	*	*	*	.2C	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	H#7
8	*	*	*	*	*	*	*	*	*	*	G	*	*	*	.1C	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	H#8
9	*	*	*	*	*	*	*	*	*	*	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	C	H#9	
10	*	*	*	*	*	*	*	*	*	C	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	H#10
11	G	*	*	C	*	C	*	*	*	*	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	U#1	
12	G	*	*	C	*	*	C	*	*	*	G	*	*	*	.2C	.1C	T	*	*	C	*	*	*	*	/	/	/	*	*	*	*	*	U(2)	
13	G	*	T	*	*	*	*	*	*	*	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	U#2
14	G	*	T	*	*	*	*	*	*	*	G	*	*	*	.1C	*	G	*	*	*	*	*	*	C	T	*	C	*	T	*	*	*	USb	
15	G	*	*	*	A	*	A	*	*	*	G	T	*	*	.1C	*	T	C	*	*	*	*	*	*	*	*	*	*	*	*	*	*	J'	
16	G	*	*	*	*	*	*	*	*	T	G	T	*	*	.1C	*	T	C	*	*	A	C	*	*	T	*	T	*	*	*	*	*	J1b1	
17	G	*	*	*	*	*	*	*	*	*	G	*	*	*	.1C	*	*	*	*	*	*	*	*	*	*	*	*	T	T	*	C	*	T2#1	
18	D	G	*	*	*	*	*	*	*	*	G	*	*	*	.1C	.1C	*	*	C	*	*	*	*	*	*	*	*	T	T	*	C	*	T2#2	
19	G	*	*	*	*	C	*	*	*	*	G	*	*	*	.2C	.1C	*	*	C	*	*	A	*	*	*	*	*	T	T	*	C	*	T2#3	
20	(G)	*	*	*	*	*	*	*	*	*	G	*	*	*	.1C	/	/	/	/	/	/	/	/	X	X	X	*	*	T	T	*	*	nd#1	

• = identical to CRS. / = impossible to determine. () = undetermined sequence polymorphism. X = area was not sequenced. D = deletion. nd = undecided into which haplogroup it belongs.

The mt-DNA haplotypes found in 37 of the 40 individuals are reported in table 17 on p. 85. The mt-DNA haplotypes of 3 individuals could not be determined at all, while the incomplete mt-DNA haplotype of one individual (# 20 in the table above.) could not be assigned unambiguously to a haplogroup. The haplogroup distribution of the 36 individuals whose mitochondrial DNA could be assigned to a haplogroup is shown in figure 21 on p. 87. Figure 21 is reproduced here. Of course, it is very likely that members of the same (extended) family, as was also proposed this thesis, were buried in this cave. Thus, the mt-DNA haplogroup distribution of the people in the Lichtenstein cave cannot be considered to be an accurate reflection of the haplogroup distribution of the peoples settling in the vicinity of the Lichtenstein cave in the Urnfield culture time period (1000 to 700 B.C.E.).

mt-Haplogruppenverteilung (Gesamt)



4.) Investigation of Y-Chromosomal DNA:

The following 12 Y-DNA markers were investigated in all 19 males: DYS 393, DYS 390, DYS 19, DYS 391, DYS 385a, DYS 385b, DYS 439, DYS389-1, DYS 392, DYS389-2, DYS 437, and DYS 438. This minimal haplotype could be determined in 15 of the 19 males (table 18 on p. 93). Within these 15 males, 5 distinct haplotypes were found. They are predicted by the author of this document to belong to haplogroups I-M170+ (80 %), R-U106(S21)+ (7 %), and R-SRY10831.2- (13 %). The closest www.ftdna.com kit to each one of these haplotypes should be deep-clade SNP tested. Of course, it is very likely that members of the same (extended) family, as was also proposed in this thesis, were buried in this cave. Thus, the Y-DNA, as was also the case for the mt-DNA, haplogroup distribution of the people in the Lichtenstein cave cannot be considered to be an accurate reflection of the haplogroup distribution of the peoples settling in the vicinity of the Lichtenstein cave in the Urnfield culture time period (1000 to 700 B.C.E.).

Haplotype (# of Individuals)	suggested Haplogroup based on Matches within FT-DNA's public Projects	closest FTDNA Kit	3 9 3	3 9 0	1 9	3 9 1	3 8 5 a	3 8 5 b	4 3 9	3 8 9 1	3 9 2	3 8 9 2	4 3 7	4 3 8
A (6)	I-M170+	66196	13	25	16	11	13	17	11	12	11	28	15	10
B (3)	I-M170+	66196	13	25	15	11	13	17	11	12	11	27	15	10
C (1)	R-U106(S21)+ (R1b1b2g, formerly R1b1c9)	N18407	13	23	14	11	11	14	12	13	13	29	15	12
D (2)	R-SRY10831.2- (R1a)	106116	13	25	15	11	11	13	11	13	11	30	14	11
E (3)	I-M170+	88756	13	24	16	11	13	17	11	12	11	28	15	10

5.) Investigation of CCR5:

Of the 40 individuals whose remains were discovered in the Lichtenstein cave, 17 were tested for the $\Delta 32$ deletion of CCR5 (p. 190). Interestingly, in 4 (2 males and 2 females) of them the $\Delta 32$ deletion was found to be present. All 4 individuals were heterozygotic for it.