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CASE REPORT

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An Illicit Love Affair During the Third Reich: Who is My Grandfather?*

ABSTRACT: More than 60 years after an illicit love affair had occurred between Erika H, wife of a Wehrmacht soldier, and a Polish slave worker during World War II, we could clarify the blood relationships of her daughter Uta. When Erika H had become pregnant both of the men could have fathered the child. Erika H was found guilty of fraternization and imprisoned at Ravensbrück concentration camp. She gave birth to Uta and died there in 1944. Uta survived the war as did Erika's husband Gustav, who accepted Uta as his child. Blood samples from family members were taken and DNA extracted. A panel of 16 short tandem repeat (STR) loci were amplified and separated by capillary electrophoresis and the likelihoods calculated using the MLINK software. The combined genotypes yielded a cumulative likelihood ratio of over 200,000 against paternity of Gustav H. This case serves to illustrate the utility of STR profiles for complex deficiency kinship analysis.

KEYWORDS: deficiency case, DNA typing, forensic science, paternity testing, slave worker

To meet the increasing demand by Germany's war industry, the Nazis seized an estimated 7–8 million people from occupied countries and forced them to work as slave workers under inhumane conditions (1). To strictly prevent any contact between the civilian population and the slave workers, a suite of stringent legal regulations was implemented in 1940 (2). Despite these measures, however, many cases were reported in which the laws were circumvented by German people, often with fatal consequences. One such case involved Erika H (Fig. 1), wife of Gustav H and mother of two sons. She worked on a farm together with slave workers from Poland, and started a relationship with one of them. Gustav H had been called up for military service in 1939, and coincidently was on leave at the time Erika H became pregnant. Thus, both he and the slave worker could have been the biological father of Erika H's child.

The extra-marital relationship of Erika H was reported to the Nazis and she was found guilty of "an indecent relationship with a member of an inferior race." In early 1943, Erika H was deported to the Ravensbrück concentration camp, some 90 km north of Berlin. The Ravensbrück camp was built during 1938–1939 by the SS, mainly for the detainment of women. Approximately 132,000 people were imprisoned there between 1939 and 1945, and exploited to work at an industrial yard inside the camp. An estimated 70,000 prisoners died of famine or mistreatment until Ravensbrück was eventually freed by the Red Army on April 30, 1945. For reasons still unknown, Erika H was allowed to give birth to a daughter, named Uta, outside the camp in September 1943, but was immediately imprisoned again. The newborn was taken care of by Erika H's parents. Erika H died in the concentration camp in December 1944, at the age of 29 years. Her body was cremated (remains of prisoners were routinely used for road works inside the camp, as has been indicated by many original documents). Nothing is known about the fate of the slave worker, but an offence such as his would typically have received the death penalty.

In 1945, Erika H's husband was released from being a prisoner of war by the allies and he accepted Uta as his own child. He remarried and later became father to another son. Gustav H died in 1994, not knowing whether he was in fact Uta's biological father. Against this background, Uta and her son, Erika's grandson, decided to have the case resolved by means of molecular genetic testing.

Materials and Methods

Blood samples were obtained from six members of the extended family of Erika and Gustav H (Fig. 2). DNA was extracted (3) and assessed by photometric measurement. For genotyping, the PowerPlex16 and Power PlexES kits (Promega, Madison, WI) were used and polymerase chain reaction (PCR) was performed taking approximately 5 ng DNA in a total volume of 25 μL and 30 cycles according to the manufacturer's instructions. Amplification was carried out using a GeneAmp PCR-System 9600 (Perkin Elmer Applied Biosystems, Weiterstadt, Germany). One microliter of amplification product was separated and analysed using an ABI PRISM 310 GeneScan Analysis.

Biometrical evaluation of the genotype data was carried out using the linkage program MLINK V5.1 (4), which was originally conceived for likelihood calculations in genetic epidemiology—but

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FIG. 1—*Only existing photograph of Erika H.*

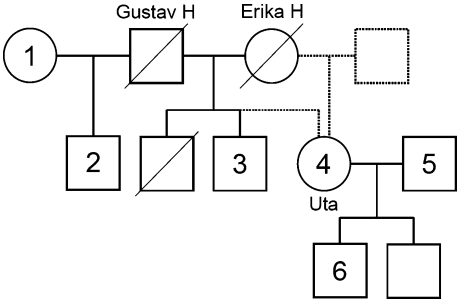

FIG. 2—*Pedigree of the extended family of Erika and Gustav H.*

which can also be used for the purpose of kinship testing (5). The required marker orders and approximate marker positions on chromosomes 5 and 21 were taken from publicized map data (Marshfield, NCBI). The results were expressed as the likelihood ratio of two different hypotheses about the relatedness of the individuals involved: X, Uta's biological father is unrelated to the remaining family members, except her son; Y, Gustav H was Uta's biological father.

Likelihood calculations were based upon allele frequencies as estimated from a North-Central European genotype database.

Results and Discussion

The usefulness of short tandem repeat (STR) loci for kinship testing has been documented in many instances, particularly for deficiency cases (6–8). In the present case, STR profiles comprising 16 loci were obtained for the second wife of Gustav H (1) and her son (2), an earlier son from Gustav's marriage with Erika H (3), from Uta (4), her husband (5), and Erika's grandson (6; see Fig. 2). Individual STR genotypes are listed in Table 1.

At STR loci D13S317 and FIBRA, the genotypes of the two half-brothers (2 and 3) and of Gustav H's second wife (1) ruled out hypothesis Y (i.e., fatherhood of Gustav H). Both markers are located on different chromosomes (13 and 4). Gustav H's D13S317 genotype must have been 11–14, whereas Uta's is 10–12. Although the mutation rates of forensic STRs are generally low (e.g., 0.3% for D13S317), the possibility of a germ line mutation in one of the three meioses of interest still had to be taken into consideration (9,10). However, the case was almost conclusively solved by a second exclusion constellation at marker FIBRA, where Gustav H's genotype must have been 20–22 or 22–23, but where Uta's was 21–26. This notwithstanding, as none of the other markers allowed a clear-cut exclusion of Y, further clarification of the case was sought by subjecting the remaining genotype data to a formal biometrical analysis. A cumulated likelihood ratio of 19.2 was obtained (Table 1). This implies that, on aggregate, and making the highly conservative assumption that the likelihood ratios corresponding to the exclusions at D13S317 and FIBRA are both equal 100 (i.e., the inverse of an upper limit for the mutation rate of

TABLE 1—*STR genotypes of six members of Erika H's extended family.*

		Family Member						
STR	Chromosome	1	2	3	4	5	6	LR(X/Y)*
TPOX	2	8–11	11–12	8–8	8–12	8–9	8–8	0.08704
D3S1358	3	13–14	13–17	17–19	17–19	16–17	16–17	0.28526
FIBRA	4	22–22	22–23	20–22	21–26	20–22	22–26	n.a.
SE33	5	18–23.2	18–21	21–28.2	23.2–28.2	28.2–30.2	28.2–28.2	5.51989
D5S818		9–11	11–12	12–12	12–13	11–13	12–13	
CSF1PO		9–10	10–10	10–13	11–12	11–12	11–12	
D7S820	7	10–11	10–11	10–10	8–10	8–12	8–12	1.40391
D8S1179	8	10–15	14–15	13–14	12–15	13–13	13–15	2.73200
TH01	11	7–9	9–9.3	9–9.3	9–9.3	9–9.3	9–9.3	0.45170
VWA	12	16–18	14–18	14–19	18–21	15–16	16–21	2.38000
D13S317	13	11–14	14–14	11–11	10–12	12–13	12–13	n.a.
PENTA_E	15	12–13	13–14	12–14	7–13	12–12	7–12	2.23600
D16S539	16	9–11	10–11	9–10	9–12	12–15	9–12	2.05230
D18S51	18	14–17	12–17	12–21	14–21	14–14	14–14	2.00882
D21S11	21	29–31.2	29–31.2	30–32.2	28–30	28–28	28–28	3.68553
PENTA_D		10–12	10–13	11–13	13–16	12–13	13–13	

*LR(X/Y): likelihood ratio of hypotheses X (no blood relationship between Uta's biological father and the remaining family members, except Uta's son) and Y (Gustav H was Uta's biological father). The cumulated likelihood ratio, i.e., the product of all entries in this column except for FIBRA and D13S317, equals 19.2. For numbering of family members, see Fig. 2.

1%), the exclusion of Gustav H as Uta's father was found to be at least 200,000 times more likely than not.

In summary, over 60 years after Uta was born, we were able to prove that Gustav H was unlikely to be her biological father and hence unlikely to be the grandfather of Uta's son. This result highlights the fact that even complex deficiency cases can be solved by means of STR profiling.

Based on the information provided by family members, the slave worker is most likely to be the biological father of Uta. We hoped to learn more about his fate and requested information at the International Tracing Service in Bad Arolsen, Germany. This process is still under way.

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