Three intriguing identification cases.

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Introduction:
The use of DNA analysis has proved to be a powerful tool in cases where identification by ordinary means is impossible. The three cases presented here, involved highly decomposed bodies.
I. A decapitated body was found in the sea March-94 in northern Norway. The police related the finding to a missing person - a man born in 1916 who was last seen December-93. The only relative was a nephew.
II. A young Norwegian sailor disappeared at Crete in November-93. A headless body was found at the seaside of Crete in January-94 and remains of the clothing indicated that this might be the missing man. Relatives: parents.
III. A body with a high degree of adipocere was found in a lake in september-94. The only missing person in the area was a man born in 1896 who disappeared in 1972. His only relatives were two sons living in the USA.

Materials:
Different kinds of samples were taken from all three bodies, including soft tissue, organs and cartilage.

Methods:
Preparation and quantitation of DNA:
DNA was extracted from all the samples, using the common procedure with proteinase K, phenol extraction and ethanol precipitation.Then the DNA was purified by dialysis.
The DNA was quantified by the slot-blot system detailed by Walsh et al.(Nucleic Acids Research 20: 5061-5065), using the QuantiBlot™ Human DNA Quantitation Kit(Perkin Elmer).

HLA DQ A1:
HLA DQ A1- typing was performed using the Amplitype™- kit from Perkin Elmer.

STR-primers:
HUMTHO1 (Polymeropoulos et al. 1991a), HUMF13A1 (Polymeropoulos et al. 1991b), HUMFES(Polymeropoulos et al. 1991c), HUMVWA (Kimpton et al. 1992), D8S347 (Lu et al. 1993), D8S306 (Nelson et al. 1993), D3S1349 (Li et al. 1993).

STR amplification conditions and fragment analysis:
Amplification was performed in a Perkin Elmer 9600 thermo cycler. The fragments were analysed in an ABI model 373 Seqencing System using Genescan 672 software.

Statistics:
Odds calculations were performed using the PATER computer program (Mostad et al. 1995).

Results:

Case I:

	The body	Nephew
HLA DQ A1	1.2/2	1.2/2
HUMTHO1	9,3 (173)	6/9,3 (158/173)
HUMVWA	16/18 (147/155)	16 (147)
HUMF13A1	5/7 (187/195)	7 (195)
D3S1349	129/134	129/134
D8S306	255/270	256/264
APOA1	285/287	280/286

Case II:

	The body	Mother	Father
HLA DQ A1	3/4	1.2/3	4
X/Y	107/113	107	107/113
HUMTHO1	7/9,3 (162/173)	7/9,3 (162/173)	7/9 (162/170)
HUMFES	10/11 (221/225)	10/12 (221/229)	10/11 (221/225)
HUMVWA	14/17 (139/151)	15/17 (143/151)	14/18 (139/155)
HUMF13A	6 (191)	6 (191)	6 (191)
D3S1349	134	134/138	134
D8S347	352/356	352/372	356/380
D8S306	256/264	256/280	264

Case III:

	The body	son no. 1	son no. 2
HLA DQ A1	1.1/4	1.1/4	1.1/4
HUMFES	10/12 (221/229)	10 (221)	10/12 (221/229)
HUMACTBP2	249/263	249/298	263/298

The odds in favour of the missing persons were 22 (case I), 46454 (case II) and 5339 (case III).

Discussion:
In these three cases, the bodies were heavily decomposed and the DNA yield in the samples was low/degraded. Positive results were therefore not expected.
In case I and II the presence of inhibitors made amplification difficult. This was most likely related to the seawater. To avoid the inhibitors, the samples were diluted and reamplified. The results of reamplification have to be interpreted with care regarding contamination. When such results match with the patterns of the relatives, this may be regarded as a positive identification. However, a non-match cannot be used as a proof of nonidentity.

Comparing the different kinds of samples, cartilage proved to be the best source of DNA for PCR.
Even though the bodies were heavly decomposed, HLA DQ A1 and the STR's gave sufficient information for the identification purpose.

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