USE OF PCR IN FORENSIC CASEWORK IN THE AREA BERLIN - BRANDENBURG: ALLELE FREQUENCY DISTRIBUTION OF SIX MICROSATELLITES

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Introduction:

During the last few years a great variety of polymorphic DNA loci was introduced into forensic science.
In the forensic police laboratories of Berlin and Brandenburg (Germany) we routinely amplify the polymorphic loci D1S80, VWA31A, F13A1, TH01 (TC11), FESFPS and ACTBP22 (SE33). At these six DNA loci we analysed the allele distributions in the region of Berlin - Brandenburg (population size ca. 500 individuals) according to the recommendations of the ISFH.

Material and Methods:

DNA was isolated according to standard methods (Gill et al 1987).
Amplification of D1S80 was carried out with the commercial kit from Perkin Elmer Kasai et al. (1990); the analysis of the four STR systems VWA31A, F13A1, TH01 and FES was performed as described by Edwards et al. (1991) and Kimpton et al. (1993), amplification of SE33 as described by Polymeropoulos et al. (1992) with modifications according to an optimized protocol developed by the LKA Hessen, Germany.
The AMFLP system D1S80 can easily be separated by vertical or horizontal native PAGE (6%), whereas the STR systems (especially SE33) require an improved and standardized separation on denaturing PAGE (6%). In our hands we found that analysis of the above mentioned STRs were easiest and most reliable by working on the DNA sequencer (ABI 373A) in connection with the Genescan 350-ROX or 500-ROX fragment size standard. The evaluation was done with the Genescan and Genotyper software from Applied Biosystems on a Macintosh computer.

Results:

The distribution of the observed allele frequencies at six DNA loci in a population sample of about 500 unrelated individuals is shown in the following table. The results were compared with the data of other european studies (see references). In spite of the heterogeneity of the population in the Berlin - Brandenburg region which is composed of several national groups the allele frequency distribution does not differ significantly from these data.

The most useful system is SE33, but the non-standardized nomenclature presents a problem still to be solved.

D1S80 (n=635)

Allel	%	Allel	%	Allel	%	Allel	%	Allel	%
14	0	**20**	2,7	**26**	1,5	**32**	0,3	**38**	0
15	0,1	**21**	2,3	**27**	0,9	**33**	0,3	**39**	0,1
16	0,4	**22**	4,4	**28**	6,9	**34**	0,2	**40**	0,2
17	0,3	**23**	0,9	**29**	3,8	**35**	0,3	**41**	0,1
18	22,3	**24**	35,6	**30**	1,4	**36**	0,6	**>41**	0,2
19	0,7	**25**	5,3	**31**	8	**37**	0,3		

SE33 (n=568)

Allel	%	Allel	%	Allel	%	Allel	%	Allel	%
227	0,1	**246**	4,2	**264**	1,5	**284**	3,9	**314**	0,2
231	0.1	**250**	6,6	**266**	2,9	**288**	4,4	**316**	0,5
235	1,3	**253**	0,2	**268**	1,9	**292**	6,7	**320**	0,1
237	0,1	**254**	8,2	**270**	0,9	**296**	8,2	**323**	0,1
238	3,9	**256**	0,1	**272**	4,6	**300**	6,5	**326**	0,1
240	0,1	**258**	7	**276**	3	**304**	6,3		
242	4,1	**260**	0,4	**280**	3	**308**	2,4		
244	0,1	**262**	4,6	**282**	0,3	**312**	1,5		

F13 (n=552)

Allel	%	Allel	%	Allel	%	Allel	%
3.2	9,4	**7**	32,2	**11**	0,1	**15**	1,4
4	3,4	**8**	0,4	**12**	0,5	**16**	1,6
5	19,2	**9**	0	**13**	0,5	**17**	0
6	29,8	**10**	0	**14**	1,4	**18**	0,1

VWA (n=597)

Allel	%	Allel	%	Allel	%	Allel	%
11	0	**14**	10	**17**	27,4	**20**	1,3
12	0,1	**15**	10,7	**18**	21,6	**21**	0,1
13	0,6	**16**	20,8	**19**	7,5		

FES (n=460)

Allel	%	Allel	%
7	0,2	**12**	23,7
8	1,9	**13**	5,4
9	0,2	**14**	0,1
10	25,9	**15**	0,1
11	42,4		

TC11 (n=589)

Allel	%	Allel	%
5	0,1	**9.3**	30,1
6	22,4	**10**	2,5
7	16,2	**11**	0,0
8	11,2		
9	17,5		

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