SHORT COMMUNICATION

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Detection of RNA viruses in sudden infant death (SID)

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Abstract Continuing previous work, reverse transcriptase polymerase chain reaction approaches for the detection of RNA viruses (influenza A+B, parainfluenza virus 3, respiratory syncytial virus) were developed. A total of 118 infant deaths, including 13 cases of non-natural death (nND), 78 cases of natural death (ND) without morphological signs of interstitial pneumonia (IP), 27 cases showing IP (ND+IP), were investigated using frozen lung tissue (N= 100) and paraffin-embedded material (N=18). In five of the autopsy cases (ND+IP) the influenza B virus genome could be detected and the other types of viruses were completely negative. Together with previous results (detection of adenoviruses and cytomegaloviruses) in the same groups, the frequency of virus detection in the cases with IP was 48% compared with 14% in the ND without IP and 7% in the nND. Significant differences in the frequency of virus detection were also obtained when the cases were divided in SIDS and non-SIDS. The results obtained indicate an association between IP and some viruses and support the hypothesis that respiratory virus infections could act as trigger in sudden infant death.

Keywords Sudden infant death · Interstitial pneumonia · RNA viruses · Reverse-transcriptase polymerase chain reaction

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Introduction

It has been assumed that infectious diseases can act as triggers in the Sudden Infant Death Syndrome (SIDS) [1, 2, 3]. However, it can become difficult to unequivocally diagnose the underlying disease especially if incipient stages and/or general infections are involved and the same applies to the clear demonstration of the causal bacterial infection. Interstitial pneumonia (IP) as caused by viruses is defined histologically [4, 5] but as early stages can be non-specific [6] detection of the virus would therefore verify the diagnosis. Because virus isolation is rarely positive in autopsy samples we have developed nested PCR approaches to detect different RNA viruses (influenza A and B viruses, parainfluenza virus, respiratory syncytial virus: RSV). These approaches have been applied to autopsy samples from SIDS cases and controls.

Materials and methods

Cases

A total of 105 subsequent cases of sudden infant death (natural deaths ND) and 13 non-natural deaths (nND) were investigated by full autopsy using a standard autopsy protocol [7, 8, 9] which included comprehensive histology of 28 organs and tissues and a broad toxicological screening [8, 9, 10].

Histology of the lungs (all 5 lobes, H&E, alcian blue-PAS, semi-thin sections) revealed a subgroup (N=27) showing different grades of IP [6, 8]. The remaining 78 cases of ND were without pulmonary disease.

Frozen lung specimens existed in 100 cases while in 18 cases only paraffin-embedded tissues (4% buffered formaldehyde, fixation time <24h) were available. Three specimens taken from the right lung lobes were stored at -80° C for up to 48 months before the investigation was performed.

Virus detection

Viral RNA was extracted using the RNeasy total RNA kit (Qiagen, Hilden, Germany), eluted from the spin column in $30 \,\mu$ l DEPC-treated water and $11.5 \,\mu$ l of the eluate was used for the first strand cDNA-synthesis (cDNA Cycle Kit, Invitrogen, De Schelp, NL).

Table 1 PCR	parameters u	used for the	detection of	of the	different types	of viruses
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	Primer sequences	MgCl ₂	Cycle parameters	Sensi-	
		tration (mM)	°C/s	Cycles	tivity ⁶
Influenza A [11]	p 1: CCGTCAGGCCCCCTCAAAGC p 2: GACCAGCACTGGAGCTAGGA	1.5	1. PCR		10
	p 3: CAGAGACTTGAAGATGTCTT p 4: TGCTGGGAGTCAGCAATCTG	1.5	94/60 52/60	30	
Influenza B [11]	p 1: TGTCGCTGTTTGAGACACA p 2: AGTTTTACTTGCATTGAATA	1.5	72/180		1
	p 3: GAAGGCAAAGCAGAACTAGC p 4: TGGCCTTCTGCTATTTCAAA	1.5	1.5 2. PCR		
Para-Influenza [12]	p 1: CTCGAGGTTGTCAGGATATAG p 2: CTTTGGGAGTGGAACACAGTT	2.5	94/30 52/60	31	10
	p 4: ATCTGTATTTAGGAGTGCT	2.5	72/90		
RSV ^a	p 1: GGTGTTGATCTGCAATCGCCA p 2: AACTTTTTCTGATCATTTGT	3.75	94/60, 56/60, 72/90	each 31 cycles	100
	p 3: AAGTGCTCTACTATCCACA p 4: CACTAAATTCCCTGGTAATC	2.25	94/30, 55/30, 72/60	each 35 cycles	

^aThe primer sequences were obtained according to the sequence of the fusion protein (F) (GenBank U31559).

^bThe sensitivity is given as number of cDNA template molecules.

Nested PCR was carried out in a final volume of $25\,\mu$ l and from the cDNA synthesis 1 μ l was used as template in the first and second rounds of nested PCR. The amplification protocols were optimised in a stepwise fashion for the detection of the different viruses (Table 1). To the primers (1 μ M) 0.25 U of Taq polymerase was added, as well as 200 μ M of each dNTP.

Samples including positive and negative controls (positive: cDNA samples from virus infected cell cultures; negative: samples without template) were analysed in 8% acrylamide gels and visualised by silver staining [11, 12]. For the sensitivity study, the product of the first PCR was quantified by UVB spectrometry, then serially diluted 10-fold down to 1 molecule in 25 μ l. These dilutions were reamplified as aforementioned. The fragments obtained in the positive cases were sequenced by Taq cycle sequencing on an ABI DNA sequencer 373A (ABI, Foster City, CA) [13].

The primer annealing sites for influenza A and B are located in the highly conserved M1 matrix protein (general primer)[14], those for parainfluenza 3 are in the conserved region of the haemagglutinin-neuraminidase-(HN)-gene [15], and primers for the detection of RS-virus were designed to anneal in the fusion protein gene (GenBank U31559).

Results

The methodology developed was specific and sensitive, sequence analysis in all positive cases resulted in cDNA sequences corresponding to the literature [14]. A minimum of 1–100 templates cDNA could be detected after the second PCR (Table 2). The detection of virus genomes using paraffin-embedded material from SIDS cases (N=18) was negative in all instances.

Virus detection was positive for influenza B in 5 cases of ND+IP (18.5%, Fig. 1) but negative in the other groups and for all other viruses (Table 2). In four out of these five cases the IP (grade 1: N=2, grade 2: N=2 [6, 8]) was characterised by typical morphology: dilatation and congestion of alveolar capillaries, protein-rich oedema, necrosis of the alveolar epithelium, denudation of the tracheobronchial mucous membrane, detachment of pneumonocytes, alveolar haemorrhages, hyalin membranes, and

 Table 2 Results of the influenza B virus detection (column 2). Additionally previous results of the DNA virus detection in the same cases are given [7, 8].

Groups total number		Influenza B positive		AV positive [8]		CMV positive [7]		Total number in each group	
Groups tota N=118 NND ND + IP ND, no IP SIDS		N	%	N	%	N	%	N	%
NND	N=13	0		0		1	7.7	1	7.7
ND + IP	N=27	5	8.5	7	26.0	3 ^a	11.1	13 ^a	48.1
ND, no IP	N=78	0		8	10.3	3	3.8	11	14.1
SIDS	N=93	5	5.4	14	15.0	6 ^a	6.4	23ª	24.7
Non-SIDS	N=25	0		1	4.0	1	4.0	2	8.0

^aIn two out of the three cases a combined viral infection has to be assumed (CMV + AV).



Fig. 1 Detection of influenza B virus. The 302 bp fragment in *lane* 9 indicates the presence of influenza cDNA. Positive (*pos*) and negative (*neg*) controls are included. The 123 bp ladder (Gibco BRL) is used as fragment size control (L)

lymphomonocyte infiltration of the alveolar septa [4, 5]. In the fifth case peribronchiolitis was found separately.

Discussion

Coumbe et al. [16] investigated tissue samples from 40 SIDS cases using in situ hybridization for cytomegalovirus (CMV) and human herpesvirus-6 and obtained only negative results. The results of An et al. [17] and our own group [8] indicate that adenoviruses (AV) could be the most frequent cause of respiratory viral infections in infants. Other investigations led to the conclusion that viral myocarditis and enteritis are more common in SID than assumed [18, 19, 20, 21].

In the present study influenza B was associated with IP in all five cases. The atypical peribronchiolar type of IP in one case could indicate an early stage of inflammation [22].

The negative results in the group with preceding formalin fixation of samples can have two reasons: (1) negative for the viruses investigated, (2) negative due to RNA degradation caused by the fixation. Because of lacking adequate controls to resolve this question, this group has been left out of further statistical considerations. In conclusion influenza B infection was associated with SIDS in 6.6% (5 out of 75, 0% in non-SIDS, p<0.001).

If the results of DNA virus detection as previously reported [7, 8] are added, viruses causing IP were detectable in 48% (Table2). Moreover, the investigation was successful in 25% of the SIDS cases compared to 8% of the non-SIDS cases. The totally negative results for the detection of influenza A virus, parainfluenza virus 3 and RSV can be due to epidemiological reasons. An especially short postmortem period cannot be made responsible for the positive results because this period was on average 32 h in the whole group as compared to 30 h in the positive cases.

The results of the present study provide further evidence for the viral aetiology of IP in some SIDS cases. IP caused by AV and influenza B does not seem to be a rare disease in infants dying suddenly and unexpectedly and therefore these infections have to be considered at least as a trigger for the death in SIDS.

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