

# Possible Prevalence and Transmission of Acute Respiratory Tract Infections Caused by *Streptococcus pneumoniae* and *Haemophilus influenzae* among the Internally Displaced Persons in Tsunami Disaster Evacuation Camps of Sri Lanka

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## Abstract

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**Objective** The objective of this prospective study was to investigate the status of acute respiratory tract infections caused by *Haemophilus influenzae* and *Streptococcus pneumoniae* in tsunami disaster evacuation camps.

**Methods** Nasopharyngeal swabs (NP) of 324 internally displaced persons (IDP) in 3 different tsunami disaster evacuation camps of Sri Lanka were collected between March 18th and 20th, 2005, and analyzed for MIC,  $\beta$ -lactamase production, serotypes, PCR and pulsed-field gel electrophoresis (PFGE).

**Results** Many IDP had respiratory symptoms and the prevalence of cough and/or sputum was 84%, 70.5% and 64.7% in the three camps. Twenty-one *H. influenzae* from 20 IDP and 25 *S. pneumoniae* from 22 IDP were isolated from the NP. All *H. influenzae* isolates were nontypeable, and 5 were  $\beta$ -lactamase producing. Seventeen pneumococci were susceptible, 5 showed intermediate resistance and 3 were fully resistant to penicillin G. Molecular analysis showed the 21 *H. influenzae* strains had 13 PFGE patterns and 25 pneumococci had 16 PFGE patterns. All 4 different PFGE patterns of *H. influenzae* strains were detected in a few IDP in camps 1 and 3, and 5 different PFGE patterns of serotype 3, 22A, 9A, 10A and 11A pneumococci were detected in a few IDP in camps 1 and 3.

**Conclusion** Our data indicate acute respiratory tract infections caused by various types of *H. influenzae* and *S. pneumoniae* appear to have been prevalent, some of which were potentially transmitted from person to person in tsunami disaster evacuation camps.

**Key words:** *Haemophilus influenzae*, *Streptococcus pneumoniae*, tsunami, internally displaced persons, acute respiratory tract infection, evacuation camp

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## Introduction

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The tsunami that occurred on December 26th, 2004 struck

southeast Asia and affected 12 countries. At least 310,000 people died, and many millions were left destitute (1). After the tsunami, many people continued to live in evacuation camps in the affected countries for various periods of times.

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It has previously been reported that acute respiratory infections were one of the leading causes of death among Bhutanese refugees in refugee camps in Nepal (2) and cases of pneumonia increased after the Hanshin-Awaji earthquake in Japan (3). *Haemophilus influenzae* and *Streptococcus pneumoniae* are bacteria that colonize the human nasopharynx and can cause a variety of infections, including otitis media, meningitis, bronchitis and pneumonia (4-6). It is well known that *H. influenzae* and *S. pneumoniae* can be transmitted from person to person at day care centers (7) or in the home (8, 9). Furthermore, these two organisms are becoming increasingly resistant to antibiotics (4, 10). The objective of this prospective study was to investigate the status of acute respiratory tract infections caused by these two organisms in tsunami disaster evacuation camps in Sri Lanka.

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## Material and Methods

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All studies described herein were approved by the Human Ethics Review Boards of Sri Lanka, and a signed consent form was obtained from each internally displaced person (IDP).

### **IDP, evacuation camps and bacterial strains.**

Nasopharyngeal swabs (NP) were collected from 324 (100, 105, 119) IDP living in 3 different tsunami disaster evacuation camps in Batticaloa, the eastern district of Sri Lanka that was affected by the tsunami between March 18th and 20th, 2005. These 3 camps were selected at random among the camps which more than 500 IDP lived. Most IDP lived in the camps for a while after the tsunami. In the camps, we announced the content of our study to IDP who were there, and examined those who agreed with participation in our study. Numerous IDP had respiratory symptoms after entering the camps and the prevalence of IDP who had cough and/or sputum was 84%, 70.5% and 64.7% (totally 72.5%) in each camp. After collection of the NP, they were transferred from the camp to the Department of Microbiology of the University of Peradeniya, Sri Lanka within 24 hours to identify the organisms. As a result, 21 *H. influenzae* from 20 (10, 4 and 6 in each camp) IDP and 25 *S. pneumoniae* from 22 (6, 4 and 12 in each camp) IDP were isolated from the NP.

### **Serotyping and $\beta$ -lactamase production.**

*H. influenzae* isolates were serotyped by slide agglutination with antisera purchased from Difco Laboratories (Detroit, MI, USA) and  $\beta$ -lactamase production was detected by a nitrocefin impregnated disk (Becton Dickinson, Sparks, MD, USA). *S. pneumoniae* was serotyped on the basis of capsular swelling (quellung reaction) observed microscopically after suspension in pneumococcal diagnostic antisera (Statens Serum Institut, Copenhagen, Denmark).

### **Antimicrobial susceptibility test.**

The Minimum inhibitory concentration (MIC) was deter-

mined by the agar dilution method according to the guidelines of the Clinical and Laboratory Standards Institute (11). The susceptibility of 21 *H. influenzae* and 25 *S. pneumoniae* isolates to the following 18 antibiotics was tested: penicillin G (PCG, Meiji Seika Kaisha, Tokyo, Japan), ampicillin (AMP, Meiji Seika Kaisha), amoxicillin-clavulanic acid (GlaxoSmithKline, Tokyo), cefazolin (Astellas Pharma Inc., Tokyo), cefaclor (Shionogi Co., Osaka Japan), cefotiam (Takeda Chemical Industries, Osaka), ceftriaxone (Chugai Pharmaceutical Co., Tokyo), cefotaxime (Aventis Pharma, Tokyo), imipenem (Banyu Pharmaceutical Co., Tokyo), minocycline (Lederle (Japan), Tokyo), chloramphenicol (Sankyo Co., Tokyo), erythromycin (Dainippon Sumitomo Pharma Co., Osaka), clarithromycin (Taisho Pharmaceutical Co., Tokyo), clindamycin (Pfizer Japan Inc., Tokyo), gentamicin (Schering-Plough K.K., Osaka), levofloxacin (Daiichi Pharmaceutical Co.), vancomycin (Shionogi Co.), and sulfamethoxazole-trimethoprim (Shionogi & Co., Osaka).

### **Identification of resistant genes by PCR.**

PCR was carried out for 21 of the *H. influenzae* isolates to identify resistant genes using mixed primers (Wakunaga Pharmaceutical Co., Hiroshima, Japan), as described previously (12). PCR was also performed for the 25 pneumococcal isolates to detect alterations in the penicillin-binding protein genes *pbp1a*, *pbp2x*, and *pbp2b* and macrolide resistance genes *mef (A)* and *erm (B)* using mixed primers (Wakunaga Pharmaceutical Co.), as described previously (13).

### **Pulsed-field gel electrophoresis.**

Pulsed-field gel electrophoresis (PFGE) was performed on 21 *H. influenzae* and 25 *S. pneumoniae* isolates to determine genetic relatedness, as described previously (7). The DNA was digested with *Sma*I (Takara Shuzo Co., Shiga, Japan). CHEF Mapper Pulsed Field Electrophoresis Systems (Bio-Rad Life Science Group, Hercules, CA, USA) were used for the electrophoresis, with a potential of 6 V/cm, switch times of 0.47 and 63 seconds, and a run-time of 20 hours and 18 minutes. After staining with ethidium bromide, the interpretation of PFGE patterns was based on the criteria described by Tenover et al (14).

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## Results

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### **Epidemiological characteristics of IDP in tsunami disaster evacuation camps.**

Table 1 shows the sex, age, respiratory symptoms, antibiotic use within the past 48 hours, and the results of the swab cultures. Man to woman ratios of the sample was comparable for each camp. Regarding age distribution, the rate for children less than 5 years of age was similar. However, in camp 3 many children who were 6-15 years of age joined this study, whereas in camp 2 more adults tended to be involved. The rate of IDP who had cough and/or sputum

**Table 1.** Epidemiological Characteristics of Internally Displaced Persons in Tsunami Disaster Evacuation Camps of Sri Lanka

		Camp 1 (n=100)	Camp 2 (n=105)	Camp 3 (n=119)
Sex	Male / Female	45 / 55	34 / 71	57 / 62
Age (years)	0- 5	14 (14.0%)	17 (16.2%)	17 (14.3%)
	6-15	15 (15.0%)	16 (15.2%)	48 (40.3%)
	16-25	16 (16.0%)	11 (10.5%)	19 (16.0%)
	26-35	26 (26.0%)	13 (12.4%)	18 (15.1%)
	36-45	10 (10.0%)	11 (10.5%)	6 ( 5.0%)
	46-55	7 ( 7.0%)	19 (18.1%)	6 ( 5.0%)
	56-65	9 ( 9.0%)	15 (14.3%)	2 ( 1.7%)
	66-	3 ( 3.0%)	3 ( 2.9%)	3 ( 2.5%)
Respiratory symptom	Cough	79 (79.0%)	68 (64.8%)	74 (62.2%)
	Sputum	61 (61.0%)	40 (38.1%)	57 (47.9%)
	None	16 (16.0%)	31 (29.5%)	42 (35.3%)
Antibiotic use within the past 48 hours	Used	16 (16.0%)	17 (16.2%)	2 ( 1.7%)
	Not used	80 (80.0%)	62 (59.0%)	93 (78.2%)
	Unknown	4 ( 4.0%)	26 (24.8%)	24 (20.2%)
Swabs culture	<i>S. pneumoniae</i>	6 ( 6.0%)	4 ( 3.8%)	12 (10.1%)
	<i>H. influenzae</i>	10 (10.0%)	4 ( 3.8%)	6 ( 5.0%)

**Table 2.** Distribution of MICs against Antibiotics for *H. Influenzae* and *S. Pneumoniae* Strains Isolated from The Nasopharyngeal Swabs from Internally Displaced Persons in Tsunami Disaster evecuation Camps of Sri Lanka

Antibiotic	<i>H. Influenzae</i> (n=21)			<i>S. pneumoniae</i> (n=25)		
	Range	50%	90%	Range	50%	90%
Penicillin G	0.125-128	0.25	16	≤0.004-4	0.016	2
Ampicillin	0.25-64	0.25	8	0.008-8	0.032	4
Amoxicillin-clavulanic acid	0.125-1	0.25	0.5	ND	ND	ND
Cefazolin	16-64	16	64	0.063-16	0.125	4
Cefaclor	4-16	8	16	0.25-128<	1	128<
Cefotiam	0.5-2	1	2	0.063-16	0.25	4
Ceftriaxone	≤0.004-0.016	0.008	0.008	≤0.004-4	0.032	1
Cefotaxime	0.008-0.032	0.016	0.032	0.008-8	0.032	2
Imipenem	0.25-8	4	8	≤0.004-0.5	0.008	0.25
Minocycline	1-2	2	2	0.125-64	0.5	16
Chloramphenicol	1-16	2	16	4-64	4	8
Erythromycin	2-4	4	4	0.063-128<	0.125	128
Clarithromycin	4-8	8	8	ND	ND	ND
Clindamycin	ND	ND	ND	0.032-128<	0.125	128
Gentamicin	0.5-4	1	2	4-16	8	16
Levofloxacin	0.016	0.016	0.016	1-4	2	4
Vancomycin	ND	ND	ND	0.125-1	0.5	0.5
Sulfamethoxazole-trimethoprim	8- 128<	128<	128<	2-128<	32	128<

ND: not determined

were 84%, 70.5% and 64.7% (totally 72.5%) in each camp. In particular, more than 60% in each camp had a cough. Al-

though the extent of pre-antibiotic use was unknown, more than half the IDP had not used antibiotics within the past 48

**Table 3.** Epidemiological Characteristics of *H. Influenzae* Strains Isolated from Internally Displaced Persons in Tsunami Disaster Evacuation Camps of Sri Lanka

Camp No.	Room No.	IDP No.	Isolate No.	Age (ys)	Symptom	Serotype	$\beta$ -lactamase	MIC against AMP ( $\mu$ g/ml)	Resistance gene identified by PCR	PFGE pattern
1	1	1	1	2	Cough, Sputum	Nontypeable	-	0.25	None	A
1	1	1	2	2	Cough, Sputum	Nontypeable	-	0.25	None	B
1	1	2	3	6	Cough, Sputum	Nontypeable	-	0.25	None	B
1	2	3	4	0	Cough, Sputum	Nontypeable	-	0.25	None	B
1	3	4	5	34	Cough, Sputum	Nontypeable	-	0.25	None	C
1	3	5	6	12	Cough, Sputum	Nontypeable	-	0.25	None	C
1	4	6	7	4	Cough, Sputum	Nontypeable	-	0.25	TEM	D
1	5	7	8	1	Cough	Nontypeable	+	4	TEM	E
1	5	8	9	46	Cough, Sputum	Nontypeable	+	8	TEM	F
1	6	9	10	18	Cough, Sputum	Nontypeable	+	64	TEM	G
1	7	10	11	34	None	Nontypeable	-	2	TEM	H
2	8	11	12	61	Cough, Sputum	Nontypeable	-	0.25	TEM	B
2	9	12	13	9	Cough	Nontypeable	-	0.25	None	D
2	10	13	14	5	Cough, Sputum	Nontypeable	-	0.25	None	I
2	11	14	15	13	Cough, Sputum	Nontypeable	-	0.25	None	J
3	12	15	16	25	Cough, Sputum	Nontypeable	-	0.5	TEM	B
3	13	16	17	45	Cough, Sputum	Nontypeable	-	0.5	TEM	K
3	14	17	18	20	Cough, Sputum	Nontypeable	+	4	TEM	K
3	15	18	19	0	Cough, Sputum	Nontypeable	-	0.25	None	L
3	16	19	20	1	Cough, Sputum	Nontypeable	-	0.25	None	L
3	17	20	21	8	Cough, Sputum	Nontypeable	+	8	TEM	K

TEM: TEM-1-type  $\beta$ -lactamase gene

hours. *H. influenzae* and *S. pneumoniae* were detected in each of the camps. However, the detection rate in camp 2 tended to be lower than in the other camps. No IDP had both *H. influenzae* and *S. pneumoniae* simultaneously.

#### Antimicrobial susceptibility test and characteristics of organisms.

Table 2 shows the MIC range, the MIC<sub>50</sub> and the MIC<sub>90</sub> values for 18 antibiotics against 21 *H. influenzae* and 25 *S. pneumoniae* isolates from the NP. Twelve (60%) of the 20 IDP with *H. influenzae* isolates were children under 15 years of age. Twenty-one of the *H. influenzae* isolates were nontypeable, 16 (76.2%) were  $\beta$ -lactamase-negative, and 5 (23.8%) were  $\beta$ -lactamase-producing. Furthermore, 10 *H. influenzae* isolates had the TEM-1-type  $\beta$ -lactamase gene, including 5  $\beta$ -lactamase-producing isolates. The MIC against AMP of one  $\beta$ -lactamase-negative *H. influenzae* isolate (Isolate No. 11) with TEM-1-type  $\beta$ -lactamase gene was 2  $\mu$ g/ml and that did not have such resistant gene as  $\beta$ -lactamase-negative AMP-resistant (BLNAR) strains (Table 3). On the other hand, 18 (72%) of 22 IDP with *S. pneumoniae* were children less than 15 years of age. The 25 pneumococci were associated with 13 serotypes, including 3, 6A, 6B, 9A, 10A, 10F, 11A, 15B, 17A, 19A, 22A, 22F and 23F. Of the 25 *S. pneumoniae* isolates, 17 (68.0%) were susceptible, 5 (20.0%) showed intermediate resistance (MIC, 0.12 to 1.0  $\mu$ g/ml) and 3 (12.0%) were fully resistant (MIC,  $\geq$  2.0  $\mu$ g/ml) to PCG. The macrolide resistance gene *erm(B)* was found in 2 of 3 fully resistant strains and the 3 of 5 intermediate resistant strains had alterations in *pbp1a*, *pbp2x*, and *pbp2b* with and without macrolide resistance gene *erm(B)*

(Table 4).

#### Interpretation of PFGE.

Molecular typing by pulsed-field gel electrophoresis (PFGE) showed that the 21 *H. influenzae* strains consisted of 13 patterns (A-L) (Fig. 1) and the 25 *S. pneumoniae* strains consisted of 16 patterns (a-p) (Fig. 2). Regarding *H. influenzae*, PFGE pattern B isolates from 3 IDP and PFGE pattern C isolates from 2 IDP were detected in camp 1, and PFGE pattern K isolates with the TEM-1-type  $\beta$ -lactamase gene from 3 IDP and PFGE pattern L isolates from 2 IDP were detected in camp 3. Regarding *S. pneumoniae*, PFGE pattern a isolates of serotype 3 were found for 3 IDP and PFGE pattern b isolates of serotype 22A were found for 2 IDP in camp 1, and PFGE pattern h isolates of serotype 10 A with the macrolide resistance gene *erm(B)* for 2 IDP, PFGE pattern f isolates of serotype 11A for 2 IDP and PFGE pattern j isolates of serotype 9A with alterations in the penicillin-binding protein genes *pbp1a*, *pbp2x*, and *pbp2b* for 2 IDP were detected in camp 3. Some of the IDP, in whom the same PFGE pattern of the organism was detected, lived in the same room at the camp, but not necessarily all (Table 4). Two different *H. influenzae* isolates with PFGE pattern A and B were detected from one IDP (IDP No. 1, Table 3). Similarly, 2 different pneumococci (serotype 3 and 22A) with PFGE pattern a2 and b1, and 3 different pneumococci (serotype 17A, 22A and 22F) with PFGE pattern o, b2 and p were detected from each one IDP (IDP No. 3 and 22, Table 4).

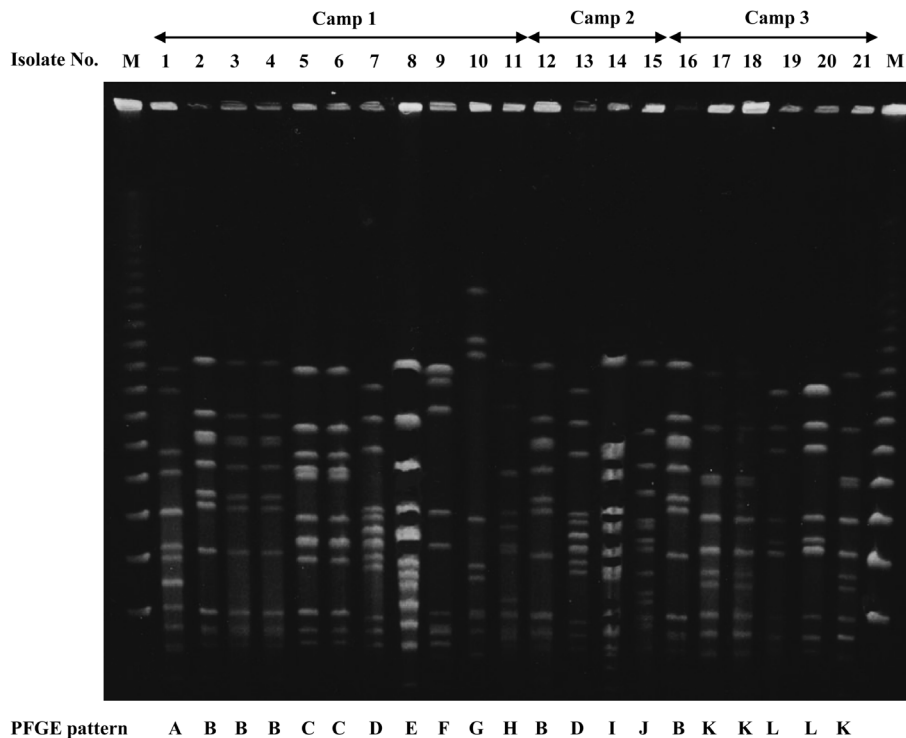
**Table 4.** Epidemiological Characteristics of *S. Pneumoniae* Strains Isolated from Internally Displaced Persons in Tsunami Disaster Evacuation Camps of Sri Lanka

Camp No.	Room No.	IDP No.	Isolate No.	Age (ys)	Symptom	Serotype	MIC against PCG (µg/ml)	PCR result					PFGE pattern
								<i>pbp1a</i>	<i>pbp2x</i>	<i>pbp2b</i>	<i>mef(A)</i>	<i>erm(B)</i>	
1	1	1	1	47	Cough, Sputum	3	0.5	-	-	-	-	-	a1
1	2	2	2	3	Cough, Sputum	3	2.0	-	-	-	-	-	a1
1	3	3	3	5	Cough	22A	0.016	-	-	-	-	-	b1
1	3	4	4	3	Cough	22A	0.016	-	-	-	-	+	b1
1	4	5	5	35	Cough, Sputum	19A	0.5	+	-	-	-	-	c
1	3	3	6	5	Cough	3	0.008	-	-	-	-	-	a2
1	4	6	7	12	Cough	9A	≤ 0.004	-	-	-	-	-	d
2	5	7	8	41	Cough, Sputum	22A	≤ 0.004	-	-	-	-	-	b2
2	6	8	9	0	Cough	6A	≤ 0.004	-	-	+	-	-	e
2	7	9	10	37	Cough	11A	0.032	-	-	-	-	-	f1
2	8	10	11	2	Cough	23F	1.0	+	+	+	-	+	g
3	9	11	12	12	Cough, Sputum	10A	0.008	-	-	-	-	+	h
3	10	12	13	14	None	10A	≤ 0.004	-	-	-	-	+	h
3	11	13	14	12	Cough, Sputum	10A	4.0	-	-	-	-	+	i
3	12	14	15	11	Cough, Sputum	11A	0.032	-	-	-	-	-	f2
3	13	15	16	10	Cough, Sputum	11A	0.032	-	-	-	-	-	f1
3	14	16	17	3	Cough, Sputum	9A	1.0	+	+	+	-	-	j
3	15	17	18	9	None	9A	1.0	+	+	+	-	-	j
3	16	18	19	12	Cough, Sputum	6B	2.0	-	-	-	-	+	k
3	17	19	20	10	Cough, Sputum	6B	≤ 0.004	-	-	-	-	+	l
3	18	20	21	13	Cough, Sputum	10F	≤ 0.004	-	-	-	-	-	m
3	19	21	22	7	Cough, Sputum	15B	0.016	-	-	-	-	-	n
3	12	22	23	12	Cough, Sputum	17A	≤ 0.004	-	-	-	-	-	o
3	12	22	24	12	Cough, Sputum	22A	≤ 0.004	-	-	-	-	-	b2
3	12	22	25	12	Cough, Sputum	22F	≤ 0.004	-	-	-	-	-	p

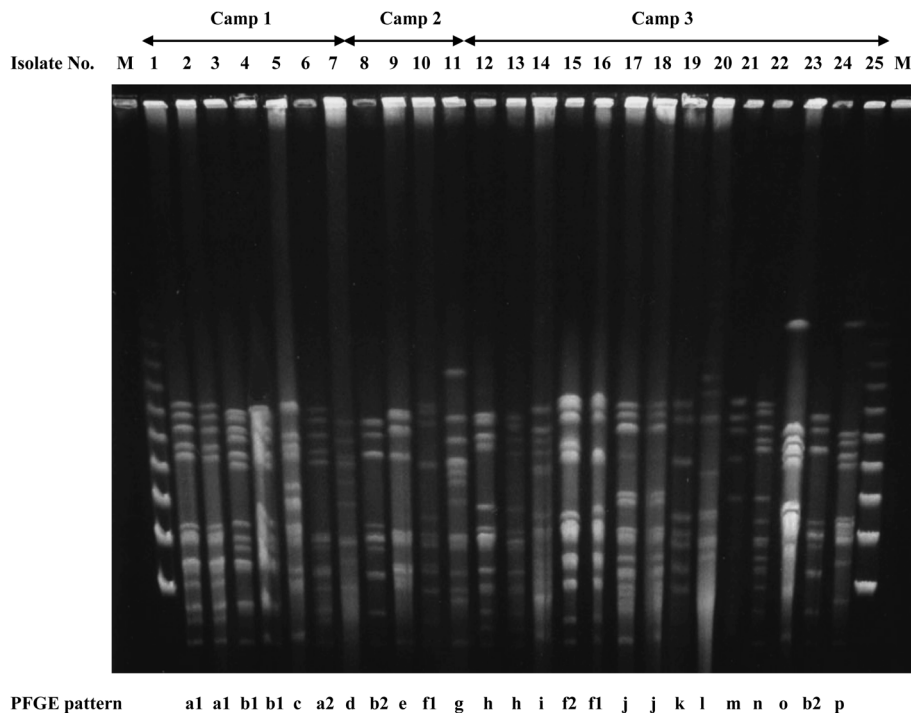
## Discussion

Displaced population due to disasters often inevitably seek refuge in evacuation camps that usually accommodate a large number of people in limited space, leading to overcrowding and poor hygiene. On January 5th, 2005, 10 days after the tsunami, WHO issued an alert for the prevalence of infectious diseases. Its major outbreaks of infectious diseases related to a tsunami have never been reported to date. However, since poor hygiene and crowded conditions in evacuation camps can be potential transmission sites for supporting a variety of communicable diseases, we focused our attention on acute bacterial respiratory tract infections in the camps. In particular, infants and young children tend to acquire *H. influenzae* and *S. pneumoniae* in the upper tract because of their low immunity (7), and colonization can become a risk factor of invasive diseases (15). In our study, many infants and young children were living in the camps. In fact, most organisms were detected in children and most person to person transmission of such organisms appeared to occur via children. Since most IDP had respiratory symptoms after entering the camps and PFGE patterns in *H. influenzae* and *S. pneumoniae* were relatively different in each camp except for a few patterns, person to person transmission of such organisms in IDP who had the same bacteria with a similar PFGE pattern in the same camp should be reasonable. In addition, some investigators have reported the presence of multiple strains in the same person's throat or nasopharynx isolates (16, 17); multiple genetic types of *H.*

*influenzae* and *S. pneumoniae* were identified in a few IDP in our study. In this respect, the mismatched strains might be tested instead of the matching ones, even in discordant IDP in the same camp. Although some of IDP who had the same organism with a similar PFGE pattern did not necessarily live in the same room at the camp, they might have had the chance to contact each other. Indeed, they said that some people had slept outdoors together because of the fear of tsunami. Their residential space was restricted and many people, including adults, had respiratory symptoms, although the detection rate of *H. influenzae* and *S. pneumoniae* was not necessarily higher compared to the previous report (18). However, we accumulated the NP in the camps and transferred them from the camps to the University of Peradeniya within 24 hours to identify the organisms, since the University of Peradeniya is far from the camps, some organisms would potentially die under the situation. Regarding resistant isolates, multidrug-resistant pneumococci are now widespread all over the world (4) and it was previously reported that the rate of penicillin-nonsusceptible pneumococci in Sri Lanka is 41.2% (19), and such resistant pneumococci was found even in the evacuation camps. Previous studies indicated that the Spanish multidrug-resistant 23F pneumococci or the Taiwan multidrug-resistant 19F and 23F pneumococci were spreading in Asia (19, 20). However, the prevalence of such international pandemic clone was not found in our study. It has also recently been reported that BLNAR *H. influenzae* strains have increased in some countries (10, 21), although their global prevalence remains low (22). In our study, the prevalence of BLNAR *H. influenzae* strains was



**Figure 1.** PFGE patterns of *Sma*I-digested DNA from 21 *H. influenzae* isolates from the nasopharyngeal swabs (NP) in 20 internally displaced persons (IDP). Molecular typing by PFGE demonstrated that the 21 *H. influenzae* strains consisted of 13 patterns (A-L), and PFGE pattern B isolates from 3 IDP and PFGE pattern C isolates from 2 IDP were detected in camp 1, and PFGE pattern K isolates from 3 IDP and PFGE pattern L isolates from 2 IDP were detected in camp 3.



**Figure 2.** Pulsed-field gel electrophoresis (PFGE) patterns of *Sma*I-digested DNA from 25 *S. pneumoniae* isolates from the nasopharyngeal swabs (NP) in 22 internally displaced persons (IDP). Molecular typing by PFGE demonstrated that the 25 *S. pneumoniae* strains consisted of 16 patterns (a-p), and PFGE pattern a isolates of serotype 3 were found for 3 IDP and PFGE pattern b isolates of serotype 22A were found for 2 IDP in camp 1, and PFGE pattern h isolates of serotype 10A for 2 IDP, PFGE pattern f isolates of serotype 11A for 2 IDP and PFGE pattern j isolates of serotype 9A for 2 IDP were detected in camp 3.

not found. Our data indicate that various types of *H. influenzae* and *S. pneumoniae* possibly caused acute respiratory tract infections and some were transmitted from person to person. Of course, since we investigated only common bacterial pathogens, the classification of such infections such as *Mycoplasma pneumoniae*, *Chlamydia pneumoniae*, *Mycobacterium tuberculosis*, *Influenza virus*, etc are unknown. Because these are also communicable diseases (23-26), further investigations are clearly warranted. In addition, knowledge of the incidence of meningitis and pneumonia caused by *H. influenzae* and *S. pneumoniae* in evacuation camps would be highly desirable, although this issue was not addressed in this study.

In conclusion, our results demonstrated that acute respiratory tract infections caused by various types of *H. influenzae* and *S. pneumoniae* were prevalent and some of them, including resistant isolates, were potentially transmitted from person to person in tsunami disaster evacuation camps in Sri Lanka. Therefore, we should consider the introduction of preventive measures, such as improved ventilation, rapid relocation and highly effective vaccines to IDP in evacuation

camps for preventing invasive disease caused by *H. influenzae* and *S. pneumoniae*.

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Hiroshi Watanabe and Ranjith Batuwanthudawe contributed equally to the work described in this paper.

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