Thalassemia is one of the most important genetic disorders in Thailand. A model for prevention of thalassemia by combining 4 strategies including education, carrier screening, counseling and prenatal diagnosis was developed by a thalassemia task force. Thalassemia working group was formed in order to develop a mechanism to integrate the model for real use on Samui Island where thalassemia is common and a specific disease oriented program is required. 200 health professionals working on Samui Island were participated in the thalassemia educational courses. The specific training courses were also provided for obstetricians, medical technologists and counselors. A team of well-trained health professionals was established to manage public education. Information booklets, posters, brochures and mass media including spot radio and newspapers were used as educational materials. For carrier screening, blood samples of pregnant women from all health care organizations on Samui Island were collected and screened for thalassemia carriers by using OF/DCIP tests at Samui Hospital. Samples with positive results were sent to Regional Medical Sciences Center in Suratthani for thalassemia diagnosis. When a carrier was identified, her spouse was offered testing. For at-risk couples, details of the disorder were included in counseling to help them reach a decision that was right to them, in the context of their unique medical, moral and social situations. Amniotic fluid samples
were collected for prenatal diagnosis. All patient information was registered by using computer software. After 1 year of integration by using facilities of the Ministry of Public Health service system, a wide range of problems were identified. They underlined the need for effective health service structure co-operation, adequate education of responsible health professionals, explicit policies and a clear line of responsibility at local, regional and national levels for service development and quality management. It is hoped that all information conducted in this study could be useful for health authorities to develop an explicit policy and promote the health service structure co-operation in the country that finally leads to remarkably successful in reducing the frequencies of severe thalassemia in the future.
Avian influenza A (H5N1) virus causes human influenza-like illness with a high mortality and complications. Early diagnosis is crucial for prompt management. We report a case of avian influenza pneumonia who was admitted with severe community-acquired pneumonia. The patient had been exposed to infected and dead chickens before his illness. The patient presented with a short history of high-grade fever, dyspnea, bilateral infiltration and respiratory failure. The hospital course was complicated by pneumomediastinum and pneumothorax. The diagnosis of avian influenza pneumonia was confirmed by the viral culture.
Influenza A viruses are classified into subtypes (hemagglutinin and neuraminidase subtypes) based on antigenic differences in their surface glycoproteins. Of 15 identified hemagglutinin (H1-H15) and 9 neuraminidase subtypes (N1-N9), only 3 hemaglutinin subtypes (H1, H2 and H3) and 2 neuraminidase subtypes (N1 and N2) have established stable lineages in humans. Because the natural reservoir of known influenza A subtypes is found in birds and waterfowl, subtypes other than those typically found in humans have the potential to cross the species barrier and infect humans.

Avian influenza A virus H9N2 was isolated from two children in Hong Kong in 1999 and avian influenza H7N7 infected 89 persons during a simultaneous outbreak in poultry in the Netherlands in 2003, although these infections resulted in only mild illnesses. The first outbreak of a highly pathogenic avian influenza (H5N1) in humans occurred in Hong Kong in 1997; 6 of 18 people with confirmed infection died. Despite attempts to prevent disease, two cases of influenza A H5N1 occurred in Hong Kong in February 2003, Followed by outbreaks in Vietnam and Thailand in January 2004. Data are limited on the epidemiologic characteristics, signs and symptoms and outcomes of avian influenza H5N1 exposure in
healthcare workers. We report atypical avian influenza H5N1 and follow-up surveillance of 35 exposed healthcare workers; we also review relevant literature in this area.

2004-04

**Title:** Seroprevalence of anti-H5 antibody among Thai health care workers after exposure to Avian influenza (H5N1) in a tertiary care center

**Authors:** Anucha Apisarnthanarak*, Steven Erb*****, Iain Stephenson*****, Jacqueline M. Katz*****, Malinee Chittaganpitch***, Somchai Sangkitporn***, Rungrueng Kitphati***, Pranee Thawatsupa***, Sunthareeya Waicharoen***, Uayporn Pinitchai**, Piyaporn Apisarnthanarak*****, Victoria J. Fraser******, Linda M. Mundy

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**Source:** Clinical Infectious Diseases 2005 Jan 15; 40(2): e16-8. Epub 2004 Dec 17

**Language:** English

**Abstract:**

After the initial atypical presentation of a patient with avian influenza (H5N1) infection, paired acute-phase and convalescent-phase serum samples obtained from 25 health care workers (HCWs) who were exposed to the patient were compared with paired serum samples obtained from 24 HCWs who worked at different units in the same hospital and were not exposed to the patient. There was no serologic evidence of anti-H5 antibody reactivity or subclinical infection in either of the groups.

In recent years, infection with avian influenza (H5N1) virus in humans has been associated with high morbidity and mortality. The first human outbreak of H5N1 infection occurred in Hong Kong in 1997, followed by 2 cases of H5N1 infection in Hong Kong in February 2003. Subsequent outbreaks of H5N1 infection occurred in Vietnam and Thailand in January 2004. Twenty-two patients in
Vietnam and 12 patients in Thailand had confirmed cases of H5N1 infection; 23 (67%) of 34 infected patients died. To date, there is a paucity of data regarding the effect of occupational exposure to H5N1 virus among health care workers (HCWs). One prior study suggested that, although rare, human-to-human transmission to HCWs occurred during the 1997 Hong Kong outbreak of H5N1 infection. To further characterize occupational exposure to H5N1 infection, we conducted an epidemiologic investigation and seroprevalence study comparing HCWs in our institution who were exposed to and index case patient with H5N1 infection with those HCWs who were not exposed.
2004-05

Title: Evaluation of nested PCR for the diagnosis of scrub typhus among patients with acute pyrexia of unknown origin

Authors: Watcharee Saisongkorh*, Mongkol Chenchittikul*, Khachornsakdi Silpapojakul**

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**Department of Medicine, Faculty of Medicine, Prince of Songkla University, Hat-yai, Songkla, Thailand

Source: Transactions of the Royal Society of Tropical Medicine and Hygiene 2004; 98: 360-366

Language: English

Abstract:

A nested PCR technique was performed to detect a specific 483 bp DNA fragment of Orientia tsutsugamushi, the aetiological agent of scrub typhus, in 53 blood samples from 36 patients with acute pyrexia of unknown origin in southern Thailand. The specific primers could amplify the specific DNA from all 10 prototype strains of O. tsutsugamushi and all nine seropositive patients and three seronegative patients, while no DNA amplification was obtained with DNAs from other rickettsiae or from healthy persons or from patients with murine typhus. The specific PCR product was detectable in the blood for as long as 22 days after the onset of disease in patients without specific treatment and 27 days after receiving a single dose of doxycycline. Thus, nested PCR may be more sensitive than the serological test for diagnosis of scrub typhus and prolonged persistence of O. tsutsugamushi DNA in patients’ blood was demonstrated despite clinical recovery of the patients.
Hepatitis B is the most hazardous infectious agent and could be transmitted among medical laboratory workers. Vaccination program for risk personnel in Thailand National Institute of Health was considered. 116 (27.5 %) medical laboratory workers were prevaccination checked up before administration of hepatitis B vaccine. 31 % were already immunized with hepatitis B in prevaccination status. 69 % of nonimmunity was classified into 3 groups, 61.2 % normal, 6.9 % carrier and 0.9 % infected group. Three doses of vaccine were administered to persons who have not been vaccinated or lack of hepatitis B immunity. After completed vaccination, hepatitis B vaccine responsive status was reviewed. 98.3 % of vaccinated medical laboratory workers response to hepatitis B vaccine.
Human hepatitis A virus (HAV) is a major causative agent of acute hepatitis and the isolates are categorised into four genotypes: I(GI), II(GII), III(GIII) and VII(GVII). Although viral hepatitis has been detected under a nationwide surveillance system in Thailand, the genetic variation of HAV has not yet been determined. In the present study, serum specimens were collected from acute hepatitis patients in Thailand from 1998-2002. The IgM-class antibody to HAV was detected in 156 out of 394 sera, counting as many as 39.6% of acute viral hepatitis cases. HAV RNA in the serum specimens was amplified by reverse-transcription polymerase chain reaction (RT-PCR), and a phylogenetic analysis of the putative VP1/2A junction of the genome was performed. The isolates were grouped into two genetic groups, GIA and GIB. This is the first report to identify subgenotype IB (GIB) in Thailand. This genetic segregation was closely related to the province where hepatitis A occurred and the serum specimens were collected. In addition, genetically similar strains were identified in both 1998 and 2001-2002 isolates from two close provinces in the southern part of Thailand, suggesting that a strain indigenous to the province or district has been circulating in southern Thailand.
Title: Study of Antiretroviral Drug–Resistant HIV-1 Genotypes in Northern Thailand: Role of Mutagenically Separated Polymerase Chain Reaction as a Tool for Monitoring Zidovudine-Resistant HIV-1 in Resource-Limited Settings


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Source: Journal of Acquired Immune Deficiency Syndromes • August 15 2004 ; 36(5): 1051

Language: English

Abstract:

As the number of HIV-1–infected individuals receiving antiretroviral drugs has been rapidly increasing in developing countries, there is an urgent need for drug resistance genotype information of non-B subtype HIV-1 and for the establishment of a practical system of monitoring drug-resistant viruses. This study first sequenced the reverse transcriptase region of HIV-1 in 112 infected individuals who had been treated with zidovudine (AZT)/didanosine or AZT/zalcitabine as dual therapy at a government hospital in northern Thailand and then compared the above sequence method with mutagenically separated polymerase chain reaction (MS-PCR) for detecting M41L and K70R mutations. Concordant rates of detecting M41L and K70R mutations by the 2 methods were 96.9% (93/96) and 92.7% (89/96), respectively. The M41L and K70R MS-PCR could detect 86.4% of AZT-resistant strains with any resistance mutation, which was determined by the sequencing method. Then 292 drug-naive individuals were screened for the presence of drug-resistant HIV-1 by the MS-PCR assay and it was found that 2 individuals (0.7%) carried viruses with either the M41L or K70R
mutation. It is feasible to test a large number of samples with MS-PCR, which is sensitive, cheap, and easy to perform and does not require sophisticated equipment. The M41L and K70R MS-PCR is potentially a useful tool to monitor the spread of AZT-resistant HIV-1 in resource-limited countries.
Five strains isolated from two patients with nocardiosis in Japan and three clinical samples from Thailand were found to have morphological, biochemical and chemotaxonomic properties consistent with their classification in the genus *Nocardia*. DNA-DNA hybridization, coupled with sequence analysis of 16S rDNA, indicated that these strains belong to a novel species of the genus *Nocardia*, named *Nocardia asiatica* sp. nov. because the isolation sites were in Asian countries; the type strain is IFM 0245T (=NBRC 100129T=JCM 11892T=DSM 44668T).
2004-10

Title: Nocardia beijingensis, is a pathogenic bacterium to humans: the first infectious cases in Thailand and Japan

Authors: Akiko Kageyama*, Natteewan Poonwan**, Katsukiyo Yazawa*, Yuzuru Mikami*, Kazuko Nishimura*

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Language: English

Abstract:

Nocardia beijingensis, a recently established new species, is an isolate from soil in China. During our taxonomic studies on 450 nocardial clinical isolates in Thailand and Japan, 17 strains from Thailand and 1 strain from Japan were found to have a similar physiological characteristic to those of N. beijingensis, such as a drug susceptibility pattern to three antimicrobial agents. Our phylogenetic studies on these 18 strains by 16S rRNA gene sequence analysis confirmed that these strains belong to N. beijingensis species. Phylogenetically, these newly isolated N. beijingensis strains were found to be classified into two distinct clades: one is a Japanese clade and other is a Chinese clade, including a reference strain and 17 Thai strains. This is the first report of human infection due to N. beijingensis strains, and we propose that the bacterium be categorized as an opportunistic infectious group regardless of its original isolation from soil.
2004-11

Title: Impregnated Mosquitoes Net and Curtain with Deltamethrin against Adult *Aedes aegypti*

Authors: Thumrong Phonchevin*, Kasin Suphanpathom*, Amnat Bunkhrouaphan*, Pathom Sawanpanyalert*

Affiliations: *National Institute of Health, Department of Medical Sciences

Source: Journal of Health Science 2004; 13: 140-7

Language: English

Abstract: Persistence of insecticidal effect of deltamethrin on the bednet made from cotton, polyethylene fabric and the curtain made from cotton and silk fabric was studied by impregnating deltamethrin at dosage of 25 mg/m² on bednet and curtain using WHO Bioassay test with *Aedes aegypti* from laboratory from February 19, 2002 to September 23, 2003. The study indicated that deltamethrin had persistent effect on cotton bednet, polyethylene bednet, cotton curtain and silk curtain could maintain over percent mortality rate for 23.85, 12.29, 9.95, and 10.17 weeks respectively.
2004-12

Title: Annual Changes of Predominant Dengue Virus Serotypes in Six Regional Hospitals in Thailand from 1999 to 2002


Affiliation: *National Institute of Health, Department of Medical Sciences
**Department of Virology I, National Institute of Infectious Diseases, Tokyo, Japan


Language: English

Abstract:

A virological study was conducted in six hospitals spread across Thailand from 1999 to 2002. All four dengue serotypes were identified, of which DEN-1 was the most predominant. The predominant dengue serotypes changed every 1-2 years in three of the six hospitals and the predominant serotypes were different in different hospitals. DEN-1 was predominant in two hospitals during three years of the study period (2000-2002). DEN-4 was not isolated, or accounted for only a small percentage of the total isolates, except in one hospital in 2002.
**2004-13**

**Title:** Sustained transmission of dengue virus type 1 in the Pacific due to repeated introductions of different Asian strains

**Authors:** Atchareeya A-nuegoonpipat*, Alain Berlioz-Arthaud**, Vincent Chow***, Tim Endy****, Kym Lowry***** Le Quynh Mai****** Truong Uyen Ninh******* Alyssa Pyke******** Mark Reid******** Jean- Marc Reynes*********, Se-Thoe Su Yun*********, Hlaing Myat Thu*********, Sook-San Wong**********, Edward C. Holmes**********, John Aaskov******

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**Institute Pasteur, Noumea, New Caledonia, Australia  
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******National Institute of Hygiene and Epidemiology, Hanoi, Vietnam  
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**********Department of Pathology, Singapore General Hospital, Singapore  
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*************Department of Zoology, University of Oxford, Oxford, UK

**Source:** Virology 2004; 329: 505-512

**Language:** English

**Abstract:**

Outbreaks of dengue due to dengue virus type 1 (DENV-1) occurred almost simultaneously in 2001 in Myanmar and at multiple sites almost 10,000 km away in the Pacific. Phylogenetic analyses of the E protein genes of DENV-1 strains recovered from Asia and the Pacific revealed three major viral genotypes (I, II, and III) with distinct clades within each. The majority of strains from the Pacific and Myanmar, and a number of other Asian strains fell into genotype I. Genotype II comprised a smaller set of Asian and Pacific strains, while genotype III contained viruses from diverse geographical localities. These analyses suggested that the continuing outbreak of dengue in the Pacific has been due to multiple, direct, introductions of dengue viruses from a variety of locations in Asia followed by local transmission. There was
no evidence that the introduction of these viruses into the Pacific was associated with any adaptive changes in the E protein of the viruses.

2004-14

Title: Analysis of specific IgM responses in secondary dengue virus infections: levels and positive rates in comparison with primary infections

Authors: Sumalee Chanama*, Surapee Anantapreecha*, Atchareeya A-nuegoonpipat*, Areerat Sa-ngasang*, Ichiro Kurane**, Pathom Sawanpanyalert*

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**Department of Virology I, National Institute of Infectious Diseases, Tokyo, Japan

Source: Journal of Clinical Virology 2004; 31: 185-189

Language: English

Abstract:

Dengue viruses are a serious cause of illness in tropical and subtropical areas of the world. Laboratory diagnosis is essential for confirmation of dengue virus infections. Detection of specific IgM by IgM-capture enzymed-linked immunoassay (ELISA) has been widely used as a main serological diagnostic technique. Objectives: The levels of specific IgM in secondary dengue virus infections were compared with those in primary infections. Study design: A total of 1780 samples collected from 924 confirmed dengue cases were tested for anti-dengue IgM by IgM-capture ELISA. Results and conclusions: Specific IgM was detected in all the cases with primary dengue virus infection on disease day 9 or later. However, specific IgM cannot be detected in 28% (204/716) of the cases in secondary infections. The average titers of IgM were higher in primary infections than in secondary infections. The results confirmed that IgM detection is a reliable serological diagnostic test in primary dengue virus infections. Although IgM detection is also a useful test, other serological diagnostic tests or tests for dengue virus detection are necessary for confirmation of all the secondary dengue virus infections.
2004-15

**Title:** Performance of four sources of cholesterol oxidase for serum cholesterol determination by the enzymatic endpoint method

**Authors:** Porntip H. Lolekha*, Pornpen Srisawasdi*, Patcharee Jearanaikoon**, Nuanchawee Wetprasit***, Busarawan Sriwanthana****, Martin H Kroll*****

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**Source:** Clinica Chimica Acta 2004; 339: 135-145

**Language:** English

**Abstract:**

Background: Cholesterol oxidase is used for the determination of serum cholesterol. It can be derived from *Streptomyces, Pseudomonas fluorescens, Cellulomonas*, and *Brevibacterium*. This study compared the performance characteristics of four enzymes in the endpoint cholesterol determination. Methods: Using the Mega analyzer, we studied assay optimization, linearity, precision, recovery, interference, stability, and compared 110 patient samples. Results: The linearity for the four enzymes was up to 13.0 mmol/l at the optimal enzyme activity. The average within-run CVs ranged from 1.6% to 1.9% and between-day ranged from 2.8% to 3.0%, within the NCEP analytical criteria. The analytical recoveries obtained from four reagents (≈96.5%) were excellent. The assays using these enzyme sources compared favorably with the commercial method and appeared accurate near the clinical decision cut-points. Hemoglobin concentration at 1.9 g/l interfered with the *P. fluorescens* cholesterol oxidase. Bilirubin caused a negative interference while lipemia
generated a positive interference with all enzyme sources. Reagents were stable up to 6 weeks. Conclusions: *Streptomyces*, *Cellulomonas*, and *Brevibacterium* were essentially analytically equivalent. *Streptomyces* and *Cellulomonas* cholesterol oxidase are one-quarter as expensive *Brevibacterium*. *Cellulomonas* is a new source of cholesterol oxidase for determining serum cholesterol by the endpoint method.
Title: Pathogenic Organisms in Natural Hot Spring Water


Affiliation: * National Institute of Health, Department of Medical Sciences, Ministry of Health
** Provincial Public Health Office, Mae Hong Son Province
*** Academy of Science, The Royal Institute, Bangkok

Source: Journal of Health Science 2004; 13: 27-31

Language: Thai with English Abstract

Abstract: Water specimens were taken from 18 natural hot springs in the four northern provinces of Thailand, namely, Mae Hong Son, Chiang Mai, Chiang Rai, Lampang and sent to the laboratories of the National Institute of Health, Department of Medical Sciences, Ministry of Public Health in Nonthaburi for determining the presence of the legionella organism and free-living ameba. Legionella pneumophila serogroup 6 was isolated from water specimen collected in Mae Hong Son province; ameba was not isolated from any the specimens. There was a clue suggestion that temperatures of the hot spring water might play an influential role in their existence of viable pathogenic organisms.
In Rachaburi Province, there are two significant natural hot springs: Boe Klueng in Suan Pueng district and Bann Pu Namron in Baan Ka subdistrict. On November 30, 2003, a pollution survey conducted at both sites revealed the presence of dissolved radon gas in water samples as high as 170,794.99 and 23,621.69 becquerels/cubic meter, respectively (safety threshold is 400,000 becquerels/cubic meter), while simultaneous measurements of gamma ray exposure and atmospheric radon gas in the vicinity of those sites showed gamma radiation intensity of 40 and 23.5 mR/h, respectively (normal background intensity does not exceed 20 mR/h) and radon gas ranges of 39.36-53.59 and 31.40-46.71 becquerels/cubic meter respectively (Safety level: 148 Bq.m$^{-3}$); and revealed the presence of *Legionella pneumophila* organisms in water samples from both hot spring source, i.e., serogr. 13 at Boe Klueng’s bathing pond, and serogr 7 and serogr 6 in water samples from the main hot spring and the bathing tanks respectively at Bann Pu Namron. Worthy of note is that the same group of researchers had succeeded in detecting legionella organism in one of the natural hot spring in Mae Hong Son province. The presence authors intend
to carry on further surveys in order to identify the hazards in natural hot springs in the Kingdom.

2004-18

Title: Serum Low-Density Lipoprotein Cholesterol and other Risk Factors of Coronary Heart Disease in Hypercholesterolemic Subjects

Authors: Pratana Satitvipawee*, Jarueyporn Suparp**, Panisa Getngern***

Affiliations: *Department of Biostatistics, Faculty of Public Health, Mahidol University
**Department of Family Heart, Faculty of Public Health, Mahidol University
***National Institute of Health, Department of Medical Sciences, Ministry of Public Health, Nonthaburi

Source: Journal of Public Health 2004; 34(2): 110-120

Language: English with Thai abstract

Abstract:

A cross sectional study was carried out to determine the association between levels of low-density lipoprotein cholesterol (LDL-C) and other risk factors of coronary heart disease (CHD) in subjects with hypercholesterolemia (total cholesterol $\geq 200$ mg/dL) from December 2001 to March 2002. Two hundred and sixteen subjects (62 males and 154 females) aged 35 to 59 years old were participated. Means (SD) of age and LDL-C level were 45.4(6.3) years and 165.4(37.8) mg/dL. Out of 216, 51.9% had a LDL-C level equal or greater than 160 mg/dL. The result revealed that there were statistical association between gender ($p=0.001$), smoking ($p=0.008$), menopause status ($p=0.017$) and serum LDL-C. Daily fruit, vegetable and whole grain intake inversely associated with LDL-C ($p<0.001$, $<0.001$ and 0.031, respectively). Those using animal or palm/coconut cooking oil and frequently eating foods cooked with coconut milk had LDL-C $\geq 160$ mg/dL more than those using other vegetable cooking oils ($p=0.017$) and those eating food cooked with coconut milk less than 3 times/week ($p < 0.001$). Those with family history of hyperlipidemia and coronary artery disease had higher LDL-C ($p = 0.041$, 0.005, respectively). Furthermore, age, BMI, total cholesterol and triglycerides were positively correlated with serum LDL-C ($r = 0.225$, $p = 0.01$; $r = 0.187$, $p = 0.008$; $r = 0.949$, $p < 0.001$; and $r = 0.147$, $p = 0.031$, respectively).
In conclusion, daily consumption of fruit, vegetable and whole grain, avoid using animal/palm/coconut cooking oils, reducing eating food cooked with coconut milk, stop smoking and weight control were associated with lower serum LDL-C and thus lower the risk of CHD in hypercholesterolemia.

2004-19

Title: LightCycler real-time PCR for quantitative detection of Mycobacterium leprae

Authors: Janisara Rudeeanaksin*, Sopa Srisungngam*, Taweerit Sithivekin**, Krisada Mahotan**, Patrick J. Brennan***, Prasit Palittapongarnpim****, and Benjawan Phetsuksiri*

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Source: Proceeding: 10th Asean Conference in Medical Laboratory Technology 2004; 264

Language: English

Abstract:

Enumeration of Mycobacterium leprae for determination of bacterial index is required for leprosy classification, monitoring of leprosy chemotherapy and diagnosis of relapse. In clinical application, quantification of M. leprae relies on microscopic examination and counting of bacilli in stained specimens. The counting method yielding results with limited specificity and sensitivity. This study is aimed to develop and evaluate the application of a fluorescence real-time PCR assay for quantifying M. leprae in skin specimens. The real-time PCR is based on a capillary format of the LightCycler using SYBR Green I fluorescent dye as a detection signal. Primers were applied to amplify a portion of 171 bp fragment of M. leprae 16S rRNA gene. Using commercial Flexigene, with modifications, resulted in high yields of isolated DNA. The PCR assay was specific for M. leprae and able to detect as low as 20 fg of M. leprae DNA. The analytical sensitivity was as
low as one cell of bacilli. The melting temperature of this PCR product was 86°C. By the use of normalized quantitative real-time PCR, *M. leprae* was detected in 40 multibacillary (MB) patients with bacilli number in the range of $9.6 \times 10^2 \text{ - } 8.5 \times 10^7$ bacilli in 6x6 mm skin biopsy specimen. The detectable number of bacilli in skin biopsies from 10 paucibacillary (PB) patients is of the order of $8.9 \times 10^2 \text{ - } 2.5 \times 10^3$ bacilli. The preliminary results demonstrated that LightCycler real-time PCR appeared to be a robust tool for quantitative detection of leprosy bacilli in clinical specimens and could be adopted as a molecular tool for quantification of *M. leprae* in other experimental settings.
Title: Combination of Mesocyclops thermocyclopoides and Bacillus thuringiensis var. israelensis: a better approach for the control of Aedes aegypti larvae in water containers

Authors: Uruyakorn Chansang*, Amaret Bhumiratana**, Pattamaporn Kittayapong***

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***Center for Vectors and Vector-Borne Diseases and Department of Biology, Faculty of science, Mahidol University, Bangkok 10400, Thailand


Language: English

Abstract: The efficacy of a local Thai-strain of the copepod, Mesocyclops thermocyclopoides and the larvicide, Bacillus thuringiensis var.israelensis (Bti), used jointly and singly, was studied against Aedes aegypti in water containers. In a laboratory test, copepods alone produced mortality of 98-100% in 1st instar larvae of Ae. aegypti at copepod: larvae ratios ranging from 1:1 to 1:4. In an outdoor field simulated experiment that ran for 16 wk, after a single inoculation, the treatment of copepods and Bti combined yielded the better, more sustainable results than the agents used individually. Numbers of mosquito larvae per sample in the combined treatment were zero during the first 8 wk; larval numbers then increased but were maintained at a very low level for the next 4 wk after which the larval numbers increased moderately but still remained below numbers in the control. Bti alone kept the larvae at the zero level for the 4 wk after which their numbers increased slightly and were at low levels up to 12 wk. Copepods alone maintained larval numbers at a low level as compared with those of the control. During the
course of the experiment the larval numbers in the control were greater than 20 per sample. Statistically significant differences were noted among treatment means ($F = 23.083$, $df = 3/60$, $P < 0.01$) over the total period of the study. The number of copepods in the joint treatment was significantly higher than in the copepod alone treatment for the first 8 wk ($t = -4.97$, $df = 4$, $P < 0.01$). The density of copepods, however, for the whole 16-wk period was not significantly different in these two treatments ($t = -1.51$, $df = 30$, $P > 0.1$).
Cockroach surveys were carried out in three provinces of the Northern region of Thailand: Chiang Mai, Chiang Rai, and Mae Hong Son, and three cities of Guangxi Province of the People's Republic of China: Nanning, Huangjiang, and Hechi. Sticky traps were used for cockroach sampling in these surveys. At least 30 houses in each province or city were randomly sampled. Traps were placed in kitchen areas for 2 nights. In Thailand, a total of 214 cockroaches was caught in 65 of 112 houses (59.4%) with an average of 1.9 cockroaches/ house. There were 5 species of cockroach caught: *Periplaneta americana* (32.7%), *Pycnoscelis surinamensis* (29%), *Periplaneta australasiae* (18.2%), *Periplaneta brunnea* (17.3%), and *Periplaneta fuliginosa* (2.8%). In China, a total of 198 cockroaches was caught in 67 of 99 houses (67.5%) with an average of 2 cockroaches/ house. There were 6 species of cockroaches caught: *P. americana* (53%), *Py. surinamensis* (12.6%), *P. brunnea* (12.1%), *P. australasiae* (12.1%), *P. fuliginosa* (9.6%), and *Neostylopyga rhombifolia* (0.6%). According to the surveys in this study, there were no significant differences among the number of cockroaches caught in the six locations of the two
P. americana was the most abundant cockroach species in both countries.

2004-22

Title: Evaluation of attractants and egg-laying substrate preference for oviposition by Aedes albopictus (Diptera: Culicidae)

Authors: Usavadee Thavara*, Apiwat Tawatsin*, Jakkrawarn Chompoosri*

Affiliation: * National Institute of Health, Department of Medical Sciences, Ministry of Public Health, 88/7 Tiwanon Road, Nonthaburi 11000, Thailand


Language: English

Abstract:

Evaluation of oviposition attractants and substrate preferences of Aedes albopictus was carried out under laboratory and field conditions. To obtain candidate oviposition substances we used a water rinse of 3 mollusk species: blood cockle (Anadara granosa), carpet shell (Paphia undulata), and sea mussel (Mytilus smaragdinus), and the giant tiger prawn (Penaeus monodon). The rinse water of carpet shell and giant tiger prawn showed higher attractiveness for oviposition than the other candidate attractants. The filter paper substrate received fewer eggs than the other two substrates. There was no significant difference between the mean number of eggs laid on hardboard paddles and sponge sheets. The hatching rate of Ae. albopictus eggs laid on hardboard paddles was higher than those from the filter papers and sponge sheets. The sponge had lethal effects on Ae. albopictus eggs, and very few eggs laid on sponge hatched. In field experiments, evaluation of attractiveness of carpet shell rinse in ovitraps lined with sponge sheet as egg-laying substrate was carried out in various habitats and different areas of Thailand. The mean number of eggs in traps containing carpet shell rinse was significantly higher than those laid in rainwater traps. These studies reveal that the carpet shell and giant tiger prawn rinses are sources of oviposition attractant for Ae.
albopictus under both laboratory and field conditions and could possibly be used as an attractant in surveillance and control.

2004-23

Title: Efficacy and longevity of a new formulation of temephos larvicide tested in village-scale trials against larval Aedes aegypti in water-storage containers

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Language: English

Abstract:

Field trials on the initial and long-term efficacy of a new formulation of temephos granules (1% on zeolite) applied at 1 ppm active ingredient (AI) were conducted in water-storage containers against Aedes aegypti in 3 villages in the Kanchanaburi Province in Thailand. A total of 316 water-storage containers of various types and sizes were included in the study. In the initial survey, we found that some containers were positive for larval Ae. aegypti, whereas others were devoid of larvae before the initiation of treatments. The containers all were numbered with paint and divided into 4 groups: with larvae and treated, without larvae and treated, with larvae untreated, and without larvae and untreated. Assessment of larval abundance was made 48 h after treatment and monthly thereafter for 5 months. Containers with larvae and that were treated exhibited almost complete absence of larval Ae. aegypti for 2 months, but a small proportion became positive after 3 months. Most of these positive containers were devoid of zeolite granules, which are visible in the containers. The number of positive containers increased in months 4 and 5, despite the fact that residues of
temephos granules were present in some of the larvae-positive containers. The containers initially without larvae and treated with temephos essentially were devoid of larvae for 2 months. After 3, 4, and 5 months, about 6-23% of the containers became positive despite the fact that some had visible amounts of temephos granules. In the 2 control groups initially with and without larvae, sustained and consistent production of larvae occurred. Even in the group initially without a larval population, the containers became positive for larvae 1 month after the start of the experiment and the positivity rate increased as the trial progressed. From these studies, the conclusion can be made that a single application of temephos zeolite granules at 1 ppm AI can provide highly satisfactory control of larval *Ae. aegypti* in water-storage containers for at least 3 months in the field under normal water-use practices.
Title: Procedures for the evaluation of field efficacy of slow-release formulations of larvicides against *Aedes aegypti* in water-storage containers

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Language: English

Abstract: In Thailand, water-storage jars, barrels, drums, pails, and tanks constitute vast developmental sites for *Aedes aegypti* in urban, semiurban, and rural areas. Earthen water jars, cement jars, and concrete tanks constitute the greatest proportion of artificial containers where *Ae. aegypti* breed. This species is a major vector of the causal agents of dengue and dengue hemorrhagic fever, and vector control by larviciding is one of the main approaches to disease control. At present, temephos sand granules (SG) (1%) are used in large-scale community-based larviciding programs. Because of the use of this larvicide over the past 30 years, the likelihood exists that *Ae. aegypti* already has become resistant to this larvicide. To develop more options for control and make them available for use, we evaluated VectoBac tablets (*Bacillus thuringiensis* var. *israelensis* [Bti] 5%) and a new formulation of zeolite granules (ZG) of temephos (1%) and compared these formulations for efficacy with temephos SG (1%) in water-storage jars. In these tests, we used 48 identical glazed earthen water-storage jars (200-liter capacity) and developed quantitative sampling procedures for larvae, pupae, and pupal skins. Pupal skins were the easiest to count
and this technique was used for the 1st time for assessing emergence of adults in water-storage containers. Three water regimens were used: full jars, half-full jars, and full jars emptied half way and refilled weekly. The 3 formulations with 3 regimens of water were assessed over a period of 6 months. VectoBac tablets at the dosage of 1 tablet or 0.37 g per 50 liters of water provided excellent control for about 112 days in full water jars. In the other 2 water regimens, VectoBac gave excellent control for 90 days. The 2 temephos formulations at the operational rate of 5 g per 50 liters of water were equal in efficacy, yielding almost 100% control for more than 6 months. Unlike temephos SG, the temephos ZG had no objectionable odor. Both the temephos ZG and Bti tablets increased clarity of the water, a feature desired by the users. Lack of odor and depression of turbidity are important attributes of Bti tablets and temephos ZG.
Cockroaches are common insects found throughout the world, especially in the tropical regions. They are generally recognized as not only household pests but also pose a high health hazard to humans. Various aspects of cockroach control including chemical and non-chemical methods have been researched on an ongoing basis. Repellents against cockroaches are considered as one of alternatives to eliminate cockroaches from dwellings and other harborage places. Attempts have been made to find and develop cockroach repellents derived from plant extracts. We evaluated 20 essential oils extracted from various plants such as basil, black pepper, eucalyptus, galanga, guava, kaffir lime, etc., for repellency against two cockroach species: the American cockroach (*Periplaneta americana*) and the German cockroach (*Blatella germanica*). The experiments were carried out against adult cockroaches in the laboratory. It was found that the tested essential oils provided various degrees of repellency against cockroaches, ranging from 40 to 100%. The essential oil extracted from kaffir
limed leaves showed excellent activity, manifesting 100% repellency against both cockroach species. The essential oils providing high degrees of repellency (>80%) were subsequently formulated as cockroach repellents and tested against cockroaches in the field. Data from both laboratory and field tests will be presented.

2004-26

Title: Novel mosquito repellents derived from essential oils of plants in Thailand

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Source: Presented in the XXII International Congress of Entomology, Brisbane, Australia, 15 – 21 August 2004

Language: English

Abstract:

Mosquito-borne diseases, such as dengue, malaria and filariasis are serious public health problems in many countries, especially in the tropical regions of the world. These diseases are caused by pathogens that are transmitted to man through mosquito biting only, thus personal protection from mosquito bites is then considered as one of the strategies to prevent them. Efforts to develop alternatives to replace chemical repellents have been increasingly considered, including extracting and evaluating plant products for repellent activity. The development and use of locally available plant products showing repellent activity thus avails an alternative strategy for prevention of mosquito-borne diseases. In this study we evaluated and reported repellent effects of essential oils extracted from plants against 4 mosquito vectors: *Aedes aegypti*, *Ae. albopictus*, *Anopheles dirus* and *Culex quinquefasciatus* under laboratory conditions using human volunteers. The essential oils were extracted from various parts of 22 plant species, belonging to 10 families, and the oils were prepared as
10% solution in absolute ethanol and some additives. The essential oils showing high degree of repellency were subsequently formulated as topical repellents and tested against day- and night-biting mosquitoes under field conditions. The results obtained from both laboratory and field evaluations will be presented.

2004-27

Title: Quantitation of Epstein-Barr Virus DNA in Sera of Patients with Nasopharyngeal Carcinoma by Real-time PCR

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Language: English

Abstract: Presence of serum EBV DNA was determined in 92 NPC patients and 36 healthy controls by using real-time PCR. EBV DNA was detected in 66% of the patients (median concentration, 726 copies/ml), while it was not found in the healthy controls. Our results suggested that the serum EBV DNA was a highly specific marker for EBV-related NPC. Nevertheless, the amount of EBV DNA in patients with early disease stages was not significantly different from those with advanced disease (Mann Whitney U test, p> 0.05). This finding was different from what has been reported by previous investigators; thus, needed to be further explored.
Leptospirosis presents as a non-specific febrile illness with clinical features similar to other tropical diseases. Early diagnosis of leptospirosis would allow clinicians to initiate effective therapy sooner in the course of illness. Although many kits are available for rapid testing in the acute setting, data on use of these tests in the field compared to gold standard testing are limited. As part of a prospective observational cohort of febrile illness patients in two areas of Thailand, acute and convalescent serum and acute urine samples were collected. At the rural hospitals, sera were tested with Panbio Multi-SDLST (MULTI) and Thailand NIH latex agglutination test (LAT). MAT testing of paired sera, the gold standard for diagnosis of leptospirosis, was performed at Thai NIH as was blinded repeat LAT testing of 88 samples. Urine samples were tested for leptospiral antigen using Leptodot. Paired sera from 749 febrile patients were tested using MAT. Sixty-six febrile patients had a four-fold rise by MAT. These patients had clinical evidence of leptospirosis (conjunctival suffusion in 24% compared
to 7.2% of MAT – (<4x rise), p<0.01; elevated creatinine in 50% vs. 21%, p<0.01; elevated bilirubin in 26% vs. 9%, p<0.01) as well as compatible risk factors (water or mud exposure in 83% vs 49%, p<0.01; lower extremity cuts or abrasions in 42% vs. 25%, p=0.01). Sensitivity of rapid tests at the acute visit were as follows: MULTI 12%, LAT at hospital 6%, LAT at NIH 26%, Leptodot 20%. For the convalescent visit, sensitivity improved to 33% for LAT at the hospital, 78% at NIH, and 73% for MULTI. MULTI and LAT were 91-94% specific at each visit at the hospitals. LAT at NIH was 57% specific and Leptodot was 90% specific. MAT testing identified patients with clinical findings and risk factors compatible with leptospirosis. No rapid test had very good sensitivity at the acute visit. Quality control is important for accuracy of rapid tests.
Background: Undifferentiated febrile illnesses are a major cause of morbidity in children who reside in or travel to tropical countries. We sought to describe the causes and clinical discriminators of febrile illness in schoolchildren in 2 areas of rural Thailand.

Methods: Patients 7-18 years of age presenting with documented fever > 38°C without focal infection provided sera for testing at reference laboratories in Atlanta and Bangkok using Leptospirosis MAT, Dengue EIA, and S. typhi dot-ELISA.

Results: Of 342 schoolchildren enrolled, 339 (99%) provided convalescent sera. Testing to date has identified dengue in 112/328 (34%), typhoid fever in 60/315 (19%), and leptospirosis in 10/208 (5%). Schoolchildren with dengue were more likely to have a rash (28% vs. 14%, p<0.01), as well as leukopenia (50% vs. 15%, p<0.01), thrombocytopenia (29% vs. 10%, p<0.01), and elevated SGOT (26% vs 7%, p<0.01). Those with typhoid fever more often had vomiting (56% vs 41%, p=0.04) and lymphadenopathy (28% vs. 17%, p=0.05) than those with other causes of fever; bloody
diarrhea, rose spots and hepatosplenomegally were infrequent (0-2%) in all patients. Schoolchildren with leptospirosis more commonly had elevated alkaline phosphatase (72% vs. 33%, p<0.01), bilirubin (45% vs. 6%, p<0.01), and creatinine (27% vs. 6%, p<0.01).

**Conclusions:** Dengue was the most important cause of fever among this group of schoolchildren in Thailand; typhoid may be important, but further microbiologic investigations are indicated. Basic clinical and laboratory findings can help to discriminate between major pathogens. Severe headache and cytopenias indicate dengue infection, vomiting and lymphadenopathy point to typhoid fever, and elevated alkaline phosphatase, bilirubin and creatinine are seen in leptospirosis.
Title: Development of a Simple Strip Test for the Detection of Hepatitis B Surface Antigen

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Language: English

Abstract:

Hepatitis B surface antigen simple strip test has been developed by using the locally produced monoclonal antibody and compared with commercial ELISA test (ABBOTT Laboratories). One thousand serum samples, 500 positives and 500 negatives, diagnosed with commercial ELISA (ABBOTT) by the National Blood Bank Center of Thai Red Cross Society were used for method comparison with the developed strip test and also commercial strip test (ABBOTT). The comparative results with the commercial ELISA test showed that the developed simple strip test had a sensitivity of 90% and specificity of 99.6%. While the commercial rapid test (ABBOTT) had a sensitivity of 94.6% and the specificity of 100% when compared with the commercial ELISA test. Due to the advantages of the simple strip test which were simple, convenience to perform, easily to interpret, the test could be used in small scale laboratory or applied to use as a tools to study in Hepatitis B virus epidemiology.
Establishment of Cytotoxic T Lymphocytes Specific for Autologous Epstein-Barr Virus in HIV-Infected Patients: The Feasibility Study of EBV-Specific Immunotherapy for Patients with EBV-Associated Lymphoma

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Journal of Medical Association of Thailand 2004; 87(suppl 2): S146-51

Cytotoxic T lymphocytes specific for Epstein-Barr virus (EBV) have previously been successfully used in immunotherapy of Posttransplant lymphoproliferative disease (PTLD) and Hodgkin’s disease. A similar strategy has never been employed in HIV/AIDS patients who also have high risk of developing EBV-associated lymphoma. A total of 5 HIV-infected patients were enrolled to evaluate their EBV-specific T cell responses by Interferon-gamma (IFNg) ELISpot assays. Most patients had detectable T cell responses, mainly directed at Epstein-Barr nuclear antigen (EBNA-3). The authors wanted to see whether it was possible to augment magnitude and spectrum of the EBV responses by stimulating patient PBMC with cells presenting autologous EBV antigens. The authors successfully established spontaneously EBV-transformed lymphoblastoid cell lines (EBVh-BCL) and used them for generation of EBV-specific CTL (EBV-CTL). The EBVh-CTL lines established in the present study were not only highly cytotoxic against the autologous virus but also able to secrete...
IFNg detected by ELISpot. The authors are now in the process of generating these lines in a large number and in a clinical grade for adoptive immunotherapy.

2004-32

Title: Molecular epidemiology of enterovirus 71 infection in the Western Pacific Region

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Source: Pediatrics international 2004; 46: 231-235

Language: English

Abstract:

Background: recently, there have been large outbreaks of hand, foot and mouth disease (HFMD) mainly caused by enterovirus 71(EV71) associated with severe neurological disease in the Western Pacific Region (WAR). To monitor the realtime trend of EV 71 transmission throughout the WPR, the authers conducted a molecular epidemiological analysis of EV71 infection.

Methods: Viruses were isolated from clinical sample from patients with HFMD of those with neurological complications. The EV71 isolation were identified by microneutralization assay. The VP4 and/or VP1 regions of recent EV71 isolates were sequenced and subjected to phylogenetic analysis using reference EV71 strains.

Result: The phylogenetic analysis of EV71 isolated from the WPR revealed two major genogroups, B and C, base on the nucleotide sequence alignment of the VP1 or VP4 region. These two major genogroups were further divided into subgenogroups, B1, B2, B3, and B4 and C1, C2, C3 and C4, respectively.

Conclusion: the molecular epidemiological analyses of recent and previous EV71 isolates in the WPR indicated that two major genogroups of EV71 are co-circulating in Australia, Malaysia, Singapore, Taiwan
and Japan. Recent EV71 isolates in Mainland China constitute a new distinct genetic cluster, subgenogroup C4. Two major lineage of EV71 are the major causative agents of the present HFMD epidemics in the WPR and both are considered to be neurovirulent.

2004-33

**Title:** First Report from the Asian Rotavirus Surveillance Network


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**Source:** Emerging Infectious Diseases 2004; 10(6): 988-995

**Language:** English

**Abstract:**

Rotavirus remains the most common cause of severe, dehydrating diarrhea among children worldwide. Several rotavirus vaccines are under development. Decisions about new vaccine introduction will require reliable data on disease impact. The Asian Rotavirus Surveillance Network, begun in 2000 to facilitate collection of these data, is a regional collaboration of 36 hospitals in 9 countries or areas that conduct surveillance for rotavirus hospitalizations using a
uniform World Health Organization protocol. We summarize the Network’s organization and experience from August 2001 through July 2002. During this period, 45% of acute diarrheal hospitalizations among children 0-5 years were attribution to rotavirus, higher than previous estimates. Rotavirus was detected in all sites year-round. This network is a novel, regional approach to surveillance for vaccine-preventable diseases. Such a network should provide increased visibility and advocacy, enable more efficient data collection, facilitate training, and serve as the paradigm for rotavirus surveillance activities in other regions.
Stool specimens collected between November 2002 and April 2003 from hospitalized infants with acute gastroenteritis from four distinct geographical regions in Thailand were examined for norovirus (NoV) and sapovirus (SaV) by reverse transcription-PCR and sequence analysis. Of the 80 specimens examined, we identified 11 NoV and 9 SaV single infection, and 3 NoV/SaV mixed infections. The majority of NoV strains (64%) belonged to genogroup II/genotype 4 (GII/4; Lordsdale cluster). Other NoV strains co-circulating belonged to GII/1, GII/3, GII/6, and one new genotype cluster (GII/New). The majority of SaV strains (83%) were from the Manchester cluster. One isolated SaV strain represented a recently discovered novel genogroup within the SaV genus (SG-V), and another isolated SaV strain represented a novel SaV genogroup II cluster.
Title: Cloning and characterization of the gene encoding the z66 antigen of Salmonella enterica serovar Typhi


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Source: FEMS Microbiology Letters 2004 May 15; 234(2): 239-46

Language: English

Abstract:

Z66 antigen-positive strains of Salmonella enterica serovar Typhi change flagellin expression in only one direction from the z66 antigen to the d or j antigen, which is different from the phase variation of S. enterica serovar Typhimurium. In the present study, we identified a new flagellin gene in z66 antigen-positive strains of S. enterica serovar Typhi. The genomic structure of the region containing this new flagellin gene was similar to that of fljBA operon of biphasic S. enterica serovars. A fljA-like gene was present downstream of the new flagellin gene. A rho-independent terminator was located between the new flagellin gene and the fljA-like gene. Hin-like gene was not present upstream of the new flagellin gene. We generated a mutant strain of S. enterica serovar Typhi, which carries a deletion of the new flagellin gene. Western blotting revealed that the 51-kDa z66 antigen protein was absent from the population of proteins secreted by the mutant strain. Southern hybridization demonstrated that the z66 antigen-positive strains of S. enterica serovar Typhi carried the new flagellin gene and fliC on two different genomic EcoRI fragments. When z66 antigen-positive strains were incubated with anti-z66 antiserum, the flagellin expression by S. enterica serovar Typhi changed from z66 antigen...
to j antigen. The new flagellin gene and the fljA-like gene were absent in the strain with altered flagellin expression. These results suggested that the new flagellin gene is a fljB-like gene, which encodes the z66 antigen of *S. enterica* serovar *Typhi*, and that deletion of fljBA-like operon may explain why *S. enterica* serovar *Typhi* alters the flagellin expression in only one direction from the z66 antigen to the d or j antigen. Copyright 2004 Federation of European Microbiological Societies

*Title:* Prospective population-based incidence of *Haemophilus influenzae* type b meningitis in Thailand


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*Source:* Vaccine 2004 Feb 25; 22(8): 975-83

Comment in:
- Vaccine. 2005 Apr 15;23(21):2687-8

*Language:* English

*Abstract:*

There are limited prospective data for Haemophilus influenzae type b (Hib) disease in Asia, where some countries are considering vaccine introduction. A prospective population-based study was conducted to measure the incidence of Hib meningitis in children in two northern provinces of Thailand. Children <5 years with symptoms consistent with bacterial meningitis were enrolled in the study if inclusion criteria were met. The study enrolled 598 children with clinical meningitis, 76% of whom received lumbar puncture. The rate of probable bacterial meningitis was 26.6/100,000 children <5 years per year. There were four cases of laboratory confirmed Hib meningitis (rate 3.8/100,000 children <5 years per year). These findings suggest a relatively low incidence of Hib meningitis. However, additional data from studies of pneumonia are needed to define the Hib disease burden in Thailand.
Detection of gamma-glutamyl transpeptidase (GGT; ggt ) activity is one of the useful methods for a specific identification of Neisseria meningitidis. However, we previously happened to isolate a ggt -deficient N. meningitidis strain (NIID113) from a healthy carrier. In this study, in order to re-examine the reliability of the marker, we again investigated the GGT activity of 245 N. meningitidis human isolates and identified two other GGT-defective N. meningitidis isolates besides NIID113. The isolation frequency (1.2%) of ggt mutants among human isolates strongly confirmed the 98.8% reliability of GGT activity as the identification marker for N. meningitidis.
We serotyped 44,087 *Salmonella* isolates from humans and 26,148 from other sources from 1993 through 2002. The most common serovar causing human salmonellosis in Thailand was *Salmonella enterica* Weltevreden. Serovars causing human infections in Thailand differ from those in other countries and seem to be related to *Salmonella* serovars in different food products and reservoirs. *Salmonella enterica* is one of the most common causes of human gastroenteritis. The infection is caused primarily by improper handling and digestion of uncooked food; a large number of food animal sources have been identified as reservoirs of the bacteria (1). More than 2,500 serovars of *S. enterica* have been identified; most have been described as the cause of human infections, but only a limited number of serovars are of public health importance. *S. enterica* serovars Typhimurium and Enteritidis have been reported to be the most common causes of human salmonellosis (1,2). However, in some regions other serovars are of greater importance (3,4). Different serovars in one country can be of global importance.
because of travel and animal and food product trade. Knowledge about the occurrence and epidemiology of different serovars in different countries and geographic regions may assist in the recognition and tracing of new emerging pathogens. We review the trends in serovars of *Salmonella* causing infections in humans and potential reservoirs in Thailand during 1993 to 2002.

**2004-39**

*Title:* Improving Public Health Practice Activities of the WHO Global Salm-Surv Asian Regional Center

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*Source:* International Conference on Emerging Infectious Diseases 2004: 67

*Language:* English

*Abstract:*

**Background:** The Center for Antimicrobial Resistance Monitoring of Foodborne Pathogens in Thailand (ARM-Asia) was established with the cooperation of the World Health Organization (WHO) in 1999. The Center’s objectives were to establish a laboratory for antimicrobial resistance monitoring of foodborne pathogens, support standardization of antimicrobial susceptibility testing in important foodborne pathogens isolated from food-animal and food of animal origin in Asian Counties, and assist in development of sustainable national policy for prudent use of antimicrobials in food-animals. In the year 2000, ARM-Asia became part of WHO Global Salm-Surv (WHO-GSS), a network created to improve laboratory capacity and decrease the burden of foodborne illnesses worldwide, and later became an official WHO Global Salm-Surv Regional Center.

**Methods:** Though not an official Regional Center when the courses began, WHO-GSS International Training Courses have been held in Asia since 1999. The training courses in Asia have been
successfully completed with the collaboration of WHO, Geneva, Switzerland; Danish Veterinary Institute (DVI), Denmark; Centers for Disease Control and Prevention (CDC), USA; and Animal Sciences Group (ID-Lelystad), the Netherlands. These training courses are a main activity for the Regional Center. **Results:** Since 1999, five regional training courses have been hosted by AMR-Asia (Figure 1) with participants from Cambodia, China, India, Indonesia, Korea, Laos, Myanmar, Malaysia, Nepal, Papua New Guinea, Philippines, Sri Lanka, Vietnam, Singapore, and/or Thailand. **Conclusions:** The future goals for the WHO Global Salm-Surv Asian Regional Center include continuing to supply *Salmonella* antisera to regional WHO-GSS Asian members, being established as a Reference Laboratory for Salmonella serotyping, and serving as a sub-station of EQAS (External Quality Assurance System). Additionally, the Regional Center will be conducting a National Program for Antimicrobial Resistance Monitoring in Foodborne Pathogens and a National Program for Promoting Prudent Use of Antimicrobial Drugs in Food-Animals.
Since 1998, pathogen reduction regulations for poultry have been enforced through the Food Safety and Inspection Service of the U.S. Department of Agriculture and through hazard analysis critical control point evaluation. This enforcement has focused attention on pathogen control and sanitation in the United States and in other countries, including Thailand. The objective of this study was to evaluate reduction in salmonellae achieved by Thai commercial exporters of frozen broiler chickens. A total of 188 broiler samples and 56 water overflows from two chillers were collected from nine processing lines of frozen broiler exporters at four identified critical control points (CCPs): CCP1, washing; CCP2, chilling; CCP3, deboning; and CCP4, packing. Samples were screened for salmonellae by enzyme-linked immunosorbent assay, and bacterial identification was confirmed through biochemical and serological
patterns. The overall prevalence of Salmonella was 24.6% (60 of 244 samples), with 12 serovars identified. Salmonella Albany was predominant (33.3%, 20 of 60 samples). Salmonella prevalence was 20.0% (6 of 30 samples) prior to CCP1 and was 12.5% (4 of 32), 22.7% (15 of 66), 33.3% (10 of 30), and 23.3% (7 of 30) after CCP1, CCP2, CCP3 and CCP4, respectively. The critical limit was 20% positive samples, and three CCPs failed to meet standards. Three corrective interventions were used at CCP2: 30 mg/liter hydrogen peroxide, 0.5% peracetic acid, and 125mg/liter ozone. After these interventions, 65 broiler samples were collected for analysis of Salmonella prevalence. Results were compared with those obtained after chlorine was applied individually as a control. The Salmonella prevalences after intervention treatments were 16.0% (4 of 25), 5.0% (1 of 20), and 15.0% (3 of 20) after hydrogen peroxide, peracetic acid, and ozone treatments, respectively. All values were below the 20% critical limit, and the application of 0.5% peracetic acid produced significantly lower prevalences (P<0.05). Repeated sampling after 1 to 4 months indicated that saititation at these three plants was inconsistent (P<0.05).
Sir—While management of asymptomatic food workers who are non-typhoidal salmonella (NTS) carriers needs additional convincing evidence, there is inadequate information about duration of excretion of NTS in healthy asymptomatic adults. We found in our previous report that 98.8% (254/257) of the asymptomatic adult NTS excretors had eradicated their initial NTS infection at the first bacteriologic assessment (day 12 after a positive screening culture), [1] which was a shorter time than an earlier study had reported. [2] An examination of 32 studies including 2,814 patients who were observed after being diagnosed with salmonella infection showed that median duration of NTS excretion was approximately five weeks, and that the duration of convalescent salmonella carriage varies with host factors, salmonella serotype, patient’s entry point, and criteria used for determining salmonella eradication. [2] We had an opportunity to confirm our finding during a preparation for Asia Pacific Economic Cooperation Forum in Bangkok 2003. A
screening for NTS carriers was performed by rectal swab culture in asymptomatic adult hotel workers. Hygienic education about enteric infection and prevention of spreading was given to all participants at the beginning of the study. A repeated rectal swab culture was performed in the initial NTS carries 21-28 days after the first culture. Microbiological methodology was the same as in our previous study. [1]

Three thousand asymptomatic adults from 16 hotels in Bangkok were include, 142 (4.7%) had *Salmonella* spp. isolated from a rectal swab culture. Eleven (7.7%) of the 142 initial NTS carriers had salmonella detected in the second rectal swab culture; none had the initial *Salmonella* serotype which indicates 100% elimination rate of the initial *Salmonella* spp. Detection of the new *Salmonella* serotypes in the 11 initial NTS carriers indicates new infection. None of the NTS carries were treated with an antimicrobial drug before the second culture. Our previous finding (that there was no benefit of antimicrobial therapy for adults NTS carriers) [1] was implemented; therefore, no antimicrobial drug was given to any adult salmonella carrier detected by this surveillance. They were assigned to work without food contact until a negative culture was obtained. The short duration of NTS excretion of healthy adults asymptomatic carriers, whose onset of NTS infection is unknown, is confirmed by this study.

Routine rectal swab culture and giving an antimicrobial drug to salmonella carriers is still a common practice in several parts of the world. Evidence of short duration of NTS excretion and no benefit of antimicrobial treatment [1,3] lead to a strong recommendation against microbiological screening and antimicrobial therapy, but for regular education and support for hygienic practice of workers.
Food pathogens in ready-to-eat traditional Thai fermented products
(Fermented shrimp, Fermented Crab and Fermented fish)

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Food Journal (1) January – March 2004

Abstract:

Three hundred samples of Thai traditional fermented products [34 samples of fermented shrimp, 66 samples of fermented fish (pla-jom), 100 samples of fermented fish (pla-ra) and 100 samples of fermented crab] sold in retailed markets around Bangkok and Nonthaburi were investigated for pH, salt percentage and pathogenic microorganisms such as Salmonellae, Shigellae, Escherichia coli O157 : H7, Vibrio cholerae, V. parahaemolyticus, Staphylococcus aureus and Bacillus cereus. The results revealed that the average pH of fermented shrimp, fermented fish (pla-jom), fermented fish (pla-ra) and fermented crab was 4.02, 4.26, 4.79 and 7.44 respectively, while the average salt percentage from each aforementioned fermented product was 8.06, 8.75, 14.85 and 15.23 respectively. Results in detection of pathogenic microorganisms from the products indicated that 21 samples (7.00 %) were found contaminated with food pathogens. Among these positive pathogenic microorganisms samples, Salmonellae revealed to be the most detectable pathogen of these fermented products (3.00 %)
[from one sample of fermented shrimp (S. Paratyphi B var. java), one sample of pla-ra (S. Rissen), 3 samples of pla-jom (S. Bredeney, S. Hadar and S. Hvittingfoss) and 4 samples of fermented crab (S. Hvittingfoss, S. Stanley, S. Braederup and S. enterica subsp. enterica 41:b:-), following by V. parahaemolyticus (2.67 %) [from 6 samples of fermented crab and 2 samples of pla-jom] and B. cereus (1.33 %) [from 3 samples of fermented shrimp and one sample of pla-ra]. Shigellae, V. cholerae, S. aureus and E. coli O157 : H7 were not detected in any of these samples. The pH of Salmonellae, V. parahaemolyticus and B. cereus positive samples was between 4.11 – 7.88, 4.11 – 4.48 and 3.79 – 4.86 respectively, and the salt percentage of each pathogenic positive samples was between 1.37 – 16.89, 3.27 – 17.41 and 6.69 – 17.17 % respectively. Determination of antimicrobial susceptibility of contaminated gram positive pathogens against a panel of 9 antibiotics implied that all detected serovar of Salmonellae and all strains of V. parahaemolyticus were sensitive to most of studied antimicrobial agents except S. Hadar resisted to Nalidixic acid and Tetracycline, S. Braenderup resisted to Nalidixic acid, Tetracycline and Co-trimoxazole, and all detected strains of V. parahaemolyticus resisted only to ampicillin.
2004-43

Title: Consistency of Identification of Pseudomonads and Related Organisms


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Source: Present at the ASM Annual Meeting 2004

Language: English

Abstract:

Those wanting identification of unknown bacteria need to know the reproducibility of identifications, especially to determine possible pathogenicity. One way to evaluate reproducibility is to distribute identical cultures to independent laboratories for analysis. Sponsored by Health Canada, 8 laboratories studied 300 isolates of Pseudomonas, Burkholderia and related genera (of medical and ecological interest) to support regulatory determination of potential hazard. The laboratories vary in mission, methodologies, and location. A distributing laboratory sent randomly encoded cultures
to each laboratory. Using their normal methods, each laboratory submitted best estimates of the identities of the isolates with supporting data. We created databases of genera, species, subspecific identifications; identification failures; and the primary data. We report 1) the proportion of laboratories with the same identification by isolate and 2) for 20 isolates sent in duplicate, the proportion of agreement by laboratory and by isolate. The modal best estimates comprised the species names for calculation of the average consistency. Consistency of reported identification varied widely with taxon. The 46 species averages, with at least 2 laboratories agreeing, spanned 88% (P. aeruginosa) to 50% (16 species) and 49% to 25% (30 species). The intra-lab consistency for the duplicate isolates spanned 75% to 45%. Consistency/isolate was 100% to 25%. However, 80% of modal names assigned to the duplicates agreed. The data demonstrate two overlapping classes of isolates, those consistently identified and those not, largely regardless of the methods used. Identifications based on multiple methods usually were more consistent than single methods. We found no “gold standard” for validating the identifications. The boundaries of the taxa are unknown (unknowable?). From the data and the rules of nomenclature, we conclude there is no absolute measure of the “correctness” of an identification. Only consensus and usage dictate correctness. The underlying taxonomy is continually in flux which further confounds identification reporting.
Identification of type cultures belonging to the Pseudomonas and related organisms by a cooperative double blind study

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Present at the ASM Annual Meeting 2004

Type strains have always been regarded as standards for the bacterial species they represent. They are usually well characterized, and thus are frequently used for comparison between species as well as nomenclature and taxonomy studies. Sponsored by Health Canada, we conducted a three year international double blind study of 300 isolates from bacterial taxa important in biotechnology: Pseudomonas (Ps.), Burkholderia (B.) and closely related genera. Among them were twenty five type cultures obtained from Belgian Coordinated Collection of Microorganisms (BCCM/LMG) and American Type Culture Collection (ATCC). Eight independent laboratories used eighteen different methods for identification; these included traditional phenotypic and biochemical tests, commercial identification kits (API and BIOLOG), Polyacrylamide Gel Electrophoresis (PAGE), Fatty Acid Methyl Ester analysis (FAME), and 16S rRNA sequencing. The accuracy of identification was organism-specific, varying from 83% to less than 10%. Type cultures of Ps. aeruginosa, Stenotrophomonas maltophilia, Ralstonia pickettii and Ps. luteola were correctly identified by more than 80% of the methods/participants. Commercial ID kits performed well for members of the B. cepacia complex. Overall, PAGE gave the best identification for all the type strains, followed by BIOLOG. Traditional
characterization methods identified Ps. tolaasii and Ps. corrugata poorly, but PAGE compensated for these species. Most of the time type cultures were better identified than other strains within the same species. It is interesting to note the type strain of B. vesicular was our worst case of misidentification. However, 14 out of the 18 tests used in this study indicated it as Achromobacter xylosoxidans. Thus, further investigation is needed to resolve the status of B. vesicular type strain.

2004-45


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Source: Poster presentation in The 9th Western Pacific Congress on Chemotherapy and Infectious Diseases (9th WPCCID) “Regional Infectious Disease Problems of Global Concern” December 1-5, 2004. Queen Sirikit Convention Center, Bangkok, Thailand. Program & Abstracts page 185

Language: English

Abstract:

Introduction: Limited data is available concerning the prevalence and resistant patterns of gram-negative bacilli (GNB) causing bloodstream infections (BSIs) in Thailand.

Objective: To report the National Susceptibility Data of 7 most common GNB causing BSIs submitted to the National Antimicrobial Resistant Surveillance Center, Thailand (NARST) from 2000-2003.

Methods: Data of antimicrobial susceptibility patterns of 7 most common GNB causing BSI collected from 33 hospitals 2000 to 2003 were reviewed. At each hospital laboratory, bacterial cultivation and identification were performed using of standard conventional methods. Antimicrobial disk susceptibility test and interpretation were according to the National Committee for Clinical Laboratory Standards (NCCLS). Patient data and inhibition
zone in mm. were input in WHONET software and sent to the National Institute of Health, Thailand for analysis.

**Results:** Of 25,459 BSI isolates, the prevalence of 7 most common GNB were *Escherichia coli* 43.8%, *Klebsiella pneumoniae* 20%, *Pseudomonas aeruginosa* 19.6%, *Salmonella* non-typhi 8.7%, *Acinetobactor baumannii* 7.1%, *Burkholderia pseudomallei* 7% and *Enterobacter cloacae* 3.4%. Resistance of the Enterobacteriaceae species to most of the commonly prescribed first line antimicrobials in Thailand, such as, ampicillin (98% in *K. pneumoniae*, 72% in *E. coli*), gentamicin (21% in *K. pneumoniae*, 15% *E. coli*), and co-trimoxazole (59% in *E. coli*, 32% in *K. pneumoniae*) was high. Resistant to certain broad-spectrum antimicrobials, such as, ESBL producing *K. pneumoniae* (33%), ESBL producing *E. coli* (15%), ceftazidime resistant *A. baumannii* (44%), ciprofloxacin resistant *E. coli* (21%), and imipenem resistant *A. baumannii* (16%) was high. There is a trend of increased resistance of these selected microorganisms over time. Differences in geographic regions were associated with certain forms of resistance.

**Conclusions:** Antimicrobial resistance among gram-negative bacilli causing bloodstream infections is prevalence in Thailand. Attempt should be made to control for antimicrobial utilization and to develop a better surveillance system for the country.
Title: Genotypic Identification and Antimicrobial Susceptibility of *Acinetobacter* isolated in Thailand


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Source: Poster presentation in The 9th Western Pacific Congress on Chemotherapy and Infectious Diseases (9th WPCCID) “Regional Infectious Disease Problems of Global Concern” December 1-5, 2004. Queen Sirikit Convention Center, Bangkok, Thailand. Program & Abstracts page 203

Language: English

Abstract:

**Introduction:** Acinetobacter spp. have been ranked as the most top five isolates from clinical specimens for at least 7 consecutive years. Routine identification in hospitals is limited by few phenotypic tests (conventional biochemical tests) and reported in non-standardized phenotypic names—not in the recent 21 genomospecies (gsp.). Lack of gsp. information prevented detailed examination of epidemiology as well as antimicrobial susceptibility by species.

**Objective:** (1) To report the susceptibility data of Acinetobacter spp. by gsp. (2) To examine the trend of antimicrobial resistance of each gsp. by years.

**Methods:** One hundred and fifty eight strains of *Acinetobacter* spp. were randomly selected from Department of Medical Sciences, Thailand-Culture Collection (DMST-CC). These isolates were received during 1980-2004 from 28 hospitals located in various regions of Thailand. They were originally identified by
conventional biochemical test and in this study by PCR-RFLP technique using primers amplifying recA gene and subsequently digested 426 bp of PCR product with TasI restricted enzyme. The susceptibility against 15 antimicrobial agents were determined by standardized disk diffusion and agar dilution technique as described by the National Committee for Clinical Laboratory Standards (NCCLS).

**Results:** Of 158 *Acinetobacter* isolates, 61 originally labeled as *A. baumannii* by conventional biochemical test was identified as gsp.2 (*A. baumannii*) 49 strains (71%), TU13 =10 (15%), gsp.3 =5 (7%), gsp.10 =1 (1%), gsp.5 =1 (1%), and unidentified =4(6%). Out of 158 isolates 109 (75%) could be identified by PCR-RFLP into 11 gsp. as follows: *A. baumannii* =49 isolates, *A. junii* =21, TU13 =16, gsp.3 =15, close to TU13 =8, *A. haemolyticus* =3, gsp 8 =2, gsp.10 =2, gsp.1 =1, gsp 6 =1, TU14 =1 isolate. On the basis of genotypic identification (PCR-RFLP), *Acinetobacter* identified as *A. baumannii* was the only gsp. which resistant to imipenem (8%). All isolates of other gsp. are susceptible to imipenem. *A. baumannii* is resistant to other 14 drugs in the range of 24-78%. Besides imipenem, *A. baumannii* has lowest resistance against ampicillin-sulbactam at the percentage of 24. Gsp.3 and gsp. TU13 which are 2 of 6 gsp. in *A. calcoaceticus-baumannii* complex (*Acb cpx*) were resistant to 15 drugs at the rate 0-80 and 0-63% respectively. Gsp.5 (*A. junii*) which was the most prevalence among none *Acb cpx* has low rate of resistant to 15 drug at the range of 0-14%. In the two different periods of 1980-1999 and 2000-2004, resistance of *A. baumannii* against 15 drugs was increased at the rate of 5-27% whereas *Acinetobacter* of all other gsp. were at the rate of 3-14%.

**Conclusions:** Antimicrobial resistance among *Acinetobacter* is dependent on genospecies. To obtain the accurated trend and rate of antimicrobial susceptibility result in a surveillance study, these group of organisms should be definitely identified to genospecies.
National Antimicrobial Resistant Surveillance (NARST) was established in the Thai-National Institute of Health (Thai-NIH) since 1998 under the sponsorship of World Health Organization and Thai Ministry of Public Health for the purpose of systematic collection, analysis, interpretation and dissemination of reliable information for planning, implementation and evaluation of public health practice.

Thirty three hospitals located in every region of Thailand participate in the program. The activities are directed by Steering Committee and consulted by the Technical Subcommittee which consists of experts from relevant fields. Technical workshop and/or seminar are regularly organized for the participants at least once a year, in order to maintain laboratory quality standards and performance. The data from each hospital are collected by the Thai-NIH and analyzed using WHONET software. After analysis, the information is
disseminated country-wide by means of brochure, annual report, and through the website: http://narst.dmsc.moph.go.th.

In 2002, the 156,104 records of the routine isolation from 29 hospitals were analysed. The result shows that 30% of *Staphylococcus aureus* are MRSA which is higher when compared to the 24% in 1998. *Streptococcus pneumoniae* isolated from sterile site has lower resistant to penicillin (33%) than from nonsterile site (48%) whereas pneumococci isolated from children <= 5 years old is higher resistant to penicillin (61%) than patients aged more than 5 (41%). The rate of PRSP in patients aged more than 5 is steady since 1998 but PRSP isolated from children age <=5 increasing significantly from 46% in 1998 to 61% in 2002. Among common isolates of gram-negative bacteria *Pseudomonas aeruginosa* and *Acinetobacter* spp. have relatively higher resistant to imipenem. Imipenem resistant *P. aeruginosa* was increasing slowly from 10% in 1998 to 13% in 2002 while imipenem resistant *Acinetobacter* spp. was increased sharply from 2% in 1998 to 19% in 2001.

Resistant rates in Thailand are high. Resistant Surveillance Network from each country is essential and inter-country network is needed in order to have a global cooperation to combat the resistant problem.
**Title:** Study of Nature Hot Springs in Southern Thailand


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**Source:** Intern Med J Thai 2004; 20: 277-281

**Language:** English

**Abstract:**

Water samples collected from nature hot spring and their annexes in nine provinces in southern Thailand during the period January – June 2004 were examined for dissolved radon gas and pathogenic organisms. High levels of dissolved radon gas, especially in Suat Thani and Chumphorn provinces, and *Legionella* spp. (esp. *pneumophila*), *Naegleria* spp. and *Acanthameba* spp. were present in hot spring water obtained from most of the provinces investigated.
2004-49

**Title:** Study of Nature Hot Springs in Central Thailand

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**Source:** Intern Med J Thai 2004; 20: 304-307

**Language:** English

**Abstract:**

Water samples collected from nature hot spring in Lop Buri, Petchabun, Kamphangphet, and Uthai Thani during the period May – August 2004 were examined for dissolved radon gas and pathogenic organism. Tests revealed the presence of radon gas in all specimens, some of which exceed the safety limit, and the presence of *Legionella* spp., *Naegleria* spp. And *Acanthameba* spp. in sample collected from some hot spring.
Surveys for potential hazards in nature hot springs, carried out in Chonburi and Chanthaburi, as representatives of the eastern provinces of Thailand, yielded positive results for pathogenic Legionella organism growth in both sites; other parameters examined were not remarkable.
Title: Study of Nature Hot Springs in Nakorn Si Thammarat and Surat Thani Provinces


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Language: English

Abstract:

Surveys for potential hazards in nature hot spring in Nakorn Si Thammarat and Surat Thani provinces revealed the presence of Legionella pneumophila and Pathogenic free-living amebas Naegleria and Acanthameba; radon gas ubiquitous in hot spring waters, with extremely high level encountered in certain specimens obtained from Surat Thani province.
Water specimens were taken from 18 natural hot springs in four northern provinces of Thailand, namely, Mae Hong Son, Chiang Mai, Chiang Rai, Lampang, and sent to the laboratories of the National Institute of Health, Department of Medical Science, Ministry of Public Health in Nonthaburi for determining the presence of the legionella organism and free-living ameba. *Legionella pneumophila* serogroup 6 was isolated from a water specimen collected in Mae Hong Son province; ameba was not isolated from any of the specimens. There was a clue suggesting that temperatures of the hot spring water might play an influential role in the existence of viable pathogenic organisms.
In Rachaburi Province, there are two significant natural hot spring: Boe Klueng in Suan Pueng district and Baan Pu Namron in Baan Ka subdistrict. On November 30, 2003, a pollution survey conducted at both sites revealed the presence of dissolved radon gas in water samples as high as 170,794.99 and 23621.69 becquerels/cubic meter, respectively (safety threshold is 400,000 becquerels/cubic meter), while simultaneous measurements of gamma ray exposure and atmospheric radon gas in the vicinity of those sites showed gamma radiation intensity of 40 and 23.5 mR/h, respectively (normal background intensity does not exceed 20 mR/h) and radon gas ranges of 39.36-53.59 and 31.40-46.74 becquerels/cubic meter, respectively (safety level : 148 Bq.m³) ; and revealed the presence of *Legionella pneumophila* organisms in water samples from both...
hot spring source, i.e., serogr. 13 at Boe Klueng’s bathing pond, and serogr 7 and seroogr 6 in water samples from the main hot spring and bathing tanks respectively at Baan Pu Namron. Worthy of note is that the same group of researchers had succeeded in detecting leionell organism in one of natural hot spring in Mae Hong Son province. The present authors intend to carry on further survey in order to identify the hazards in natural hot spring in the Kingdom.

2004-54

Title: Clinical and Epidemiological Predictors of Leptospirosis in Acute Febrile Illnesses Patients

Authors: Rungrueng Kijphati*, Wimol Petkanchanapong*, Piyada Wangroongsarb*, Supraluk Yasang*, Pimjai Naigowit*, Pathom Sawanpanyalert*

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Source: Bulletin of the Department of Medical Sciences 2004; 46(1): 1-15

Language: Thai with English abstract

Abstract: The purpose of this study is to determine the clinical features and epidemiological factors suggesting the diagnosis of leptospirosis among patients with acute febrile illnesses in the endemic area of Thailand using the data from laboratory request form. One hundred and sixty-three illnesses were diagnosed as leptospirosis (76 cases) and non-leptospirosis acute febrile illnesses (87 cases) used leptospirosis diagnosis criteria. Clinical features and epidemiological factors were analyzed by univariate analysis. Unconditional multivariable logistic analysis was used for controlling variables and developing logistic equation to estimate the probability of leptospirosis among acute febrile illnesses patients. The epidemiological risk factor strongly associated with the illness of leptospirosis was the working in the moisture area without wearing the boots. Other symptoms associated with the illness were suffusion conjunctivitis and hemoptysis. Patient who had the epidemiological history and clinical manifestations of
suffusion conjunctivitis and hemoptysis had the highest of predictive value. Good planning in collecting patient data in the laboratory request form was useful for a study to suggest the probability of the disease based on epidemiological, clinical and laboratory information.

2004-55

Title: Blood Lead Level of Traffic Police in Bangkok Before and After the Unleaded Gasoline Usage Policy

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Source: Bulletin of the Department of Medical Sciences 2004; 46(1): 16-24

Language: Thai with English abstract

Abstract:

Since lead has been recognized its toxicity to human health, the national phase out of lead in gasoline by the Royal Thai Government has been done in 1996. However blood lead level in the high risk groups have to be monitored. A survey on blood lead levels (BLLs) of 810 traffic policemen in the Bangkok Metropolitan area had been done during 8-22 November 2000 by Graphite Furnace Atomic Absorption Spectrometry. The average BLLs was 5.49 ± 2.48 µg/dl. Then, this studied demonstrated relationship between before and after unleaded gasoline usage policy. The data collection specific 3 police stations, 53 traffic policemen compared with the previous studied, 93 traffic policemen of the same stations in 1991, have shown decreasing trends of BLLs. There is a statistically significant decrease in BLLs from 20.94 ± 10.81 µg/dl. to 6.90 ± 2.57 µg/dl. of Pathumwan police station, form 24.81 ± 4.44 µg/dl. to 5.10 ± 1.20 µg/dl. of Yannawa police station and from
13.22 ± 5.01 µg/dl to 7.30 ± 1.70 µg/dl of Watprayagrai police station at $P$ value 0.011, <0.001 and 0.044, respectively. This result suggested that the lowering of policemen BLLs should come from the implementation of the unleaded gasoline usage policy.

2004-56

**Title:** Serological observation of Thailand virus infection in human and rodent in Thailand

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**Source:** Presented at: The 6th International Conference on Hantavirus (HFRS and HPS), Seoul, Korea, 23-25 June 2004

**Language:** English

**Abstract:**

Hemorrhagic fever with renal syndrome (HFRS) and hantavirus pulmonary syndrome (HPS) are rodent borne viral zoonosis caused by hantavirus. So far 23 virus species has been registered in the hantavirus genus. Among them, the etiologic agents of HFRS are Hantaan (HTNV), Seoul (SEOV), Puumala (PUUV), and Dobrava (DOBV) viruses whereas Sin Nombre (SNV) and related viruses are leading causes of HPS. In Thailand, observations of Hantann-like virus infection have been reported since 1985 in rodents as well as in humans without clinical symptoms. More recently, there were patients hospitalized for pyrexia of unknown origin, who had
specific immune reactions to agents related to leptospira, rickettsia, influenza, dengue, and hantaviruses. We, therefore, demonstrated serological evidence of hantavirus infection among 519 serum specimens from seronegative cases for leptospirosis in Surin, Thailand. The human sera were screened for indirect immunofluorescence antibody (IFA) with HTNV and PUUV followed by Western blotting (WB). Three of 519 human sera shown to be positive. One of the serum (#277) was strongly positive for IgG and IgM antibody to HTNV by ELISA but having lower titer to PUUV. The other two sera showed lower titers to both antigens. The #277 serum was further examined by FRNT with HTNV, SEOV and Thailand virus (THAIV). It showed the highest FRNT titer to THAIV (1 : 160) but was negative (<40) to HTNV and SEOV.

In addition, a total of 48 rodent sera (15, Bandicota indica; 2, B. savilei; 19, Rattus rattus; 7, R. exulans; 5, R. norvegicus) were collected in Buriram, which is close to Surin, were examined in 1999. We found that (2, B. indica; 1, R. rattus) of the 48 rodent sera were positive by IFA, ELISA and WB. Furthermore, one of the B. incica sera showed FRNT titer of 1 :80 to THAIV but negative to HTNV and SEOV.

Although the THAIV was isolated from Bandicota indica in Thailand, no virological evidence for human infection has been reported so far. The present study showed that THAIV infection is existing in both humans and rodents in Thailand. Since the patient (#277) showed high IgM antibody and developed symptoms compatible with HFRS, such as high fever, conjunctival suffusion, proteinuria, high blood level of transaminase (SGOT and SGPT), it is suggested that THAIV is the causative agent of this case of HFRS.