

HEALTH SCIENCES

HSD No. 1

CHARACTERIZATION OF PLAQUE-PURIFIED DENGUE VIRUSES AS REAGENTS FOR IgM CAPTURE ELISA

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Dengue virus antigen is one of the key reagents for IgM-capture ELISA, a method which is now widely used for detection of dengue infection. However, since this reagent is not commercially available, the laboratory where the test is done, has to produce the antigen in-house. In our laboratory, 11 plaque-purified dengue virus isolates - four DEN-1, four DEN-2 and three DEN-3 - were evaluated for their potential as antigen reagents. Dengue viruses were isolated by inoculating infected culture fluids into host *Aedes albopictus* C6/36 cells. The isolated viruses were serotyped by Reverse Transcription-Polymerase Chain Reaction. To produce the antigens, infected cells were maintained in Minimum Essential Medium with 2% fetal bovine serum and incubated at 28°C until the 12th day post inoculation. Evaluation of the antigens was done by 3 different methods: (1) determination of antigen titer by antigen sandwich ELISA, (2) monitoring of the presence of infectious virus particles by infectivity assay, and (3) construction of growth curves. Results showed that the peak of antigen production was on day 7 post-inoculation for DEN-1 isolates, day 6 for DEN-2 isolates, on day 12 for one Dengue 2 and all DEN-3 isolates. Highest titers were obtained for DEN-3 followed by DEN-2. This information helps determine the schedule of culture fluid collection, and which assay antigen is most useful for IgM-capture ELISA.

Keywords: Dengue virus, IgM capture ELISA, Plaque-purified viruses, antigen production, infectivity assay, growth curves

HSD No. 2

**ANTIMICROBIAL EFFECTS OF β -MONOGLYCERIDE
FROM COCONUT OIL AND ITS POTENTIAL IN
THE TREATMENT OF URINARY TRACT INFECTIONS**

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β -monoglyceride (β -MG) is a macromolecule synthesized from coconut oil, freeze-dried BIOTECH lipase, and n-butyl alcohol. This research was conducted to determine the inhibitory effect of β -monoglyceride on the growth of *Proteus vulgaris*, *Enterococcus faecalis*, and *Candida albicans*, microorganisms which cause urinary tract infections (UTI), as well as to compare β -MG to that of commercially-available antibiotics namely Amoxicillin and Co-trimoxazole (Bactrim). It was also performed to assess the potential use of β -monoglycerides in the treatment of UTI in dogs. The antimicrobial assay using the broth dilution method was employed. It involved optical density determination and comparison with McFarland standards which gave an estimate of the microbial growth. A viable plate count employing the Miles and Mizrahi method was performed. To test the potential of β -monoglyceride as a medication for the UTI, the *in vivo* section of this research involved the case study of dogs with UTI. These dogs were subcutaneously injected with β -MG given in 10 mg/kg dosage for five days. The effect of β -MG on the dogs was evaluated through White Blood Cell (WBC) count and urinalysis. The Minimum Inhibitory Concentration (MIC) was between 10 and 25 ppm for *P. vulgaris*, between 125 and 150 ppm for *E. faecalis*, and between 6000 and 8000 ppm for *C. albicans*. The Minimum Lethal Concentration (MLC) was 25 ppm for *P. vulgaris*, 150 ppm for *E. faecalis*, and 8000 ppm for *C. albicans*. For *P. vulgaris* and *E. faecalis*, there was 100% kill at 150 ppm β -MG, while 94.70% kill was the highest value achieved when treated with 500 ppm Amoxicillin and Bactrim. β -monoglyceride caused a decrease in the bacterial count from the urine samples and achieved a 43.65% decrease in the WBC count of the dogs with UTI. Therefore, β -monoglyceride is a potential antimicrobial agent against various pathogenic microorganisms which cause UTI.

Keywords: β -monoglyceride, β -MG, coconut oil, antimicrobial, urinary tract infections

HSD No. 3

**DIAGNOSING PULMONARY EMBOLISM USING
ARTIFICIAL NEURAL NETWORKS**

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Pulmonary Embolism (PE), an obstruction of pulmonary blood flow to the distal lung is a life-threatening condition causing chest pain and difficulty of breathing. Hence, prompt diagnosis is necessary so to render medical attention immediately. The standard way of diagnosing PE is through Lung Scintigraphy analyzed by Nuclear Medicine physicians. An expert system using artificial neural network (ANN) is created to diagnose PE with its probability based on Prospective Investigation of Pulmonary Embolism Diagnosis (PIOPED). A set of patients who underwent lung scan due to PE formed the training group while another set of patients formed the test group. None of the training group scans was included in the test group. The training group was trained by ANN using the back propagation method and Delta Rule while the test group was used to measure the performance of the expert system. All scans were examined independently by one expert nuclear medicine physician based on PIOPED criteria. The expert system is a standalone application with user-friendly interface. It shows all the 8 standard projections of lung scan. White spots and hot spots are detected and effectively reduced in the images to warrant more accurate diagnosis. Spaces around the lung images are also removed ensuring proper alignment of the ventilation and perfusion images to the template. Likewise, the system is able to quantify the mismatched between the ventilation and perfusion images. Based on the evaluation of the test group, the system is able to match the diagnosis of the expert physician by 80 %. The expert system can be used as a temporary substitute when there are no immediate help from expert physicians. It can also be used as a teaching tool by resident doctors training in radiology or nuclear medicine and is not meant to replace the expert physicians diagnosis.

Keywords: artificial neural networks, expert system, lung scan, pulmonary embolism

HSD No. 4

**THE VALIDITY OF A POLYMERASE CHAIN REACTION
ASSAY IN THE DETECTION OF *MYCOBACTERIUM
TUBERCULOSIS* IN LIVER BIOPSY SPECIMENS OF CHILDREN**

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Childhood hepatic tuberculosis remains a diagnostic dilemma as conventional bacteriologic methods has a low sensitivity for detection of *Mycobacterium tuberculosis*.

This study was done to determine the validity of a PCR assay of the IS6110 gene and 38kDa protein to detect *M. tuberculosis* in liver biopsy specimens of children.

Eighty consecutive children admitted for percutaneous liver biopsy for various indications were included in the study. Patients were divided into those with hepatic tuberculosis (n=12) and those with other liver disorders (n=68). Liver biopsy specimens obtained underwent acid-fast stain and culture, histopathology and PCR assay using the IS6110 gene and 38kDa protein.

The sensitivity of the PCR of the IS6110 gene and the 38kDa protein in detecting *M. tuberculosis* in liver biopsy samples was 50% and 8%, respectively; specificity was 47% and 81%, respectively. Our study shows that the PCR assay using both the IS6110 gene and the 38kDa protein has a low sensitivity and specificity for the detection of *M. tuberculosis* in liver biopsy specimens of children. Thus, it could not be used as a diagnostic tool for childhood hepatic tuberculosis.

Key words: Acid-fast bacilli, granuloma, caseation necrosis, hepatic TB

HSD No. 5

**THE IMPACT OF DISEASE DATABASE SYSTEMS ON THE
MOLECULAR DIAGNOSTIC SERVICES DEVELOPED
AT ST. LUKE'S MEDICAL CENTER, PHILIPPINES**

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Advanced laboratory testing for various infectious diseases, such as dengue, hepatitis B and C, tuberculosis, Japanese encephalitis, herpes simplex encephalitis and meningitis is offered only at St. Luke's Medical Center in the Philippines. The Research and Biotechnology Division has developed molecular diagnostic tests for the detection, identification, and monitoring of different pathogens in a wide range of biological specimens by Polymerase Chain Reaction, Reverse Transcription-PCR, and IgM-capture ELISA. Samples include serum, cerebrospinal fluid, sputum, pleural fluid, gastric aspirates, ocular fluid, synovial fluid, bone marrow and liver biopsies taken from patients from various hospitals in the Philippines.

A comprehensive database for each infectious disease is maintained containing a description of the specimen, pertinent patient information, clinical data provided by the doctor, the initial and final diagnoses, laboratory test results and pathogen identification. These disease information systems are vital instruments not only for efficient record-keeping and data retrieval, but also:

- Enable valuable epidemiological tracking of the disease, especially its geographical location, seasonality and yearly trends, the prevalent strains, and the age and sex of the affected population.
- Provide the necessary information needed for monitoring the effectiveness of applied therapy or drug treatment on eliminating the pathogen load.
- Facilitate research advances by enabling correlations between molecular data and clinical indicators, and biostatistical analysis to be made.
- Make available periodic data summaries as guide to clinicians, health researchers and government officials in their practice, research and policy-making.

Keywords: Molecular diagnostics, Disease databases, Infectious diseases, Polymerase Chain Reaction

HSD No. 6

**EXISTENCE OF *HELICOBACTER PYLORI* IN THE ORAL CAVITY OF
FILIPINO PATIENTS WITH GASTRODUODENAL DISEASES**

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Helicobacter pylori, a Gram-negative, spiral-shaped microaerophilic bacterium is correlated with the development of various gastroduodenal diseases such as gastritis, gastric and duodenal ulcers, gastric carcinoma and MALT lymphoma. It has been demonstrated that eradication of *H. pylori* by antibacterial therapy resulted in the treatment of *H. pylori* - associated gastroduodenal diseases. However, the route of infection by *H. pylori* has not been established. Researchers have suggested that the oral-oral route would be the most probable mode of transmission.

The objective of this study was to determine the existence of *H. pylori* in the oral cavity of Filipino patients in order to test the hypothesis of transmission by an oral route. A total of 54 patients (28 males and 26 females) of the Institute of Digestive Diseases, St. Luke's Medical Center were enrolled in the study. Endoscopic diagnosis showed that 38 patients have gastritis, 8 with gastric ulcers and 8 with duodenal ulcers. Saliva samples were collected from the enrolled patients prior to endoscopy. Biopsy samples were also taken both from the antrum and corpus. Cytotoxin genotypes were determined by PCR using both biopsy and saliva samples. All saliva and gastric biopsies were positive for *H. pylori* using 16S rRNA gene. *cagA* gene was detected in 80% of patients from both saliva and corporal biopsies and 74% of patients from both saliva and antral biopsies. Predominant *vacA* genotype is s1a/m1 in both saliva and gastric biopsies with 30% observed agreement in saliva and corporal biopsies and 52% agreement in both saliva and antral biopsies.

Our study has provided evidence of the presence of *H. pylori* in the oral cavity of Filipino patients with gastroduodenal diseases. This shows that there is a possibility of an oral transmission of the infection. Moreover, different strains may exist in the stomach and saliva of patients.

Keywords: *Helicobacter pylori*, gastroduodenal diseases, biopsies, *vacA* genotypes, *cagA* gene, 16s RNA

HSD No. 7

**SIMULTANEOUS DETECTION USING MISMATCH AMPLIFICATION
MUTATION ASSAY (MAMA)-MULTIPLEX PCR, AND
CHARACTERIZATION OF ENTEROHEMORRHAGIC AND
ENTEROPATHOGENIC *Escherichia coli***

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A total of 45 diarrheagenic *E. coli* isolates from three different hospitals in Metro Manila were screened for EHEC-associated genes using mismatch amplification mutation assay (MAMA)-multiplex PCR. The multiplex (pentavalent) PCR amplifies a region of the *stx1*, *stx2*, *uidA*+93 (transversion mutation marker for *E. coli* O157:H7/H-), *ehxA*, and *eae*f[×] (also present in EPEC O55:H7), respectively. Based on PCR results, 3 isolates were identified as EHEC and 4 belong to the O55:H7 EPEC group. One of the EHEC isolates, PGH36 (*uidA*+93 positive), was validated as *E. coli* O157:H7 by latex agglutination. Subsequent assay for sorbitol fermentation and glucuronidase (GUD) expression reveal that PGH36 is a phenotypic variant (sorbitol fermentation and GUD positive). Other than these phenotypic tests, the multiplex PCR-positive isolates were also assayed for enterohemolysis and sensitivity to 9 antimicrobial agents. All 3 EHEC demonstrated EHEC-specific enterohemolytic patterns on sheep-blood agar plates while majority of the isolates were sensitive to most of the antimicrobials tested.

The relative pathogenicity of the local multiplex PCR-positive isolates was also investigated by performing standard *in vivo* and *in vitro* cytotoxicity assays. Intraperitoneally injected C3HeJ mice (10⁸ CFU/mice) showed 100% death rate for four of the isolates (3 EHEC and 1 EPEC), and 33 to 83% for the remaining 3 EPEC. *In vitro* cytotoxicity assay using three cell lines - Vero, HT-29 colon cancer and human fibroblast cells reveals cytotoxic response using spent medium crude toxin concentrates indicating the production of a cytotoxin other than shiga-like toxins.

Keywords: *Escherichia coli*, Enteropathogenic, Enterohemorrhagic, Shiga-toxin, Mismatch amplification mutation assay (MAMA), diarrhea, multiplex PCR

HSD No. 8

**DIABETES AND BODY MORPHOMETRICS:
A CASE STUDY OF A MARANAO MUSLIM CLAN**

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Diabetes is a global health problem of enormous magnitude. By the year 2010, global projections are that there will be a 2-fold increase in diabetes to over 200 million worldwide. Many are afflicted with the disease especially in newly industrialized nations and among minorities in developed countries. Studies involving ethnic groups especially those practicing consanguineous marriages are good sources of information in determining relationships of the disease with genetics, body morphometrics including height, weight, facial, dermatoglyphics and digits measurements. Several families with known diabetic members of a Muslim Maranao clan from Marawi City, Lanao del Sur were included in the study. Pedigree analysis was done to determine inheritance of the disease. Blood glucose analysis was also performed for confirmation if the individuals perceived to have diabetes are really afflicted with the disease. Results showed close associations between body morphometrics and the disease. Diet and genetics were observed to be the major factors of the high prevalence of the disease in the clan.

Keywords: diabetes, pedigree analysis, genetics

HSD No. 9

**INACTIVATION OF A ROGUE p53 MUTATION USING siRNA
REVERSES RESISTANCE TO CHEMOTHERAPEUTIC
AGENTS IN BREAST TUMOR CELLS**

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The guardian of the genome, *p53*, is considered as the most frequently mutated gene in all human cancers, and its mutation paradoxically leads to an insidious resistance to anti-cancer drug treatments observed in most clinically aggressive tumors. Because majority of the mutations are missense, localized in specific “hotspots”, and have a trans-dominant effect on the wild-type allele, here, we demonstrate the ability of mutant homing of siRNAs (small inhibiting RNAs) to inactivate a point mutation and normalize *p53* pathways in breast tumor cells. The effect of suppression of the mutant *p53* leads to the reversal of cellular resistance to specific anti-cancer agents via the down-regulation of the multiple drug resistance gene (*MDR1*). Therefore, the combination of *p53*-targeted siRNAs and standard chemotherapeutic drugs would provide an attractive personalized combination therapy that optimally utilizes data on drug action and the genetic information of the patient’s tumor.

Keywords: p53, small inhibiting RNAs, breast cancer therapy, MDR1

HSD No. 10

**MUTATION DETECTION IN MISMATCH REPAIR GENES OF A
FILIPINO FAMILY WITH HNPCC (HEREDITARY
NONPOLYPOSIS COLORECTAL CANCER)**

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Hereditary nonpolyposis colorectal cancer (HNPCC) is an autosomal dominant inherited cancer predisposition caused by mutation in one or more of the six mismatch repair (MMR) genes (hMLH1, hMSH2, hMLH3, hMSH6, hPMS1 and hPMS2). These genes encode for proteins that ensure fidelity of DNA replication. Mutation in one or more of these genes result in instability of the microsatellite repeats, also known as microsatellite instability (MSI). In recent years, different methods of mutation detection have been developed in order to identify individuals prone to HNPCC.

In this study, peripheral blood samples were collected from members of a family with history of colon cancer in three generations. DNA was isolated using phenol-chloroform extraction method. Appropriate PCR primers were then used to amplify the different exons of the hMLH1 gene and the amplified products were subjected to dHPLC for mutation screening. The type of mutation present in each exon was determined by DNA sequencing. Mutations in exons 15 and 16 of the hMLH1 gene have been commonly reported in other Asian countries such as Japan and Korea. However, our initial results show that these regions appear to be normal in our Filipino family. Result of mutation screening by dHPLC revealed a mutation in exon 4 of the same gene.

Keywords: Hereditary nonpolyposis colorectal cancer, autosomal dominant, mismatch repair genes, exons, dHPLC, DNA sequencing, HMLHI gene, PCR

HSD No. 11

DUCK EMBRYOGENESIS: EFFECTS OF 3 PLANT EXTRACTS

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Three medicinal plants commonly used in treating a variety of diseases are *Annona squamosa*, *Hibiscus rosa-sinensis* and *Sarcandra glabra*. Using light microscopy and scanning electron microscopy, this study investigated the individual activities, as well as antiteratogenic potential against the known teratogen, retinoic acid, of different concentrations of their methanol extracts on the basis of their effects on the chondrogenesis and myogenesis in the limbs of a 3-day old duck embryos. The limbs were subjected to fixation, dehydration, paraffin embedding, serial section, hydration, and staining with hematoxin and eosin, before they were mounted on slides. Standard SEM protocol was used for scanning electron microscopy. Based on histological grading, it was found that *A. squamosa* has an inhibiting activity on myogenesis. *S. globra* proved to induce myogenesis and to diminish chondrogenic cells at 50 micrograms/milliliter dosage. Only *H. rosa-sinensis* exhibited slight antiteratogenicity when combined with retinoic acid. More studies should be done to further test the activities of the three extracts in the duck chondrogenesis and myogenesis.

Keywords: *Annona squamosa*, *Hebiscus rosa-sinensis*, *Sarcandra glabra*, retinoic acid antiteratogenesis

HSD No. 12

**EFFECTIVENESS OF PEDIAH.E.A.R.T (HOLISTIC
EDUCATION AGAINST RHEUMATIC THREATS) ON
THE HEALTH STATUS OF RHD PATIENTS**

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Today, about 12 million people are currently affected by rheumatic heart disease (RHD), many requiring repeated hospitalization, or often, unaffordable heart surgery in the next 5 to 20 years.

This 4-month study sought to investigate the effectiveness of a holistic health educational program - "PediaH.E.A.R.T. (Holistic Education Against Rheumatic Threats)" in improving the health status of adolescent outpatients aged 12 -19 with RHD.

Utilizing a randomized clinical trial, 35 patients for the intervention group received a 3-hour teaching program, twice a month. Topics were the heart and circulatory system; the nature of RHD, its medical and surgical management for the first session; and diet, exercise, hygiene and coping with illness for the second session. The control group (n=35 patients) received routine health teachings.

Outcome measures of health status included variables of health-related quality of life (physical, social and emotional health and general health perceptions); functional capacity tested subjectively through the Specific Activity Scale (SAS) and objectively through the 6-Minute Walk Test (6-MWT). These were assessed at baseline, one and two months.

Results showed that at 2nd evaluation, there was a significant difference in all health status components: health-related quality of life ($p=0.000$), SAS functional classification ($p=0.000$) and 6-MWT ($p=0.030$).

Findings suggest that through implementation of a holistic health educational program, the health status of adolescent RHD patients may improve. In the long run, awareness of these young people to the fact that worst complications can be prevented through self-management, is a cost-effective strategy not only for the health care system but also for the Filipino society as we ensure future productivity among these young adolescents.

Keywords: patient education, rheumatic heart disease, health status measures

HSD No. 13

DENTAL REGISTRY

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With the recent integration of information technology in the health sector, dental health care should not be limited to treating patient using only using only dental instruments and devices. An emerging discipline called Dental Informatics combines computer technology with dentistry in order to improve delivery of oral health care. At the University of the Philippines Manila, the College of Dentistry together with the College of Arts and Sciences created a working prototype entitled "Dental Patient Registry" which aims to capture patient data related to dental practice. It is currently being used already at the College of Dentistry. Dental Patient Registry (DPR) integrates patient medical and dental history, soft tissue examination, oral examination, diagnosis, treatment plan and service record. DPR consists of five modules namely 1) Medical and Dental History, 2) Soft Tissue Examination, 3) Tooth Chart, 4) Problem List Worksheet and 5) Query Module. The modules are integrated with each other, thus, data from Soft Tissue and Tooth Chart Modules for instance is reflected in the Problem List Worksheet. New fields are added in the Problem List Worksheet to incorporate additional comments. Finally treatment performed and associated service fees are clearly indicated in the Service Record. The Query Module is another feature aimed to support research. It outputs patient records matching a specific criteria. DPR is a web-based application designed to be run on server and accessed in a number of terminals by dental students and faculty. Security, patient confidentiality, data integrity and easy retrieval of records have been incorporated in the design of DPR. DPR is an example of a collaborative project aimed at integrating information technology with dental practice.

Keywords: Dental Registry, Dental Informatics

HSD No. 14

PHILIPPINE MEDICINAL PLANTS INFORMATION SYSTEM

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The Philippine Medicinal Plants Information System (PMPIS) is an output of the collaboration between two colleges from the University of the Philippines Manila: the College of Arts and Sciences and College of Pharmacy. PMPIS was conceived in order to provide an online catalog of indigenous medicinal plant information with focus on their parts, bioactivities and constituents. PMPIS is an open-source web-based database system developed under a Debian/Linux environment using a Zope web application server, PostgreSQL database and MedPlants Zope Product free software that is written in Python. Registered students and other researchers are allowed to contribute 1) core plant information which includes family, genus, species and attributed taxonomist, 2) common names with an associated language or dialect, 3) plant images, 4) plant part, bioactivity, and constituent information including references and abstract. The submitted entries are subsequently screened by a panel of experts from the College of Pharmacy acting as content administrators. Hence, the entire content of the PMPIS database is the responsibility of the College of Pharmacy. PMPIS aims to lessen the time spent on gathering plant information by providing a search engine based on plant name, plant part, bioactivity and constituent or a combination of these. PMPIS however does not contain information about preparation, compounding or dispensing of medicinal plants.

The PMPIS website is already working, however, students at the College of Pharmacy still needs to test the system and populate it with read data until such time that it may be ready for public launching as a nationwide repository of medicinal plants information.

Since PMPIS is an open-source software, it has a potential of being built upon, developed and maintained by a loosely-knit community of other free software developers.

Keywords: medicinal plants, plant biochemical constituents, plant bioactivity, open-source software

HSD No. 15

REPORTING AND QUERYING NOTIFIABLE DISEASES VIA SMS

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Health surveillance is an important monitoring tool. It involves regular collection, analysis, interpretation, and dissemination of health information that should be done immediately so that authorities can plan health programs effectively. However, several factors such as geography, transportation and weather delay the delivery of reports hence relevant data such as notifiable diseases report do not reach the city health offices immediately. Thus, it takes some time before a solution is implemented to prevent outbreaks. As a response to this problem, the Online Notifiable Diseases Information Gateway was created. It has two major components: 1) sending and querying notifiable diseases via short messaging service (SMS) to support barangay field health workers and 2) viewing notifiable diseases report via the internet to support the barangay health officials at the provincial and city levels and the Department of Health (DOH).

SMS technology enables barangay field health workers to immediately send a report on notifiable diseases such as measles and diphtheria directly to the database thus if a specific disease reach the threshold set by the epidemiologist, an SMS alert is automatically sent to barangay health officials at the city and provincial levels. Also, barangay field health workers can query total number of cases of a specific disease on a given location; list of locations where a specific disease occurred, etc. again via SMS. At the barangay, city and provincial health offices, health officials as well as the DOH, may view online the breakdown of frequency of disease by age and by gender; daily, weekly, monthly and yearly notifiable diseases report; percentage of increase of cases of a specific disease this year and the previous year, etc.

The use of wireless technology to deliver clinical information is very useful as almost everyone has access to cellular phones. Although there is a charge per text message, this is still cheaper compared to paper delivery and is a better alternative for field health workers where internet access is not possible. As reports are submitted without delay, faster analysis of data can be done. The online component on the other hand helps provide a better view of the notifiable diseases report as these cannot be viewed well via SMS.

Keywords: health monitoring, health surveillance, SMS, wireless technology, online health information systems

HSD No. 16

**BIOINFORMATICS AND DATA MANAGEMENT:
A KEY COMPONENT IN BIOMEDICAL RESEARCH AT
ST. LUKE'S MEDICAL CENTER, PHILIPPINES**

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Bioinformatics plays a crucial role in the post-genomic era, revolutionizing biomedical research and impacting medical research. The main function of the Bioinformatics and Data Management Section (BDMS) of the Research and Biotechnology Division (RBD) at St. Luke's Medical Center is to develop computerized knowledge systems of raw clinical and laboratory data as well as the interpretation and deduction of results. It oversees data management systems for medical genetics/molecular researches on infectious and non-infectious diseases.

Since 1995, RBD has spearheaded the establishment of computerized databases in SLMC starting with data banks on dengue infections, stroke and colorectal cancer. New, ongoing projects are the Cardiovascular Disease Information System, Head and Neck Tumor Information System, Liver Diseases Databank, and databanks for breast cancer, ophthalmology, and reproductive endocrinology and infertility. Other databases on CNS infections, tuberculosis, and thalassemia have been created as well. The data banks store patient information on sociodemography, medical history and physical findings, laboratory and molecular diagnostic findings, therapy, and follow-up status. Data validation rules were incorporated in the systems to facilitate encoding and minimize errors in data entry.

Composed of basic scientists, an epidemiologist, a biostatistician, and technical support staff, the BDMS has capabilities to analyze raw DNA data using DNAsis, access and retrieve DNA sequence data from public databases via the internet, design and analyze oligonucleotide primers using OLIGO v.4, and compare DNA sequence data with published sequences using BLAST. It has various softwares for the statistical analysis of the data. It has helped clinicians and scientists generate quality research studies in elucidating the etiological, epidemiological, pathophysiological and molecular pathogenesis of diseases, in determining survival and disease-free rates of the patients, and in comparing the efficacy of different treatment modalities. Numerous studies have been generated from the databanks, some of which garnered awards.

Keywords: bioinformatics, data management, biomedical research

HSD No. 17

**THE ST. LUKE'S DENGUE SERUM AND DATA BANKS:
ADVANCING DENGUE RESEARCH IN THE PHILIPPINES**

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Since the start of its Dengue Research Program in 1995, St. Luke's Medical Center has established a local repository center for the storage and maintenance of over 8000 serum samples obtained from dengue patients all over the Philippines. The Dengue Serum Bank, as it is called, serves as a valuable resource for research work on dengue virus and dengue infections in the Philippines.

Data from samples in the serum bank include the following:

- Patient socio-demographic information which includes history of travel
- Medical history
- Physical examination findings including all signs and symptoms
- Laboratory test results such as CBC, IgM-capture ELISA, RT-PCR, cytokine, antiplatelet IgG, Fibrinogen Degradation Products (FDP), chest radiographs
- Serotyping of virus isolates
- DNA sequences of dengue viral genes
- The clinical and the final diagnosis of dengue

All these information are kept as an electronic data compilation known as the Dengue Data Bank, accessible through the Data Information and Bioinformatics Section of the Research and Biotechnology Division.

With these available resources and access to data, basic and clinical researches have been done or are ongoing. These include research on the development of front-line diagnostics for dengue, development of diagnostic reagents for dengue detection, determination of annual rates of dengue serotypes, and sequencing of selected dengue genes. Clinical researches include studies on thrombocytopenia, the role of platelet-associated IgG and pathophysiology of dengue infections. One of the major projects is the national dengue surveillance program in collaboration with the Department of Health.

Keywords: dengue, serum bank, data bank, repository, electronic data compilation

HSD No. 18

**SEQUENCE ANALYSIS OF THE ENVELOPE GENE
FROM PHILIPPINE DENGUE-1 ISOLATES**

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The dengue virus is a positive single-stranded RNA virus belonging to the family Flaviviridae and consists of four serotypes. All 4 serotypes can cause mild dengue fever or severe dengue hemorrhagic fever. The viral genome is made up of genes encoding for 3 structural and 7 nonstructural proteins, typical of the Flavivirus.

The envelope gene, one of the structural genes, is made up of 1485 nucleotides and codes for the envelope protein which is found on the surface membrane of the dengue virus. The envelope protein is composed of 495 amino acids and binds to the host cell receptor prior to viral entry into the cell. Mutations in the envelope gene may affect viral infectivity. DNA sequence analysis is a useful method to investigate any sequence change in the gene.

The envelope gene of Dengue-1 isolates of different years, 1995 (1), 1999 (2), 2001(1) and 2002 (6) were amplified, cloned and sequenced. Sequence data were compared with the sequences of 1974, 1989 and 2002 Philippine isolates deposited at Genbank. Analysis of the raw sequence data with DNAsis v3.6 software showed that there were more silent mutations observed than missense mutations. This indicates selection pressure being applied to virus genome. In a span of 28 years (1974 - 2002), only 0.2% - 0.5% missense mutations were found to occur among the 1485 nucleotides of the envelope gene. However, no significant changes were observed in the structure of the envelope protein in these isolates. Phylogenetic analysis suggests that current dengue-1 isolates originate from earlier isolates and that outbreaks due to Dengue-1 are not derived from imported infections.

Ten dengue-1 envelope gene sequences were submitted to Genbank and assigned accession numbers in October 2003.

Keywords: Dengue virus, envelope gene, mutation, clone, DNA sequence analysis, phylogenetic analysis

HSB No. 19

CHROMATOGRAPHIC PROFILING OF METABOLIC DISORDERS

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Inborn errors of metabolism cause hundreds of different diseases. Each disease is individually rare but collectively account for a significant portion of illness, particularly in children. Metabolic disorders are usually caused by defects in enzymes involved in the biochemical pathways. To prevent metabolic disorders, correct diagnoses must be made. Metabolic profiling consists of a variety of biochemical and physiological tests to diagnose metabolic disorders which could be characterized by the excretion of excess or deficient amounts of organic and amino acids in biological samples. The presence of organic acids and amino acids not normally present in biological samples is also indicative of metabolic disorders.

Two chromatographic techniques were utilized in the profiling of metabolic disorders. Gas Chromatography with Mass Spectrometry (GC/MS) was utilized for analysis of organic acids in urine. Prior to GC/MS analysis, organic acids in urine samples were isolated through oximation, extraction and derivatization steps. The derivatized acids were then analyzed using the Finnigan Trace GC 2000 coupled with a GCQ GC/MS system operated with an Xcalibur software. A computerized library search was used to identify the urinary organic acids. Analysis of amino acids in plasma or urine samples was carried out by Shimadzu Amino Acid Analyzer using post column derivatization with o-phthalaldehyde and fluorescence detection. Chromatographic profiles of urine samples from healthy and sick individuals were compared.

This study will contribute to the development of proper screening of metabolic disorders in the Philippines particularly for children to avoid early death and for them to live normal lives.

Keywords: metabolic disorder, metabolic profiling, GCMS, HPLC, amino acid organic acids

HSD No. 20

**EFFECTS OF OPEN AND CLOSED STERNOTOMY DRESSING
ON WOUND HEALING AMONG CABG PATIENTS**

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The purpose of the study was to determine the effects of open and closed sternotomy dressing on wound healing of patients who underwent coronary artery bypass graft (CABG).

The study utilized randomized controlled trial. The sample comprised a total of 64 subjects who had undergone uncomplicated CABG and admitted to a surgical intensive care unit of the Philippine Heart Center from August to November 2003. Block randomization was done to categorize the subjects into control group (closed dressing) and study group (open dressing). At POD 2, initial assessment of the wound was done. The control group received daily dry, sterile gauze dressing on the sternotomy wound, while the study group received no dressing on the sternotomy wound. Wound characteristics such as serous exudates, erythema, purulent exudates, and separation of deep tissue were measured from Post Operative Day (POD) 2 to POD 6. At POD 6, additional criteria such as use of additional antibiotics, drainage under local anesthesia, debridement under general anesthesia, isolation of bacteria, and prolonged hospital stay were reviewed. Degree of wound healing was calculated by adding score points from wound characteristics and additional criteria. The study utilized Mann-Whitney U-test, Wilcoxon Paired Signed Ranked Test, and T-test for the statistical treatment.

There was a steady improvement of serous exudates for both groups, on the other hand, erythema was observed to occur at higher percentage among the closed dressing group. However, there was no significant difference between the control and study group based on daily wound characteristics from POD 2 to POD 6. Use of additional antibiotics was noted to be more common among the control group. Based on total wound scores, all subjects in the open dressing group obtained satisfactory wound healing, while 7

subjects from the closed dressing group were observed to have disturbances in wound healing.

The outcome of the study opened up critical implications for wound care. Wound exposure promotes effective wound healing. Therefore, instituting a cost-effective sternotomy dressing regimen to CABG patients is essential to post-operative wound management.

Keywords: sternotomy dressing, coronary artery bypass graft, CABG, dressing regimen

HSD No. 21

POINT MUTATION IN THE ENDOTHELIAL NITRIC OXIDE SYNTHASE (NOS) GENE ASSOCIATED WITH NON-INSULIN-DEPENDENT DIABETES MELLITUS (NIDDM) IN FILIPINO PATIENTS

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Non-insulin dependent diabetes mellitus (NIDDM) of Type II diabetes mellitus is a heterogenous, multifactorial disease characterized by impaired glucose metabolism due to insulin resistance. Recent studies showed that mutations of the endothelial nitric oxide synthase (¹NOS) gene are associated with an increased risk for progression to diabetic neuropathy in NIDDM, and that the expression of ¹NOS is reduced in subjects with impaired glucose metabolism. Polymorphism in the ¹NOS gene may therefore serve as a possible genetic marker for NIDDM.

This study involves the identification of a G to T substitution at position 894 in the ¹NOS coding sequence, corresponding to a change from Glu to Asp at codon 298, that removes a Ban II restriction site in the DNA sequence. This is the only polymorphism identified to date that changes the ¹NOS protein sequence, leading to speculation that genetic variation at this site may alter ¹NOS activity or regulation.

Genomic DNA was prepared from peripheral blood lymphocytes using standard techniques. A 248 bp product of the ¹NOS coding region was amplified from the genomic DNA by Polymerase Chain Reaction (PCR). The PCR product were digested with Ban II and resolved on 8% polyacrylamide gels. Depending on whether G or T is found in position 894, one band corresponds to TT, two bands correspond to GG and three bands may be found corresponding to GT genotypes, respectively.

A total of 133 diabetic subjects and 79 normal individuals were tested. Of the diabetic group, 77 (58%) carried the GG genotype, 53 (40%) had the GT genotype and 3 (2.3%) had the TT genotype. Among the normal subjects, a similar pattern was observed: 57 (72%) were of GG genotype, 21 (27%) GT and 1 (1.3%) had the TT genotype. These results show that a G to T substitution was more likely to occur in diabetic subjects (56%) compared to the normal group (22%).

Keywords: (NIDDM) Non-Insulin Dependent Diabetes Mellitus, (¹NOS) Endothelial nitric oxide gene, (RFLP) Restriction Fragment Length Polymorphism, Mutation, Polymorphism

HSD No. 22

A FIVE-YEAR (1996-2000) SURVEY OF THE PREVALENCE OF CANCER CASES IN ILIGAN CITY, PHILIPPINES, BASED ON HOSPITAL RECORDS

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An on-going comprehensive study on cancer is being undertaken in Iligan City, one of the highly industrialized cities in Southern Philippines. Partial data on four types of carcinomas, namely, breast, ovarian, lung, and skin were obtained from 1996 to 2000 from four main hospitals in Iligan City. Although, a significant number of cancer cases were not reflected in hospital records based on personal communications from individual medical practitioners, the data revealed a very wide gap in the incidence of ovarian

cancer cases (240%) over the other three types. This may still reflect the correct picture if all unreported cancer cases have been included. In the five-year study, 48 cases of breast cancer, 183 cases of ovarian cancer, 45 cases of lung cancer, and 36 cases of skin cancer, or a total of 312 cases, have been reported based on hospital records. Close to 75% of the reported cases were women, a serious problem in women's health and welfare in Iligan City. Apparently, most of the cases excluded from the gathered data either consisted of individuals who could not afford hospitalization, or who sought treatment in Cebu or Manila, where better diagnostic and treatment facilities are available, for those who could afford.

We are currently investigating more recent reports from the Iligan City Health Office, on increased incidence of breast cancer in a particular group of women, public school teachers belonging to the 25 to 45 years age group. Conservative estimate reveals that one out of ten (1:10) women belonging to this group is positive for breast cancer. We are suspecting chronic exposure to some environmental carcinogens prevalent in Iligan City as the predisposing factor in cancer development in susceptible individuals. Gender studies, particularly on women's health concerns, must be seriously considered, given the significant role of women in the social and economic life of the city.

Keywords: cancer, incidence, environmental carcinogens

HSD No. 23

AFLATOXIN IN ENVIRONMENTAL TOBACCO SMOKE (ETS): POTENTIAL LINK TO INCREASED INCIDENCE OF CANCER AND EMERGING AND RE-EMERGING INFECTIOUS DISEASES

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In this study, we report the presence of aflatoxin in commercial cigarettes and its imminent entry into the human body by inhalation, a pioneering study in the Philippines based on literature search.

Samples of three popular brands of commercial cigarettes were analyzed using the Veratoxä Aflatoxin System kit (Glenwood Technologies International, Inc.). Aflatoxin content of the processed samples ranging from 0.5 to 4.0 ppb,