CONFERENCE PROCEEDINGS

2018 – 7th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 17-18 December, Mauritius

17-18 December, 2018

CONFERENCE VENUE

Voilà Bagatelle Hotel, Mauritius

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Preface:

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KEYNOTE SPEAKER

Dr. Fawzi Mahomoodally

Associate Professor and Former head of Department at the Faculty of Science

University of Mauritius, Mauritius

Dr. Fawzi Mahomoodally is an associate professor and former head of department at the faculty of science, University of Mauritius. Fawzi is an alumnus of the Harvard University, USA, and recipient of several awards. He has authored 214 scientific publications (133 full scientific papers in ISSN/impact factor journals, edited 4 academic books, 36 book chapters, and 41 abstracts in international/national conferences). He is the recipient of >40 fellowships/travel grants. In 2011, he was invited as a key speaker at the 14th Asian Chemical Congress (Thailand); ASM-GM (Boston, USA), the ICAAC meeting in Colorado, USA and 6 strategic meetings in Washington DC, USA. In 2018, he was an invited speaker for at the ISE 2018, Dhaka and plenary speaker for Creative Educational Society's College of Pharmacy, India. He was invited to the Commonwealth conference (Bangalore) by the Royal Society, UK, the Young leader session with Nobel Laureates at the STS forum, Japan and Fellow of African Science Leadership Programme, South Africa. He is presently the PI/co-PI of 6 research grants/consortium (total of 13 million MUR). He has organized/instructed >15 international/national workshops/training courses. Fawzi works in the field of health sciences, with a deep-rooted interest towards documenting/validating the use of complementary/alternative medicine and indigenous/traditional knowledge pertaining to the use of natural products (medicinal herbs/spices/food plants/animal products/practices). He endeavors to develop therapeutic bio-products from medicinal herbs/food plants to address global health, wellness, and food security issues. He is presently collaborating with private companies to translate his research into commercial therapeutic bio-products.

Dayyabu Shehu
ERCICRLSH1807054

Functional Role of Tyr12 in the Catalytic Activity of Novel Zeta-like Glutathione S-Transferase from Acidovorax sp. KKS102

Dayyabu Shehu
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Abstract

Glutathione S-transferases (GSTs) are family of enzymes that function in the detoxification of variety of electrophilic substrates. In the present work, we report a novel zeta-like GST (designated as KKSG9) from the biphenyl/polychlorobiphenyl degrading organism Acidovorax sp. KKS102. KKSG9 possessed low sequence similarity but similar biochemical properties to zeta class GSTs. The gene for KKSG9 was cloned, purified and biochemically characterized. Functional analysis showed that the enzyme exhibits wider substrate specificity compared to most zeta class GSTs by reacting with 1-chloro-2,4-dinitrobenzene (CDNB), p-nitrobenzyl chloride (NBC), ethacrynic acid (EA), hydrogen peroxide, and cumene hydroperoxide (CuOOH). The enzyme also displayed dehalogenation function against dichloroacetate (a common substrate for zeta class GSTs) in addition to permethrin, and dieldrin. The functional role of Tyr12 was also investigated by site-directed mutagenesis. The mutant (Y12C) displayed low catalytic activity and dehalogenation function against all the substrates when compared with the wild type. Kinetic analysis using NBC and GSH as substrates showed that the mutant (Y12C) displayed a higher affinity for NBC when compared with the wild type, however, no significant change in GSH affinity was observed. These findings suggest that the presence of tyrosine residue in the motif might represent an evolutionary trend toward improving the catalytic activity of the enzyme. The enzyme as well could be useful in the bioremediation of various types of organochlorine pollutants.

Keywords: Acidovorax sp. KKS102, Bioremediation, Glutathione s-transferase, Site-directed mutagenesis, Zeta.

Ayman Elshayeb
ERCICRLSH1807055

Proteins of Escherichia coli and Staphylococcus aureus associated with enzymatic profiles of their allied bacteriophages

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Microbiology, Elbarkal Multi Activities, Dept. Research & Consultancy, Khartoum – Sudan

Abstract

Introduction: The mechanical action of the bacteriophage on the selected bacteria species depend on their receptors that adsorb them to their hosts. Some proteins of the bacterial outer membrane acts as the receptor for phage infection, the relationship between bacteriophages and bacteria proteins could be found by the protein profiles analysis.

Methods: To isolate the phages and identify their species, this was done through plaque assay on bacterial cultures. The analysis and protein-protein interaction assays were confirmed by proteins profile of bacteriophage and corresponded bacteria using Sodium Dodecyl Sulphate Poly Acrylamide Gel Electrophoresis (SDS-PAGE) to estimate their molecular weights; the migration of each band was compared to the standards of known weights in the molecular ladder.

Results: The mobilised proteins of the phage showed four major bands with molecular weights of 46, 35, 24 and 14 kDa. Meanwhile, the bacteria

	showed clear nine bands with molecular weight ranged between 96 and 24 kDa. The analysis showed molecular masses of 47, 34 and 16 kDa, and the protein bands distance migration on plot area of the phage and the bacteria. Protien size from 47.7 to 34.3 kDa resembles 43.3% of total phage protein which formed the capsid head and the coil, while the molecular weight mass of 22.5 formed the tail proteins. The lytic enzymes molecular weight was ranged between 18-14 kDa according to the type of the enzyme. We found that the band of 34 kDa was the common shared peak between bacteriophage and allied bacterium. **Conclusion: Protein separation resulted data during phage assembly, ensures lytic enzymes are built in the capsid head and the lysozyme in the tail, they facilitate the enzymatic decaye for bacterial host. This is related to the lytic cycle of the bacteriophages and their phenomenon in utilizing the bacterial DNA in proteins manufacturing during their multiplication inside bacteria.** **Keywords: Bacteriophage\ Bioinformatics\ Escherichia .coli\ Molecular weight\ Protein Profile**
Dr. Amlan Das **ERCICRLSH1807058**	**Pharmacological inhibition of Notch-activating enzyme?-secretase attenuatesoncogenic potential, EMT and stemnessin Triple Negative Breast Cancer (TNBC) cells andin vivo, by modulating the Autophagy/ Apoptosis balance** **Dr. Amlan Das** **Assistant Professor, Department of Biotechnology, National Institute of Technology, Sikkim, India** **Abstract** **Background: Breast cancer (BC) is the most common cancer in women, and accounts for almost 15% of all cancer-related deaths in women worldwide Notch signaling is reported to be deregulated in several malignancies, including breast. Moreover, Notch-signaling was also known to be the key regulator of stemness in breast cancer and also responsible for the acquisition of drug resistance. The enzyme γ-secretase plays an important role in the activation and nuclear translocation of Notch intracellular domain (NICD). Hence, pharmacological inhibition of γ-secretase might lead to the subsequent inhibition of Notch signaling in cancer cells.** **Results: In search of novel γ-secretase inhibitors (GSIs), we screened a series of triazole-based compounds, for their potential to bind γ-secretase and we observed that 3-(3′4′,5′-Trimethoxyphenyl)-5-(N-methyl-3′-indolyl)-1,2,4-triazole compound (also known as NMK-T-057) could bind to γ-secretase complex. Very interestingly, NMK-T-057 was found to inhibit proliferation, colony forming ability, motility in various triple-negative breast cancer cells (TNBCs) such as MDA-MB-231, MDA-MB-468, 4T1 and also MCF-7 (ER/PR positive cell line), with negligible cytotoxicity against non-cancerous cells such as MCF-10A, and PBMC and Swiss albino mice. It also inhibited epithelial to mesenchymal transition (EMT) and stemness in TNBCs. The in a silico study revealing the affinity of NMK-T-057 towards γ-secretase was further validated by fluorescence-based γ-secretase activity assay, which confirmed inhibition of γ-secretase activity in NMK-T-057 treated TNBC cells.** **Very interestingly, we also observed that NMK-T-057 induced significant autophagic responses in TNBCs and administration of the autophagy inhibitor 3-MA, attenuated NMK-T-057 induced cell death. The cell based results were further confirmed in vivo using balb/c-4T1 TNBC model,**

	where administration of NMK-T-057 drastically reduced the tumor load in female balb/c mice. **Conclusion: Hence, we concluded that NMK-T-057 could be a potential drug candidate against breast cancers, specifically TNBCs, which can trigger autophagy-mediated cell death in breast cancer cells by inhibiting the γ-secretase–mediated activation of Notch-signaling.**
Oluwafemi Oguntibeju **ERCICRLSH1807059**	**Modulatory Effects of Moringa Oleifera Leaf Extract in Hepatic Tissue and Erythrocytes of Diabetic Animal Model** **Oluwafemi Oguntibeju** **Department of Biomedical Sciences, Cape Peninsula University of Technology, Bellville, South Africa** **Abstract** **Diabetes is a global public health problem. The study examined the modulatory effects of methanolic leaf extract of Moringa oleifera (MO) (250 mg/kg) in streptozotocin-induced diabetes in animal model. The animals (rats) were randomly divided into four groups: non-diabetic control group (Control), non-diabetic Moringa treated group (Moringa), diabetic control group (Diabetic) and diabetic Moringa treated group (Diabetic + Moringa). Antioxidant capacity and inflammatory markers as well as endogenous antioxidant enzymes (SOD, CAT, GSH, GPX) were evaluated in the plasma, serum, liver and erythrocytes respectively. Following treatment with Moringa oleifera in normal and diabetic rats daily for 6 weeks, significant improvement in antioxidant enzyme activities, improved antioxidant capacity and a reduction in inflammatory cytokines and chemokine were observed. Pancreatic histological sections revealed the protective effect of MO in non-diabetic and diabetic rats. Moringa oleifera exerted modulatory effect in STZ-induced diabetes by its antioxidant and anti-inflammatory activities.** **Key words: Moringa oleifera, diabetes, methanolic extract, streptozotocin, oxidative stress, antioxidant and inflammation.**
 **Maria Kihara** **ERCICRLSH180762**	**Characterization of Odorant Degrading Enzymes Encoding Genes in Glossina Morsitans Morsitans** **Maria Kihara** **Center for Biotechnology and Bioinformatics, University o Nairobi, Kenya** **Abstract** **Odorant degradation is an important process that involves ODEs, which facilitate insect sensitivity to odor molecules in its surrounding and chemoreception. Progress over the years has been made in characterizing ODEs in dipteran species such as Drosophila melanogaster and Antheraea polyphemus. Glycosyltransferases, cytochrome P450s, glutathione S-transferases and esterases are among the odorant degrading enzymes that have been studied in various insects, however, there is little information about ODEs in tsetse fly (Glossina morsitans morsitans), which is considered the sole cyclical vector of African trypanosomes. To understand fully, how they degrade odor from the environment, this study entailed characterization of Glossina morsitans morsitans ODEs and determining the evolutionary relationship with those in D. melanogaster. A blast search was performed against the Glossina database, Vectorbase and a number of matches were obtained for the four classes of ODEs; cytochrome p450s,**

	Esterases, glucuronosyltransferases and UDP glycosyltransferases **Multiple sequence alignments for the sequences obtained were done using MUSCLE and later edited using Jalview. Separate multiple sequence alignment analysis was done for the four classes of enzymes for the two species, D.melanogaster and G.m.morsitans, using RaXML V8 with the WAG (Whelan and Goldman) model being used and 1000 bootstrap iterations. The phylogenetic trees obtained showed that the two species had genes that were orthologous to one another.** **A De Novo RNA-Seq assembly was also done on tsetse fly antennal transcriptome sequence data with different treatments to identify the differentially expressed genes. The genes were later annotated to determine their locations and functions**
Richard Ojedele **ERCICRLSH1807064**	**Prevalence of Plasmodium Falciparum and Impact of Malaria on Haematological Parameters in Children at Lautech Teaching Hospital, Osogbo, Nigeria** **Richard Ojedele** **Medical Microbiology and Parasitology, Ladoke Akintola University of Technology, Ogbomoso, Nigeria** **Abstract** **Malaria is a major problem in children particularly in developing countries. High mortality is usually compounded by various haematological complications if left untreated. The aim of this study was to determine the prevalence of P. falciparum and it's impact on haematological parameters in children at LAUTECH Teaching Hospital Osogbo.** **5mls of blood each was collected from 300 children subjected to Giemsa's stained thin and thick blood films for microscopy and also Rapid Diagnostic Test (RDT) method was used for the detection of P. falciparum. Haematological parameters were determined while Mean Cell Volume (MCV), Mean Cell Haemoglobin (MCH), Mean Cell Haemoglobin Concentration (MCHC) and Red Cell Distribution Width (RDW) were estimated using Mindray blood analyzer.** **36 (12%) were positive by RDT while 44 (14.6%) were positive by microscopy. The total parasite density was 7945.45p/µl of blood. Age group 5-10 years recorded the highest mean parasite density of 9722.22p/µl at ($P = 0.001$). The mean platelet counts for malaria positive group ($247.76 \pm 125.26 \times 103/\mu l$) was lower than non infected group ($292.79 \pm 136.38 \times 103/\mu l$) at ($P = 0.062$). The total mean leucocyte counts in infected group ($9.36.36 \times 103/\mu l$) while non-infected group (10.47 ± 8.60) ($P = 0.45$). A significant difference was observed in the mean haemoglobin of malaria infected group (11.25 ± 3.18) to non-infected group (12.25 ± 3.18) ($P = 0.025$). The PCV was also lowered among infected group (32.84 ± 7.68) to non-infected group (35.79 ± 4.93) ($P < 0.05$). The mean eosinophil count of the infected group was higher (2.45 ± 2.52) than non-malaria infected group (1.85 ± 2.10) ($P > 0.05$). The lymphocyte count of the malaria infected group was lower (37.78 ± 17.53) than non-infected group (41.03 ± 17.86) ($P > 0.05$).**
Umm-e-Laila **ERCICRLSH180765**	**Child Psychology Monitoring and Learning System** **Umm-e-Laila** **Computer Engineering Department, Sir Syed University of Engineering and Technology, Karachi, Pakistan**

Abstract

Devices such as cell phones, tablets, laptops, etc. have become children's material support when they are being neglected by parents. Without emotional support, there is little parental guidance and children will eventually suffer from insecurity, depression, and anxiety. Thus, to bridge this gap that is called emotional detachment between parents and their children, we came up with the idea of CPMLS.

This paper explores the different aspects of Child Psychology and introduces an android based application, called Child Psychology Monitoring and Learning System (CPMLS) which is designed to assist parents in monitoring the psychological state of their child. It is designed for children between the ages of 3-9 year and is grouped into three categories i.e. 3-5, 6-7 and 8-9. Within this application, there is a variety of digital games that will test the level of emotional and social intelligence within the child. As a result, parents can keep track of what their child is experiencing on a psychological level.

Keywords—-Play, Child Psychology, Monitoring, Mental growth, Development stages

Manoj M.C.
ERCICRLSH1807068

Master's Degree Dissertation thesis

Manoj M.C.
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Abstract

Introduction: Emergence of Methicillin Resistant Staphylococcus aureus (MRSA) strain has become a global concern in 21st century. So, it is necessary to recover new antibiotics against this pathogen. Objective: The main objective of this study was to screen Bacillus with anti-MRSA activity from different soil samples. Materials and Methods: Serially diluted soil samples were spread plated on Nutrient Agar plates and Bacillus colonies with zone of inhibition around them were selected. They were screened first against S. aureus ATCC 25923 followed by clinical isolates of MRSA by spot inoculation technique. From the isolates of Bacillus with positive screening test, antimicrobial compounds were produced. The yield, MIC value and proteinaceous nature of the extract was determined and tested against other drug resistant isolates of bacteria. Results: From 60 soil samples, Altogether 11 isolates of Bacillus with anti-MRSA were screened as antibiotic producing strains from which only 6 isolates revealed anti-MRSA in secondary screening. Among them maximum antimicrobial effect was revealed by Bacillus subtilis (isolate 4X6) with a crude yield of 749.66µg/mL and MIC value of 1097.45 µg/mL on MRSA. The extract also had antimicrobial activity against ESBL producing E. coli and Salmonella Typhi but not against Pseudomonas aeruginosa. The extract was proteinaceous in nature. Conclusion: This study concludes that Bacillus with anti-MRSA activity can be found in soil. Considering the antimicrobial effect of the isolates especially against MRSA, intended compounds can be purified that may act as lead molecules for further researches.

Key words: Bacillus, Polypeptide, anti-MRSA, Antibiotics, Soil, Drug Resistance, Spot-inoculation

Novel regulators of female reproduction

Alexander Sirotkin

Alexander Sirotkin
ERCICRLSH1807051

Faculty of Natural Sciences, Constantine the Philosopher, University in Nitra, Nitra, Slovak Republic

Abstract

Development in animal biotechnology, assisted reproduction, human and veterinary medicine requires search for new regulators of reproductive functions. This is the review of original data concerning the role of some metabolic hormones (GH, leptin, ghrelin, obestatin), growth factors (IGF-I, IGFBPs, EGF, thrombopoietin), intracellular mediators of their action (cyclic nucleotides, protein kinases, transcription factors and related cDNA, siRNA and miRNA gene constructs) on basic ovarian functions (cell proliferation, apoptosis, secretion, oogenesis, ovulation, production and viability of pups) in different species (pig, rabbit, humans and chicken). Practical applications of some these molecules for characterization, prediction and control of reproductive processes in these species was examined too.

It was shown that these hormonal and intracellular regulators are able to control apoptosis, proliferation and secretory activity in porcine, rabbit, human and chicken ovarian cells and maturation of porcine oocytes and cumulus oophorus in vivo and in vitro, as well as to suppress or promote the response of ovarian cells to other hormones (gonadotrophins, IGF-I, ghrelin). Immuno-blockade of these hormones prevented their effects. Effects of hormones on rabbit, human and chicken ovarian cells and on porcine and bovine oocytes were associated with changes in PKA, MAPK and CDK and transcription factors CREB, STAT-1 and p53 in such cells, whilst blockers of these kinases prevented or promoted hormones action. Transfection of porcine and rabbit granulosa cells with gene constructs for these transcription factors affected ovarian cell functions and prevented or reversed hormones action. Down-regulation of approx. 1./3 known protein kinases by specific siRNA constructs resulted not only decrease in accumulation of these kinases within human ovarian granulosa cells, but also changes in expression of kinase-dependent transcription factors, markers of cell proliferation, apoptosis and release of steroid hormones and IGF-I. Transfection of human granulose cells with constructs up and down regulating expression of some miRNAs are able to increase or decrease ovarian cell proliferation, occurrence of apoptosis, as well as the release of progestagen, androgen, estrogen and IGF-I . In-vivo experiments demonstrated that leptin, IGF-I, steroid hormones and some regulators of PKA, MAPK and CDK could be used to predict reproductive efficiency, for direct in-vitro control of maturation of oocytes and for in-vivo stimulation of reproduction in pigs and rabbits.

These observations suggest, that metabolic hormones, growth factors and intracellular regulators and mediators of their action (protein kinases, transcription factors, siRNAs, miRNAs) can be used for characterization of state of ovarian cells, for identification signaling pathways (hormones-growth factors-protein kinases-transcription factors-genes regulating proliferation, apoptosis and secretory activity) controlling reproductive processes, as well as for prediction and control of basic ovarian cell functions (proliferation, apoptosis, secretory activity, maturation of oocyte-cumulus complex and fertility).

Molecularly Imprinted Polymers in Cosmetics: A New Deodorant Approach

Jeanne Bernadette Tse Sum Bui
CNRS Enzyme and Cell Engineering, University of Technology of

Jeanne Bernadette Tse Sum Bui
ERCICRLSH1807057

Compiegne, Compiegne, France

Abstract

Axillary (armpit) malodors are mainly caused by volatile medium chain branched fatty acids, produced from their non-odorant glutamine conjugate precursors by the action of bacteria, commensal to the skin. In order to combat malodors, we have synthesized a molecularly imprinted polymer (MIP) that can capture the glutamine conjugate precursors in human sweat, hence preventing their transformation into malodorous acids1 (Figure 1). The MIP, blended in a dermo-cosmetic deodorant formulation, can selectively capture the undesirable molecules in human sweat, despite the presence of a multitude of other molecules contained in this complex medium.2 The diameter of the MIP particles was around 600 nm and therefore they cannot penetrate into the skin. The biological effects of the MIP in terms of epidermal cell viability and irritation (cytotoxicity and release of proinflammatory cytokines) were assessed in vitro on human keratinocytes (HaCaT cells). Furthermore, the MIP does not affect the growth of skin bacteria (staphylococcus epidermidis, corynebacterium striatum and micrococcus luteus) isolated from human sweat, indicating that the MIP will not perturb the fragile microbial equilibrium of the skin.3 This innovative application of MIPs meets the needs of cosmetic industries in the development of mild deodorant active ingredients as alternatives to the currently-used unspecific antimicrobials, hence preserving the integrity of the skin microbiota.

Maria Awuor Kihara
ERCICRLSH1807062

Characterization Of Odorant Degrading Enzymes Encoding Genes In Glossina Morsitans Morsitans.

Maria Awuor Kihara
Center for Biotechnology and Bioinformatics,University Of Nairobi,Kenya

Abstract

Odorant degradation is an important process that involves ODEs, which facilitate insect sensitivity to odor molecules in its surrounding and chemoreception. Progress over the years has been made in characterizing ODEs in dipteran species such as Drosophila melanogaster and Antheraea polyphemus. Glycosyltransferases, cytochrome P450s, glutathione S-transferases and esterases are among the odorant degrading enzymes that have been studied in various insects, however, there is little information about ODEs in tsetse fly (Glossina morsitans morsitans), which is considered the sole cyclical vector of African trypanosomes. To understand fully, how they degrade odor from the environment, this study entailed characterization of Glossina morsitans morsitans ODEs and determining the evolutionary relationship with those in D. melanogaster. A blast search was performed against the Glossina database, Vectorbase and a number of matches were obtained for the four classes of ODEs; cytochrome p450s, Esterases, glucuronosyltransferases and UDP glycosyltransferases

Multiple sequence alignments for the sequences obtained were done using MUSCLE and later edited using Jalview. Separate multiple sequence alignment analysis was done for the four classes of enzymes for the two species, D.melanogaster and G.m.morsitans, using RaXML V8 with the WAG (Whelan and Goldman) model being used and 1000 bootstrap iterations. The phylogenetic trees obtained showed that the two species had genes that were orthologous to one another.

A De Novo RNA-Seq assembly was also done on tsetse fly antennal transcriptome sequence data with different treatments to identify the

	differentially expressed genes. The genes were later annotated to determine their locations and functions.

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Upcoming Conferences

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- 2018 – 8th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 22-23 Dec, Bangkok
- 2018 – 9th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 27-28 Dec, Dubai
- 2018 – 10th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 30-31 Dec, Bali
- 2019 – 2nd International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 08-09 Feb, Bangkok
- 2019 International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 27-28 Feb, Dubai
- 2019 – 3rd International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 16-17 March, Singapore
- 2019 – 4th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 12-13 April, London
- 2019 – 5th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 04-05 May, Rome
- 2019 – 6th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 07-08 June, Prague
- 2019 – 7th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 29-30 June, Malaysia
- 2019 – 8th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 28-29 June, Lisbon

- 2019 – 9th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 29-30 June, Singapore
- 2019 – 10th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 12-13 July, Bali
- 2019 – 11th International Conference on Research in Life-Sciences & Healthcare (ICRLSH), 12-13 July, Budapest