PLENARY SESSIONS

Plenary I
Preventing HIV
Salim Abdul Karim (South Africa)
Thursday • April 3, 2014 • 9:00–9:45hrs

Plenary II
Community Directive Initiative and Neglected Tropical Diseases
Uche Amazigo (Nigeria)
Thursday • April 3, 2014 • 14:30–15:15hrs

Plenary III
Old and New Global Challenges in Infectious Diseases
Peter Piot (United Kingdom)
Friday • April 4, 2014 • 9:00–9:45hrs

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Plenary IV
Otitis Media as an Infectious Disease: the Debate Goes On
Ron Dagan (Israel)
Friday • April 4, 2014 • 14:30–15:15hrs

Plenary V
Influenza: Understanding Pathogenesis to Improve Outcomes
Jonathan McCullers (USA)
Saturday • April 5, 2014 • 9:00–9:45hrs

Plenary VI
MERS-COV
Ziad Memish (Saudi Arabia)
Saturday • April 5, 2014 • 14:30–15:15hrs

Congress Website: http://isid.org/icid/
MEET-THE-EXPERTS
Invasive Non-typhoid Salmonellosis (iNTS): Increasing Awareness and Future Vaccines
- An Overview of iNTS Epidemiology
  Myron Levine (USA)
- Bivalent Vaccine Strategies for Invasive Non-typhoidal Salmonella Infections
  Sharon Tennant (USA)
Prevention and Management of UTI and Urosepsis
Kurt Naber (Germany)

Publishing Your Work: Perspectives From the Editor in Chief of IJID
Eskild Petersen (Denmark)
The Use of Viral Load Monitoring and Virus Genotyping in the Management of Hepatitis
RK Ratho (India)

SYMPOSIA
Rickettsiosis in Africa
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  D. Raoult (France)
- Role of Delocalized Point of Care Diagnosis of Rickettsioses in Africa
  C. Sokhna (Senegal)
- Rickettsial Disease in Febrile Patients in Africa With or Without Malaria
  O. Doumbo (Mali)
- Rickettsial Disease in Eastern Africa
  TBD
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- Vaccine Confidence and Public Trust as Drivers of Vaccine Failure
  H. Larson (UK)
- Tuberculosis Vaccines
  W. Hanekom (South Africa)
- The Challenge of Vaccinating in Emergency Settings
  J. Cohn (USA)
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- New Diagnostics for Childhood Pneumonia
  D. Murdoch (New Zealand)
- Clinical Spectrum and Complications of Childhood Pneumonia in the Era of Bacterial Conjugate Vaccines
  S. Madhi (South Africa)
- Future Streptococcus Pneumoniae Vaccines
  M. Alderson (USA)
- Can Adult Pneumonia be Prevented by Adult PCV Vaccination?
  M. Bonten (The Netherlands)

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  A. Wilder-Smith (Singapore)
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  K. Edwards (USA)
- Endgame Polio: Vaccine Strategies to Achieve an End
  J. Modlin (USA)
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  K. Neuzeil (USA)

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  D. Pittet (Switzerland)
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- Getting Drug Doses Right in Children with Tuberculosis
  H. McIlleron (South Africa)
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16th ICID ~ Plenary Speakers

Salim S. Abdool Karim
Preventing HIV

Uche Amazigo
Community Directive Initiative and Neglected Tropical Diseases

Peter Piot
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Ron Dagan
Otitis Media as an Infectious Disease—The Debate Goes On

Jonathan A. McCullers
Influenza: Understanding Pathogenesis to Improve Outcomes

Ziad A. Memish
MERS-COV
Beginning in January 2014 the *International Journal of Infectious Diseases* will become an open access journal.

From January 2014 the *International Journal of Infectious Diseases* will become an open access journal with no subscription charges. An Open Access Publishing Fee (OAPF) payable by the author or research funder, will be requested after peer review and acceptance. This fee is required for all articles submitted after 16th August 2013.

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Digital Disease Detection Workshops
ProMED participated in workshops in Vietnam, Ethiopia and Morocco in November to train epidemiologists and other members of the public health community on ‘informal disease surveillance.’

Participants in the DDD Workshop in Marrakech, Morocco engage in exercises.

ProMED Deputy Editor,
Dr. Marjorie Pollack, leading the DDD workshop in Addis Ababa, Ethiopia.
The International Meeting on Emerging Diseases (IMED 2014) is organized by the International Society for Infectious Diseases (ISID) and its Program for Monitoring Emerging Diseases (ProMED-mail). Emerging infectious diseases are at the center of the world’s attention. The threats posed by pandemic influenza, bioterrorism and the realization that new infectious diseases may be recognized at any time, in any place, have dramatically raised our awareness and our need to understand emerging pathogens. What are the most important emerging disease threats? What biological, ecological, social and other factors lead to their emergence? How can we quickly detect their occurrences in order to respond in timely and appropriate ways? This meeting will fully embody the “one health” model of emerging diseases, recognizing the commonality of human and animal health.

The deadline for abstract submission will be July 2014.

**Target Audience:** Healthcare professionals including physicians, and veterinarians, public health specialists, epidemiologists, research scientists, pharmaceutical and biotechnology industry, journalists, other interested persons.

**Planned session topics include:**

- Methods and Models of Disease Surveillance, Detection and Reporting
- Emerging Zoonoses and Animal Health Threats
- Animal Reservoirs for Emerging Pathogens
- Biosecurity and Agents of Bioterrorism and Biological Warfare
- Infections Related to Travel and Migration of Humans and Animals
- Vectorborne Diseases
- Epidemiology of Emerging Pathogens
- Diagnostic Tests for Emerging Pathogens
- Foodborne and Waterborne Pathogens
- Specific Disease Threats: Pandemic, Avian, and Swine Influenza; MERS Coronavirus; Rift Valley Fever; Drug-Resistant Pathogens; Chikungunya; Anthrax; Shiga-toxin producing E. coli; West Nile Virus; Viral Hemorrhagic Fevers; Schmallenberg Virus; Transmissible Spongiform Encephalopathies; Healthcare Associated Infections and Others.
- Vaccines Against Emerging Diseases
- Social, Political and Economic Factors in Disease Emergence
- Submitted Abstracts (Oral and Poster)
2013 Small Grant Awardees:

Dr. Gbemisola Boyede, South Africa
Infectious Disease Clinic, Red Cross War Memorial Children’s Hospital
Validation of a new developmental screening tool for neurodevelopmental delays among HIV-infected South African children

Ms. Yagahira Castro Sesquen, Peru
Laboratorio de Investigación en Enfermedades Infecciosas, Universidad Peruana Cayetano Heredia
Novel nanotechnology for urine antigen detection in congenital Chagas disease

Dr. Admasu Mamuye, Ethiopia
Department of Internal Medicine, School of Medicine, College of Health Sciences, Addis Ababa University
Utilizing point-of-care test for cryptococcal screening among HIV-infected persons in Ethiopia

Dr. João Marques, Brazil
Department of Biochemistry and Immunology, Institute for Biological Sciences, Universidade Federal de Minas Gerais
RNA Interference: a tool for identifying and controlling dengue virus and other arboviruses in insect vectors

Mr. Erick Muok, Kenya
Schistosomiasis Research Unit, Center for Global Health Research, Kenya Medical Research Institute
Evaluation of schistosomiasis treatment efficacy and re-infection patterns in children co-infected with Schistosoma haematobium and S. mansoni in western Kenya

2013 ISID/ESCMID Fellowship Awardees:

Dr. Syed Hani Abidi, Pakistan
Department of Biological and Biomedical Sciences, Aga Khan University
To study at the Nuffield Department of Medicine, John Radcliffe Hospital, Oxford, UK
Epitope evolution of HIV in genetically distant populations

Dr. Rodrigue Nguema Mintsa, Gabon
Department of Parasitology–Mycology, Faculty of Medicine, University of Health Science, Libreville
To study at the Université de Pergignan, Perpignan, France
Schistosomiasis in Estuaire Province of Gabon: What is the situation?

2013 ISID Fellowship Awardees:

Mr. Johnson Mosoko Moliki, South Africa
Department of Molecular and Cell Biology, University of Cape Town
Research to be done at McMaster University, Hamilton, Ontario
Skills development and technology transfer to investigate the molecular mechanisms of regulation of primary epithelial cell tight junctions of the female genital tract by contraceptives, hormones and HIV-1

Dr. Maria de las Mercedes Pescaretti, Argentina
CONICET, PROIMI-INSIBIO, Universidad Nacional de Tucumán
Research to be done at University of Utah, Salt Lake City
Study of the secretion flagellar proteins in the rcsC11 mutant to serve as a model of vaccine against Salmonella typhimurium

Grant Application Deadlines:
Small Grants Program – April 1, 2014
SSI/ISID Fellowship – April 1, 2014
ISID Scientific Exchange Fellowship – March 1, 2014
ISID/ESCMID Fellowship – March 1, 2014
More information and application materials are available at http://www.isid.org/grants/grants.shtml
In vitro assays of 2,5-dihydroxibencil derivatives on Trypanosoma cruzi and Leishmania donovani

Rolón Miriam1, Enrique Pandolfi2, Celeste Vega1, Antonieta Rojas de Arias1

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2 Faculty of Chemistry, University of the Republic, Montevideo, Uruguay

Introduction

The effort to find more effective and affordable forms of treatment for Chagas disease and Leishmaniasis is framed in the priority list of the WHO. Currently, drugs used to treat these diseases are seriously limited given the following reasons: they are expensive and efficaciously questionable; they require prolonged treatment and regular medical supervision; and, they have significant side effects. The search for new drugs is needed to help treatment efforts in Latin America. Conservative figures show that 8 million people are infected with Chagas disease, including the 50,000 people who die annually. Moreover, for leishmaniasis, an estimated 12 million people are infected worldwide, and 350 million people are at risk of acquiring Leishmaniasis (1). Leishmaniasis is a vector-borne disease that affects 72 countries in total; 13 of these are least developed countries. Visceral Leishmaniasis (VL) is the most severe form of Leishmania infections and it annual incidence is estimated 500,000 new cases and 60,000 deaths occur each year (2, 3).

For these reason, the main objective of this project was to establish a sequential and rationale screening of new compounds by using in vitro assays on T. cruzi and L. donovani to decrease the access time in the development of new antiprotozoan drugs. The potent in vitro and in vivo pharmacological activity showed for 2 out of 14 phenolic derivatives, with high activity on T. cruzi and Leishmania sp and low toxicity on mammalian cells (Grant BID/FAPEP 1691-OC/PR–CONACYT–Paraguay) motivated this proposal. These 2,5-dihydroxybibencyl derivatives compounds have served as trypanocidal and leishmanicidal lead compound and new twelve derivatives were synthesized for their evaluation to obtain a small library of active and non-toxic compounds.

Materials and Methods

1. Chemistry. In the library design, we selected the 2,5-dihydroxybenzyl unit as active structure for combinatorial derivatization (4).

2. Epimastigote susceptibility assay: The screening assay was performed in 96-well microplates with CL-B5 of T. cruzi epimastigotes cultures. Epimastigotes were seeded at 1 x 10⁵ per milliliter in 200 µL. The plates were then incubated with the drugs at 28˚C for 72 hours, at which time 50 µL of CPRG solution was added. The plates were incubated at 37˚C for an additional 4 h and were then read at 595 nm (5).

3. Promastigote susceptibility assay: The assay was performed using L. donovani (MHOM/IN/80/DD8) promastigotes. Promastigotes (2.5x10⁶ parasites/well) was cultured in 96-well plastic plates. Different dilutions of the compounds up to 200 µL final volume were added. After 72 h at 26˚C, 20 µL of 2.5 mM resazurin solution was added and the oxidation-reduction was quantified at 570 and 595 nm (6).

4. Cytotoxicity assays: The cell lines used were NCTC clone 929 and murine J774 macrophages. The procedure for cell viability measurement is evaluated with resazurin (19) by a colorimetric method (7).

This research was supported with a grant from the International Society for Infectious Diseases (ISID).
Results and Discussion

Twelve new hydroxybenzyl derivatives compounds, called AP24, AP28, AP29, AP30, AP31, AP32, AP38, AP40, AP43, AP44, AP45, and AP47 were synthesized and tested on parasites of *T. cruzi* epimastigotes and *L. donovani* promastigotes and macrophages and fibroblast cell lines. These compounds are 2,5 dihydroxybibencyl derivatives and present different substituents, divided into five groups: AP24 and AP28 are hydroxyphenyl derivatives; AP29 and AP31 are alkyloxyphenyl derivatives; AP30, AP32, AP38, and AP47 are alkyl derivatives; AP43, AP44 and AP45 are halophenyl derivatives; and AP40 is a pyridyl derivative.

The new compounds present different substituents such as alkyl, hydroxyphenyl, alkyloxyphenyl, and halogen groups. The halophenyl derivatives were more active on *T. cruzi*, particularly AP44, a fluorophenyl derivative, with IC₅₀=38 µM, CC₅₀=351 µM and SI= 9. Only the halophenyl derivative AP45 showed a selective activity on *L. donovani* parasites with IC₅₀= 26 µM, CC₅₀= 91 µM and SI= 4. All compounds were less toxic on J774 macrophage and NCTC 929 cells, except the alkyl derivative AP47 that presented higher toxicity than both reference drugs. Six out of twelve compounds assayed showed trypanocidal activity and one of them also has leishmanicidal activity.

Conclusions

Trypanocidal and leishmanicidal activity of twelve new dihydroxybencyl derivatives were tested in vitro, six of them showed trypanocidal activity and one also presented a leishmanicidal activity. Three of these compounds are halophenyl derivative (AP43, AP44, AP45), and the other are alkyloxyphenil (AP31), alkyl (AP38) and pyridyl (AP40) derivatives.

In view of the results obtained, the tested compounds are very promising and should advance to the next stage of pharmacological screening in order to assess their potential activity against in vitro intracellular amastigotes.

References

Distribution of trypanosomes within tsetse in northern Nigeria

Clement Isaac,1,2 Alana Hamilton,2 Kathleen Scullion,2 Marc Ciosi,2 P.M. Dede,1 I.B.I. Ighinosa,1 O.P.G. Nmorsi,1 Dan Masiga,2,4 C. Michael R. Turner2

1 Ambrose Alli University, Ekpoma, Nigeria
2 Institute of Infection, Immunity and Inflammation, Sir Graeme Davis Building, University of Glasgow, 120 University Place, Glasgow G12 0PT, UK
3 Nigerian Institute of Trypanosomiasis Research, Kaduna, Nigeria
4 The International Centre of Insect Physiology and Ecology (ICIPE), Nairobi, Kenya

Background

Tsetse-transmitted trypanosomes are the etiological agents of African trypanosomiasis. This disease, a major contributor of poverty in Africa has been estimated to cause financial losses worth billions of dollars in potential agricultural production with *T. congolense*, *T. vivax*, *T. simiae*, *T. evansi* and *T. brucei brucei* being the major causative parasites. In Nigeria, several studies on the prevalence and distribution of trypanosomes in tsetse and mammalian hosts have shown varying infection rates of *T. vivax*, *T. congolense*, *T. brucei*, and *T. simiae* and *T. suis* [1,2,3,4,5]. These authors have used conventional parasitological tools in the diagnosis of trypanosomes. However, this method that employs microscopy has been greeted with some shortcomings and therefore not completely reliable. For instance, microscopic investigation cannot be specific for genetically different but morphologically similar trypanosomes including its inability to detect immature or mixed infections. Another limitation can be seen in cases of very low infections where parasites may be very difficult to detect.

In order to overcome these challenges, specific and sensitive molecular tools have to be applied. ITS1-PCR is now widely used for trypanosomes diagnosis [6,7,8]. The application of these universal primers has been seen to considerably reduce the time and costs used in trypanosome diagnosis compared to species-specific PCR diagnosis. However, the use of any of these PCR tools is still perceived to be relatively expensive and therefore scarcely considered in disease diagnosis in Nigeria.

Presently, there is no epidemiological data showing the distribution of trypanosome parasites in Nigeria (NITR-conference communication, 2013). In order to attain elimination through an effective control programme, accurate information regarding the prevalence and distribution of *Trypanosoma* species in tsetse and mammalian hosts is urgently needed. In an attempt to partly achieve this, we screened tsetse flies collected in endemic areas of Niger and Bauchi (Yankari) States using PCR diagnostic tools. Information arising from this investigation will provide evidence in reassessing the disease risks in Nigeria.

Results and Discussion

We screened 488 tsetse flies of three species for the presence of trypanosomes using ITS1 primers. All samples that were PCR positive for *T. congolense* were then screened to determine which clade of this species they belonged to. The overall prevalence data for the three species and Savannah clade shows prevalence levels of *T. brucei*, *T. congolense* and *T. congolense* Savannah in the range 2.5–14 %. In addition, one case of *T. godfreyi* was detected in *G. tachinoides*, one case of *T. simiae* detected in *G. morsitans* and five cases of *T. congolense* Forest were detected—four in *G. tachinoides* and one in *G. morsitans*. This low infection rate of *T. godfreyi* and *T. simiae* in tsetse could be an indication of low transmission rate of these parasites in Yankari, a game reserve which is home to some wildlife animals [9].

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To assess transmission potential to a little extent, DNA preparations from abdomen (ABD) and head + proboscis (H+P) samples were screened from the majority of the flies. For *T. congolense*, there were very few flies that were positive in both locations and most infections were found only in the abdomen samples ($\chi^2=8.47$, d.f.=1, $p>0.01$). We would offer two potential explanations for this result. Firstly, these data may simply reflect the known biology of the *T. congolense* life cycle [10,11]; the positive samples in the abdomens reflect immature infections and only a subset of these would expect to develop into mature infections in the mouthparts. Also, some flies would expect to be too young when trapped for mature infection to have developed. Second, many abdomen samples will have contained blood which is an inhibitor of PCR. In contrast, *T. vivax* was detected only in the H+P samples ($\chi^2=20.05$, d.f.=1, $p>0.001$), reflecting that these parasites develop only in the mouthparts [12]. The data for this parasite however give useful guidance that only active infections have been detected; any *T. vivax* parasites ingested into the midgut in the act of tsetse feeding will have been killed and the PCR procedure employed has not detected any signal from the degraded remains of the DNA from the dead parasites.

The differences in prevalence between male and female flies of each of the three species of tsetse are shown in Table 1 for all trypanosome infections, *T. congolense*, *T. congolense* Savannah and *T. vivax*. The general trend is that infection prevalences were higher in female than in male flies, except for *T. congolense* and *T. congolense* Savannah in *G. palpalis*. To investigate the differences in prevalence between the sexes and host species more rigorously we undertook a forward step-wise regression analysis, the outputs of which are summarized in Table 2. As these results show, the higher prevalence of infection in female flies compared with male is almost entirely caused by the differences in prevalence in *T. vivax* infections (Table 1). The differences for *T. congolense* show the same trend but are not significant. In contrast, the data for species differences show that it is the lower prevalence of *T. congolense* in *G. palpalis* compared with the other two species (Table 1) that is statistically significant (Table 2). This finding needs to be treated with considerable caution however, as there is the confounding variable that the *G. palpalis* samples are from Niger whereas *G. tachinoides* and *G. morsitans* are both from Bauchi (Yankari) i.e. the real effect may be a difference in site rather than species but we do not have multiple species from both sites that would allow us to analyse this potential difference.

**Table 1.** Comparison of % prevalences of trypanosomes in male and female flies.

<table>
<thead>
<tr>
<th>Species</th>
<th>sex</th>
<th>n</th>
<th>All trypanosomes (%)</th>
<th><em>T. congolense</em></th>
<th><em>T. congolense</em> Savannah</th>
<th><em>T. vivax</em></th>
</tr>
</thead>
<tbody>
<tr>
<td><em>G. palpalis</em></td>
<td>Male</td>
<td>98</td>
<td>6.1</td>
<td>3.1</td>
<td>3.1</td>
<td>3.1</td>
</tr>
<tr>
<td></td>
<td>Female</td>
<td>100</td>
<td>8.0</td>
<td>2.0</td>
<td>2.0</td>
<td>6.0</td>
</tr>
<tr>
<td><em>G. tachinoides</em></td>
<td>Male</td>
<td>40</td>
<td>2.5</td>
<td>2.5</td>
<td>2.5</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>Female</td>
<td>161</td>
<td>14.3</td>
<td>9.9</td>
<td>6.2</td>
<td>5.6</td>
</tr>
<tr>
<td><em>G. morsitans</em></td>
<td>Male</td>
<td>17</td>
<td>11.8</td>
<td>5.9</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>Female</td>
<td>72</td>
<td>13.9</td>
<td>8.3</td>
<td>8.3</td>
<td>5.6</td>
</tr>
</tbody>
</table>

continued on next page
Table 2. Logistic regression analysis of the effects of sex and tsetse species on infection with trypanosomes. Significant results are shown in bold.

<table>
<thead>
<tr>
<th>Output variable</th>
<th>Sex</th>
<th>Species</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>t-values</td>
<td>p</td>
</tr>
<tr>
<td>All trypanosomes</td>
<td>1.97</td>
<td>0.05</td>
</tr>
<tr>
<td>T. congolense</td>
<td>2.40</td>
<td>0.02</td>
</tr>
<tr>
<td>T. congolense Savannah</td>
<td>2.02</td>
<td>0.04</td>
</tr>
<tr>
<td>T. vivax</td>
<td>1.98</td>
<td>0.05</td>
</tr>
</tbody>
</table>

Conclusion
The screening of tsetse reveal that there is active transmission of trypanosomes in these areas in which T. vivax and T. congolense Savanna are likely to be the main parasites responsible for African Animal Trypanosomiasis (AAT) in livestock. We advocate that screening for trypanosomes should be extended to livestock in these endemic regions and beyond using molecular tools. This undoubtedly will provide better and more reliable information on the distribution of Trypanosoma species in Nigeria with the view of effectively adopting the most appropriate control measures in achieving disease elimination.

References
Study the secretion flagellar proteins in the \textit{rcsC11} mutant to serve as a model of vaccine against \textit{Salmonella Typhimurium}

Mercedes Pescaretti, PhD • Instituto de Química Biológica-UNT-CONICET/Argentina

Background

The members of genus \textit{Salmonella} are Gram-negative bacteria causative of foodborne diseases in human and animals (1). \textit{Salmonella} can survive and respond to adverse environmental changes through the regulation of gene expression mainly by the two component regulatory systems. The RcsCDB system controls a variety of cellular functions, mainly those genes involved in virulence (2-7).

The use of attenuated strains of \textit{Salmonella} as vaccines is a useful method to transport heterologous antigens to eukaryotic cells. We are interested in the study of the role of RcsCDB system in the \textit{S. Typhimurium} virulence responsible to produce gastroenteritis in human and typhoid fever in mice (8). Previously, we showed that the \textit{rcsC11} mutant dramatically attenuates bacterial virulence and when inoculated into mice intraperitoneally led to an immunogenic response that resulted in a protection (9). This result allowed us to postulate that the RcsCDB system is a good candidate for vaccine development. On the other hand, the RcsCDB activation by the \textit{rcsC11} mutant reduces the expression of the genes encoding invasion proteins as well as those involved in the flagellin synthesis (10,11). Here, we proposed that bypass of the flagella synthesis repression in the \textit{rcsC11} mutant could be used to increase the host immune response without modifying the mutant virulence attenuation.

Main Activities Conducted

In order to bypass the inhibition of the \textit{flhDC} expression in the \textit{rcsC11} mutant, point mutations affecting the RcsB binding site were introduced into \textit{flhDC} promoter region. The point mutations were chosen based upon an earlier mutagenesis study (Wozniak \textit{et al}., 2009). We used the following mutants: -190::A (BS#1), -189C:T (BS#4) and -198A:G (BS#5) (Wozniak \textit{et al}., 2009). The introduction of these point mutations in the \textit{S. Typhimurium} 14028s strain and the isogenic \textit{rcsC11} mutant was carried out by transduction with the phage of \textit{S. Typhimurium} P22 HT105/1 int-201.

The resulted mutants were characterized for the effect on motility. The point mutations BS#1, BS#4 and BS#5 significantly increased motility compared with the wild-type strain. Surprisingly, the introduction of these mutations in an \textit{rcsC11} strain restored the motility of this strain at wild-type levels. We selected the \textit{rcsC11} BS#1 mutant for the next assays.

Transcriptional fusion to the \textit{fliL} gene was utilized to investigate the effect of the BS#1 point mutation in the \textit{rcsC11} mutant. We observed that the BS#1 mutation in the \textit{rcsC11} mutant was able to bypass the inhibition of RcsB regulator on the \textit{flhDC} transcription.

For the analysis of the formation of flagella in \textit{rcsC11} BS #1 mutant, the swarming cell were fluorescently labeled to look for changes in number of flagellar basal structures assembled compared to the wild-type strain. We used a GFP fusion to a component of the C-ring, FliM, to analyze assembled C-rings by fluorescent microscopy. The wild-type strain displayed normal number hook-basal-bodies (HBB) per cell. Importantly, the numbers of completed

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HBBs in the rcsC11 BS #1 mutant were greatly increased. This data demonstrate that the rcsC11 BS #1 mutant bypass the inhibition of the flhDC in rcsC11 mutant, increasing the HHB structures per cell.

In order to measured the FlgE secretion in rcsC11 BS#1 mutant, we improved an established reporter system consisting of the flagellar T3S-specific substrate FlgE fused to β-lactamase lacking its own Sec-dependent secretion signal (FlgE-Bla) (12,13). The FlgE-Bla protein fusion was assayed in an flgBC mutant that results in FlgE-Bla secretion into the periplasm where it confers resistance to β-lactam antibiotics. As this fusion protein is only secreted via the flagellar-specific T3S system, this system enables us to quantify the levels of secretion of FlgE with Minimal Inhibitory Concentration (MIC) ampicillin (Ap) assays. The presence of the BS#1 point mutation in the rcsC11 mutant confers resistance to high levels of Ap. The Ap' observed in the rcsC11 BS#1 mutant strain was dependent on both the flagellar gene expression and the presence of flagellar secretion apparatus.

**Conclusion**

In conclusion, we have demonstrated that the recombinant live strain constructed in this study, the rcsC11 BS#1 mutant, is able to produce and express flagella. We propose that the expression of flagella in this attenuated bacterial strain will produce the delivery of these antigens to the immune system leading to a relevant immune response. Mouse immunogenicity and challenge experiments are underway to determine if this mutant can be used as oral vaccine able to confer protection against infections with a *Salmonella* virulent strain.

**References**

2014

2–5 April
16th International Congress on Infectious Diseases
Cape Town, SOUTH AFRICA
http://www.isid.org/icid
Encompassing all of the fields in infectious diseases with particular attention being paid to the major infectious causes of death in Africa and elsewhere, which include AIDS, malaria, TB, pneumonia and enteric infections including typhoid fever and diarrhea. In all of these fields there are exciting interventions underway in Africa, the results of which will be presented in Cape Town. The ISID has always had its focus on the global burden of infectious diseases and it is important for us to announce our return to Africa some 20 years after the last meeting of the Society there in Kenya in 1992.

6–10 May
32nd Annual Meeting of the European Society for Paediatric Infectious Diseases (ESPID 2014)
Dublin, IRELAND
http://espid.kenes.com/
Benefit from an unparalleled educational forum, where you will learn about the newest developments, innovative techniques, and advanced practices in Paediatric Infectious Diseases. ESPID 2014 will include interactive case sessions, platform presentations, educational workshops, networking sessions, meet the professor sessions and more, which will be presented by international experts. This is your opportunity to gain new knowledge in the field of Paediatric Infectious Diseases and exchange new ideas with experts and colleagues from around the world.

7–10 May
HIV in the Americas Congress
Rio de Janeiro, BRAZIL
http://www.hivamericas.org/
This meeting will bring together a scientific programme to explore through plenary sessions, discussion and networking issues of particular relevance to the region. Faculty will be drawn both from within the region and from international experts.

27 July–1 August
International Union of Microbiological Societies 2014 Congresses
Montréal, CANADA
http://www.montrealiums2014.org/
• XIVth International Congress of Mycology
• XIVth International Congress of Bacteriology and Applied Microbiology
• XVth International Congress of Virology

31 October–3 November
International Meeting on Emerging Diseases and Surveillance (IMED 2014)
Vienna, AUSTRIA
http://imed.isid.org
Email: info@isid.org
The threats posed by pandemic influenza, bioterrorism and the realization that new infectious diseases may be recognized at any time, in any place have dramatically raised our awareness and our need to understand emerging pathogens. This meeting will fully embody the “one health” model of emerging diseases, recognizing the commonality of human and animal health.

2–6 November
HIV Glasgow Drug Therapy Meeting
Glasgow, UK
http://hivglasgow.org/
The meeting will provide a relevant, meaningful and topical Scientific Programme reflecting recent progress in the research and treatment affecting the management of HIV infection. This Congress will provide practical advice and guidance to clinicians in the day-to-day treatment of their patients. The programme is being developed to offer a mix of presentation-types and styles from keynote lectures to practical case-based presentations, within a single-session plenary format. Abstract submission is encouraged and abstracts will be considered for oral presentation in the plenary programme or oral poster discussion sessions, as well as printed posters. Time is set aside within the programme to encourage discussion and audience interaction.

2015

16–18 January
International Conference on Infectious & Tropical Diseases (ICTID)
Phnom Penh, CAMBODIA
http://ictid.webs.com
Email: geo_stv_goss@hotmail.com
Focusing on infectious and tropical problems in Asia and Africa, and on other global problems such as malaria, tuberculosis, HIV/AIDS, dengue/other viral fevers, melioidosis, schistosomiasis, hemorrhagic fevers, rickettsioses, diarrheal diseases, sepsis, meningitis, respiratory tract infections, avian influenza, neglected infectious diseases, hepatitis and more.