The feasibility of rectal artesunate as pre-referral treatment for severe malaria in under fives at community level in rural Uganda

J. Rujumba[1], E.A. Mworozi[1,*], B.A. Mpeka[2], T. Lutalo[2], R. Azairwe[3]

[1] *Makerere University College of Health Sciences, Kampala, Uganda*
[2] *Ministry of Health, kampala, Uganda*
[3] *WHO- Uganda Country Office, kampala, Uganda*

Background: Malaria is the leading cause of child mortality especially in under five children. It is responsible for 1-2million deaths and 300-500million clinical cases worldwide annually (WHO 2003); 90% of the cases are in sub-Saharan Africa and majority are children under five. Most deaths result from delayed treatment due to various causes. Treatment of severe malaria requires parenteral drugs and skilled personnel yet peripheral health facilities are poorly equipped for this. Timely efficacious treatment at community can ''buy'' time for patients to reach health facilities. Artemisinin derivatives have been shown to cause rapid reduction of parasite load and resolution of clinical malaria symptoms. We conducted a study to design and evaluate systems for effective community based treatment of severe malaria in underfives in 2 rural Ugandan districts using rectal Artesunate as pre-referral treatment.

Methods: Randomized community trial carried out from 2004-2007. Study phases were formative, development of IEC materials, selection and training of drug distributors, deployment and monitoring of study drug.

Results: Acceptability of Rectal Artesunate in treatment of severe malaria in under-five children at community level was high. A total of 1502 children with severe malaria were recruited and referred. A total of 1469/1502 (98%) of treated children recovered, 33(2%) died mainly due to severe anaemia.

Conclusion: Majority (98%) of the treated children with severe malaria recovered. Use of rectal Artesunate at community level reduced mortality due to severe malaria in under-fives and community delivery systems for Rectal Artesunate are feasible and should be scaled-up in rural areas where accessibility to parental and anti malarial therapy is not feasible.

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Clinical features predicting mortality (M) in high risk febrile neutropenic cancer children (HRNTPCH) at Hospital de Niños Ricardo Gutiérrez (HNRG), Argentina

N. Rivas*, A. Viña, G. Yerino, C. Ceccoli, F. Plat, C. Hascalovici, E.L. Lopez

Hospital de Niños ''Ricardo Gutiérrez'', Buenos Aires, Argentina

Background: Mortality is the major concern in HR NTPCH. To detect associated factors on admission and during hospitalization is important to decrease it The objective was to

Methods: Prospective cohort study from 1/02 to 12/07 at HNRG. HR-NTPCH were defined according to IDSA criteria. Exclusion: All NTPCH that did not fullfied the HR criteria. Endpoint: Mortality. Predictive factors assessed for M: hospitalization in last 10 days (PH), underlying disease (UD), fever (F) and clinical focus in admission (CF), bacteremia (B), sepsis(S), positive culture (PC) and polimicrobial isolations (PI), intensity(IN) and duration of neutropenia (DN), duration of fever (DF), days of hospitalization (HD) and nosocomial infection. Demographic data were also analized. Chi 2 and Mann-Whithney test were used in the univariate analysis. All factors with $p < 0.05$ were included in a regression model.

Results: Population 501 episodes/267 pts. M 13/501 (2,6%), survivals 488/501 (97,4%). Age(med) 87 (5-219)mo, male 231/501(46.5%) and UD: hematologic tumors 350/501(70%). No significant difference between groups in relation to age, gender or UD was observed. 58/501pts (12%) had not a focus, 216/501(43%) had m demostrated infection and 227/501(45%) had only c findings. S was present in 85 pts, 12 of them in M group: 12/13 (92,3%) vs C 73/488(14,9%) $p < 0,001$. Nosocomial pneumonia(NP) 7/13(54%) vs 51/488(10.5) $p < 0.001$; PI 5/13 (38.5%) *vs* 15/488 (3%) $p < 0.001$, B 7/13 (54%) *vs* 85/488 (17.4%), p0,0008; PC 10/13 (77%) vs 204/488 (42%) p 0,011; and HD 22 (1- 100) vs 8(2-110)d, p0,026 also differed between M group and C. No statistical difference was found in F, CF, PH, IN,DN and DF. In multivariate analysis: S, p0.002-OR 33.6,NP, p0.009 OR 7.2 and PI, p0.048 OR 7.5 remained as independent risk factors for M. In M, PI were Gram - 7/10, Gram + 2/10 and fungi 1/10.

Conclusion: The presence of S, NP and PI should alert physicians to extreme health care attention in HR-NTPCH.

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Non-typeable *Haemophilus influenzae* and *Streptococcus pneumoniae:* Primary causes of acute otitis media in Colombian children

P. Lopez[1], A. Sierra[1,*], M.A. Zapata[1], B. Vanegas[1], R. De Antonio[2], M.M. Castrejon[2], W. Hausdorff[3], R. Colindres[4]

[1] *Centro de Estudios en Infectologia Pediatrica CEIP, Cali, Colombia*
[2] *GlaxoSmithKline Biologicals, Panama City, Panama*
[3] *GlaxoSmithKline Biologicals, Wavre, Belgium*
[4] *GlaxoSmithKline Biologicals, Rio de Janeiro, Brazil*

Background: Acute otitis media (AOM) is one of the most common bacterial infections in childhood and the most frequent reason for antibiotic use. Bacterial conjugate vaccines have demonstrated some efficacy in preventing AOM, but impact may vary according to underlying pathogen and serotype distribution. Because data from Latin America are limited, this report provides novel data regarding bacterial etiology and serotypes of AOM cases within a routine clinical setting in two medical centers in Cali, Colombia to determine what proportion of disease may be vaccine-preventable.

Methods: Children aged ''3 months to <5 years with new episodes of AOM (onset of symptoms <3 days) were included. Middle ear fluid (MEF) samples were collected by tympanocentesis or by sampling of spontaneous otorrhea (<20% of all cases). Recovered bacteria were identified and serotyped.

Results: 99 children with new episodes of AOM were enrolled between January 2008 and January 2009. 100 MEF samples from tympanocentesis (n = 84) and otorrhea (n = 16) were collected (1 subject had 1 sample collected in each ear). The median participant age was 29 months (range: 5 - 55months), and 54.5% of subjects were male. Bacteria were cultured from 63% samples with at least one pathogen under study. *H. influenzae* was isolated in 31 (31%), 30 *S. pneumoniae* (30%), 2 *S. pyogenes* (2%) and 3 *S. aureus* (3%). 14 (46.7%) *S. pneumoniae* isolates were serotypes found in the two licensed pneumococcal conjugate vaccines (14, 19F & 23F), 7 (23%) were vaccine-related types 6A (n = 5) and 19A (n = 2) and 7 were non-vaccine types. 27/31 (87%) of *H. influenzae* isolates were non-typeable. No *M. catarrhalis* was isolated.

Conclusion: Non-typeable *H. influenzae* and *S. pneumoniae* were the leading bacterial causes of AOM in Cali, Colombia. A vaccine with efficacy against both pathogens would be most useful to prevent AOM.

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Risk factors (RF) for necrotizing enterocolitis (NE) in Pediatric oncologic patients (POP) with neutropenia (NTP)

N. Rivas, A. Viña, G. Yerino, M.L. Praino, C. Ceccoli, F. Plat, C. Hascalovici, A. Cane, E.L. Lopez*

Hospital de Niños ''Ricardo Gutiérrez'', Buenos Aires, Argentina

Background: NE is a life threatening complication in neutropenic patients

Objective: To identify risk factors for NE.

Methods: Retrospective analytical study Jan 03-Nov 07 at Hospital de Niños of Buenos Aires.NE: POP with NPT and abdominal symptoms (AS) with bowel wall thickness $\geq$4 mm by CT scan and/or ultrasonography. Controls (C): POP with NTP and AS with normal imaging. Exclusion: POP with NTP without AS. RF for NE: Underlying disease (UD), Cytosine arabinoside (ARA C) use, fever (F), diarrhea (D), vomiting(V), abdominal pain (AP), abdominal tenderness(AT), sepsis(S) and platelets count (PC). Demographic data, isolations (I), treatment (T), hospitalization days (HD) and mortality (M) were also analized. Chi2 and Mann-Whithney tests were used in univariate analysis. All factors with $p < 0.05$ were included in multivariate model.

Results: Population 83 episodes/63 patients. NE 31/83 (37.3%) vs C 52/83(62.7%). Age(median) 117(5-241)mo, male 43/83 (51.8%), UD: Hematologic malignancies 60/83(72,5%). NE didn't differ from C in age, gender or UD. Groups were different in **F** 31/31 (100%) *vs* 44/52 (84%),p0.02; **D** 31/31 (100%)*vs* 42/52 (81%),p0.009; **AP** 29/31 (93,5%) *vs* 39/52 (75%), p0.03; **AT** 22/31(71%) *vs* 9/52 (17%), $p < 0.001$ and **PC**(med) 17000/ul(3000-370000/ul) *vs* 49000/ul (6000-33000),p0.02, S 14/24 (58%)vs 18/58 (31%) p 0,021.No differences were observed in the ARA C and V. In the multivariate analysis, only **AT** $p < 0.001$, OR 11.67 remained statistically associated. **I**: NE 13/31 (42%) vs C13/52 (25%) p0.1. I in NE: *Klebsiella sp* 6/13 (46%), *E.coli*.5/13 (38.5%) and *Pseudomona aeruginosa* 3/13(23%). **T** in NE carbapenems-aminoglycosides (AMG) 10/31 (32%) or 3rd gen cephalosporins -AMGmetronidazole 20/31 (64.5%). NE vs C required surgical T 5/31 (16%) *vs* 5/52 (10%), p 0.37 and HD(med) 17(2-60)d *vs* 12(3-95)d, p 0.85. M 6/83(7.2%), NE 4/31(12.9%) *vs* C 2/52(3.9%), p0,12.

Conclusion: AT was the only independent risk factor for NE. In POP with NTP and AS, images to confirm NE should be performed if AT is found

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Temporal variation of human rotavirus types circulating in Caracas during 2007-2008

E. Vizzi[1,*], O. Piñeros[1], A.C. Alcala[1], M.D. Oropeza[1], L. Naranjo[2], J.A. Suarez[2], J.L. Zambrano[1], F. Liprandi[1]

[1] *Instituto Venezolano de Investigaciones Cientificas, Caracas, Miranda, Venezuela*
[2] *Instituto de Medicina Tropical, Caracas, Venezuela*

Background: Human rotavirus (RV) is considered the main viral cause of acute gastroenteritis in children in both developed and developing countries. The recent implementation of a vaccination program promises to effectively reduce the disease burden and health care costs of rotavirus-specific diarrhea. Surveillance is needed to assess the impact of immunization on the rotavirus diarrhea incidence and variability of the circulating strains. In the last decades, RV molecular genotyping has provided valuable information about the diversity of rotavirus outer capside proteins (VP7/G and VP4/P) of strains circulating throughout the world. Previous studies have demonstrated a broad diversity in rotavirus strains circulating in Venezuela, with predominance of G1, G3 or G4 in combination with P[8] type. The purpose of the present study was to monitor the prevalence of the G/PNSP4 genotypes of rotaviruses circulating in Caracas between February 2007 and April 2008 and detect any uncommon or novel types by means of molecular characterization.

Methods: A total of 164 rotavirus-positive stools from diarrheic pediatric patients aged between 2 months and 5 years collected in Caracas, were tested by multiplex semi-nested RT-PCR and/or sequencing of the VP4, VP7 and NSP4 rotavirus gene.

Results: The analysis revealed 5 common G/P-NSP4 combinations, being G2P[4]/NSP4A and G1P[8]/NSP4B the most prevalent (43% and 38%, respectively), while G3-, G4- or G9-P[8]/NSP4B were more sporadically found. Although present throughout the period studied, G2P[4]-NSP4A rotavirus was the most widely circulating type until November 2007, from then being prevalent G1P[8]-NSP4B strains. Four isolates showed an unusual genotype G8P[14], until now only described in Latino America among animal rotaviruses, 3 of the isolates being associated with NSP4C and one with NSP4A genotype.