77.024

Characterization of community-acquired *Staphylococcus aureus* methicillin-resistant (CAMRSA) vs methicillin susceptible *Staphylococcus aureus* (CA-MSSA) infection (Inf) in Argentinean children

G.A. Yerino, M.S. Vazquez, C. Magneres, G. Abalos, C.I. Cazes, M.L. Vozza, C.I. Echave, V. Valle, M. Langard, A. Procopio, M.M. Contrini, E.L. Lopez*

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

Background: CA-MRSA inf are increased worldwide and few data are published from Latin America. Objective: to define the prevalence of CA-MRSA vs CA-MSSA in hospitalized children in our setting; to characterize the demoepidemiological, clinical and laboratory data between groups.

Methods: Restrospective study Jan'05 — March'08, at Hospital de Niños, Buenos Aires. CA *Staphylocuccus aureus* inf: positive culture)72 hs of admission consistent with CDC's ABC criteria. Exclusion: patients with health care associated infection. Likert scale for parent's education and frequency of bath score was performed. Chi2, *t* test and regression logistic model (LRM) were used.

Results: A total of 302 *Staph* inf were studied: CA-MRSA:153 (51%) and CA-MSSA:149 (49%). CA-MRSA increased frequency from 39.8% in 2005 to 60% in 2008, ($p = 0.01$).No difference between groups was observed in: age: 70.3(±61.5), median:51 mo; gender: male 187/302 (61.9%); underlying disease: 74/302 (24.5%); crowding: 125/302 (41.4%). CA-MRSA was related to lower parent's education and less frequency of bath, $p = 0.009$, respectively. Clinical and laboratory features:

Infection	CA-MRSA	CA-MSSA	*p*
Skin and soft tissue	135/153 (88.2%)	199/149 (67.1%)	<0.001
Two or more skin sites affected	50/135 (37%)	15/100 (15%)	0.0002
Subcutaneous Abscess	107/135 (79.2%)	56/100 (56%)	<0.001
Piomyositis	14/135 (10.4%)	2/100 (2%)	0.01
Lower Resp Tract Infection	18/153 (11.7%)	14/149 (9.4%)	0.5
Meningitis	4/153 (2.6%)	5/149 (3.3%)	0.7
Sepsis	19/153 (12.4%)	14/149 (9.4%)	0.4
Osteomyelitis	32/153 (20.9%)	54/149 (36.2%)	0.003
Bacteremia	34/153 (22.2%)	48/149 (32.2%)	0.005
Invasive Disease (total)	68/153 (44.4%)	92/149 (61.7%)	0.002
WB count (/mm^3)	17,226 (±6,328)	14,715 (±5,602)	0.0003
Duration of Hospitalization	11.5 (±10.2) ds	9.1 (±8.9)ds	0.13
Mortality	1/153 (0.7%)	1/149 (0.7%)	—

CA-MRSA resistance: GEN (10 (7.5%); CLI: 7 (4.5%); ERY: 7(4.5%); RIF and SXT: 1 (0.65%).

Conclusion: 1. Prevalence of CA-MRSA inf increased during last years in our setting ($p = 0.01$) 2. Independent risk factors associated to CA-MRRSA in RLM were: subcutaneous abscesses ($p < 0.0001$), two o more skin sites affected ($p = 0.002$) and use of antimicrobials during the last year ($p = 0.0001$) 3. CA-MSSA was statistically associated to invasive disease ($p = 0.002$).

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Diphtheria *tox* gene polymorphism in *%. diphtheriae* strains isolated in Russia during 2002—2009

S. Kombarova*, I. Mazurova, O. Borisova, N. Gadua, T. Kornienko

G.N. Gabrichevsky Institute of Epidemiology and Microbiology, Moscow, Russian Federation

Background: Diphtheria *tox* gene is responsible for diphtheria toxin synthesis by diphtheria causative agent. We studied diphtheria *tox* gene structure in *C. diphtheriae* strains isolated in Russia over the period of decreased and sporadic incidence of diphtheria (2002—2009).

Methods: 16 toxigenic strains from various regions of Russia (North-Western region, i.e. St.Petersburg; Central region, i.e. Moscow, Smolensk, and Tula; from Siberian region, i.e. Omsk) were used to determine the full nucleotide sequence of their *tox* gene. 13 of the strains were of the *gravis* biovar, the other 3 — of the *mitis* biovar. 2 strains were isolated from patients, 14 strains — from passive carriers. Also 115 nontoxigenic *C. diphtheriae* strains isolated between 2006 and 2009 were observed to identify nontoxigenic strains carrying a ''silent'' *tox* gene.

Results: 12 point mutations in *tox* gene were registered between 2002-2009. In comparison, we have studied 40 strains circulating before and during diphtheria epidemic in Russia (1985—1993) and only 5 point mutations were revealed. By now 13 point mutations have been registered among srains isolated in 1985—1993 and 2002—2009. Majority of mutations did not lead to substitutions in amino acid sequence of diphtheria toxin. Over the period of decreased and sporadic incidence of the disease two point mutations corresponding to substitutions on amino acid level were registered. Such changes affected 4 out of 16 strains. Futher research was done to identify nontoxigenic *C. diphtheriae* strains carrying a ''silent'' *tox* gene. No nontoxigenic strains carrying a *tox* gene were identified. Comparing these results with the data collected over many years of monitoring showed that the percentage of nontoxigenic *tox* gene carrying strains in the strain population was different in different years. Thus, at the time of of sporadic incidence of

the 1980 s and during the period of epidemic rise (1990-1995) such strains were either registered at a very insignificant level (2-4%) or not registered at all. In the period of low diphtheria incidence following an epidemic rise (1996- 2004), the concentration of nontoxigenic *tox* gene carrying strains considerably increased (up to 17%).

Conclusion: Polymorphism of *tox* gene can create wide adaptation possibilities of diphtheria causative agent.

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Staphylococcus lentus: The troublemaker

C. Mazal[1,*], B. Sieger[2]

[1] *Orlando Regional Medical Center, Sanford, FL, USA*
[2] *Orlando Regional Medical Center, Orlando, FL, USA*

Background: Staphylococcus lentus has been associated with infections in animals, however *S. lentus* has rarely been reported as a pathogen in humans. Here we report 72 cases involving *S. lentus* at our institution over a period of 9 years. Review of the literature revealed only one case of a human infection, and to our knowledge, this is the largest series of *S. lentus* infection in humans reported so far.

Methods: Cases were defined as clinically significant if there was evidence of a positive culture, in addition to signs and symptoms of pain, tenderness, swelling, fever or leukocytosis.

Results: Of the 72 cases, 20 involved only *S. lentus*, 50 had associated microbes, and 2 cases were unknown. Of the 20 cases involving solely *S. lentus*, 9 were from urine, 1 from peritoneal fluid, 7 from blood, 1 from CSF and 2 from wound cultures. All patients with culture positive *S. lentus* (both with and without associated microbes) had clinical signs of infection including leukocytosis, fever, pain, tenderness, swelling, infection noted by physician or improvement with antibiotic therapy. Analysis of demographic data revealed no particular patterns. Forty-four of the 72 cases were culture positive within 1—3 days of culture or admission. Antibiotic sensitivities revealed 83% sensitivity to Vancomycin and 29% sensitivity to Oxacillin.

Conclusion: Little is known about *S. lentus* and only one report of human infection exists. Our case study involved 72 cases of *S. lentus* positive cultures at our institution with evidence of clinical infection in all 72 cases. Based on our experience, *S. lentus* is a true pathogen that deserves attention. We feel, however, that it will require clinical sense to decide if infection with *S. lentus* is significant when analyzed on a case-by-case basis.

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Staphylococcus lugdunensis — A wolf in sheep's clothing

A. Klotchko[1,*], M. Wallace[2], A.F. Walsh[3], B. Sieger[4], C.M. Licitra[5]

[1] *Orlando Health, Orlando, FL, USA*
[2] *Orlando Health, 32806, FL, USA*
[3] *Orlando Health, Orlando, FL, USA*
[4] *Orlando Regional Medical Center, Orlando, FL, USA*
[5] *Florida Infectious Disease Group, Orlando, FL, USA*

Background: The coagulase negative staphylococci are generally much less virulent than *Staphylococcus aureus*, but there are increasing reports of *Staphylococcus lugdunensis* behaving aggressively. We analyzed our teaching hospital's experience with this pathogen.

Methods: Retrospective chart review in an 808 bed tertiary care medical center. All 70 initial isolates were reviewed, and clinical and microbiologic data compiled.

Results: There were 70 unique patient isolates; 57 were from inpatients. 21 had positive blood cultures; 5 of them met Dukes criteria or had autopsy proven endocarditis. Three endocarditis patients underwent valve replacement and survived. Two patients died, including a 26 year old healthy man who died within 48 hours of admission due to refractory shock; his autopsy revealed a ventricular wall abscess and large aortic valve vegetations. There were 13 urinary isolates; the others were primarily from skin, soft tissue and bone sites, including 6 from breast abscesses. 3 had prosthetic joint infections, and 1 had postoperative meningitis. Two deaths were attributable to *S. lugdunensis* infection. Only 12% of isolates were penicillin sensitive, and 9% were oxacillin resistant.

Conclusion: S. lugdunensis is a virulent pathogen, capable of causing life threatening infection, including both native valve and prosthetic endocarditis. Sensitivity to penicillin and oxacillin cannot be assumed. The clinical laboratory should identify to the species level all clinically important coagulase negative staphylococci.

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Association of breast milk _Lactobacilli_ and _Staphylococcus aureus_ in women with mastitis using quantitative PCR

U. Srinivasan, N. Shrivastwa, S. Ponnaluri, J. Debusscher, C. Barbossa-Cesnik, C.F. Marrs, B. Foxman*

University of Michigan, Ann Arbor, MI, USA

Background: Staphylococcus aureus is the most common causative agent of lactation mastitis; an infection of the breast that affects up to 30% of lactating women and often requires treatment with antibiotics. Commensal breast milk *Lactobacilli* inhibit pathogenic *Staphylococcus* growth *in vitro*; whether this is true *in vivo* is not known. We will test *Staphylococcus* and *Lactobacillus* levels in mastitis and healthy breast milk collected from a study of lactating mothers in Brazil and determine the association of *Staphylococcus* and *Lactobacilli* levels in breast milk.

Methods: Breast milk samples were collected from 72 healthy mothers and mothers suffering from mastitis in