COMMUNITY ACQUIRED MRSA INFECTIONS IN A PAEDIATRIC POPULATION IN GREECE

S Vourli [1], D Perimeni [1], A Makri [2], M Polemis [1], A Voyiatzi [2], A Vatopoulos [1]

We investigated the characteristics of 20 community acquired MRSA strains isolated in a paediatric hospital in Athens. Eighteen of these, all isolated from skin and soft tissue infections, carried the Panton-Valentine leukocidin (PVL) determinants, were found resistant to fusidic acid, tetracycline and kanamycin, and displayed a PFGE pattern identical to that of the well-described ST80 CA-MRSA clone circulating in various European countries.

Euro Surveill 2005; 10(5): 78-9 Published online May 2005
Key words: CA MRSA, Panton-Valentine leukocidin (PVL), pediatric infections

Introduction

Community acquired (CA) methicillin resistant *Staphylococcus aureus* (MRSA) infections caused by hypervirulent strains producing the Panton Valentine Leukocidin (PVL) are an emerging public health issue worldwide [1]. Outbreaks of CA-MRSA infections have recently been described in Australia, Europe and the United States [1-6], mainly in otherwise/ healthy schoolchildren and young adults. Molecular studies have suggested that these infections are the result of the spread of a limited number of PVL-producing MRSA clones that are genetically distinct from nosocomial strains [1,2,6]. PVL producing MRSA strains are associated with severe deep skin infections and necrotising pneumonia and usually show an unusual antibiotic susceptibility profile, being resistant only to kanamycin, fusidic acid and occasionally tetracycline.

In this study we report the emergence of PVL positive CA-MRSA infections in a paediatric population in Greece.

Materials and Methods

All *S. aureus* strains isolated from community acquired skin and soft tissue infections in Penteli Children's Hospital, a paediatric hospital in the north of Athens with a catchment population of one million inhabitants, from June to November 2004 were retrospectively analysed.

It should be noted that it is the hospital's policy to systematically culture specimens from all skin and soft tissue infections.

Antibiotic susceptibility profiles were determined by the standard disk diffusion method, according to the instructions of the National Committee of Clinical Laboratory Standards [7]. Detection of the *mec*A gene and the *lukF*-PV and *lukS*-PV genes was performed by polymerase chain reaction (PCR) as previously described [8]. *SmaI* digests of chromosomal DNA were objected to pulsed-field electrophoresis (PFGE), as described previously [9].

Results and Discussion

During the study period a total of 129 patients were presented in the outpatient department of the hospital suffering from skin and soft tissue infections, and *S. aureus* was isolated from 99 of them. On sensitivity testing, 22 of them (22.2%) were found to be MRSA, an alarmingly high rate that must be further confirmed by carefully designed prospective studies. MRSA accounted for 47% of all CA *S. aureus* infections in a recent study from Taiwan, [10].

Eighteen MRSA strains recovered from 18 patients were available for further study. Seven were recovered from abscesses, seven from cases of cellulitis, three from boils, and one from a wound infection. Two more MRSA strains isolated from outpatients during the same time period, from pus and from synovial fluid, were also included in the analysis.

The genes *lukF*-PV and *lukS*-PV were detected in all 18 skin and soft tissue isolates but not in the two isolates from pus and synovial fluid. All PVL-positive strains were resistant to fusidic acid, kanamycin and tetracycline, but sensitive to gentamicin, erythromycin and ciprofloxacin. PFGE analysis revealed high similarity among all PVL+ strains grouping them into one type (type C) divided into three subtypes (C1 displayed by 12 isolates, C2, by 4 and C3 by 2 isolates, respectively). The two PVL - strains showed different PFGE patterns (Pattern A and B respectively, data not shown).

TABLE 5

Vaccine coverage (%) by vaccine and year of birth among young adults over 14 years of age, Northern Health Region of Portugal

Vaccine / Dose No.	Year of birth			
	1987	1988	1989	1990
Td	95.5	96.4	96.7	96.7
HBV 3	92.5	91.6	92.6	95.6
MMR 2 *	93.4	94.5	94.2	96.0

* Second dose of MMR.

Interestingly, Pattern C was found similar to the PFGE pattern of the well-described MLST80 strain that seems to be spreading through Europe [FIGURE] [5,11]. Moreover, PFGE pattern C is similar to the PFGE pattern of the PVL+ clone C, established and causing hospital acquired MRSA infections in one hospital in Patras, a city in southwest Greece [12]. Although Greece has one of the highest rates of MRSA infections in Europe [13], this PFGE type is not among the types circulating in the Greek hospitals [12], indicating that community acquired MRSA infections are possibly not the result of the spread of hospital MRSA strains in the community.

In that respect, and similarly to other areas in the world, PVL producing CA MRSA seems to be a new emerging infection in Greece.

Acknowledgements

Strain CA-MRSA 3925/02 (ST80) is a generous gift from Professor W Witte.

This work was supported by the Hellenic Centre for Infectious Disease Control (KEEL, Ministry of Health).

1. Department of Microbiology, National School of Public Health, Athens, Greece.
2. Department of Microbiology, Penteli Children's Hospital, Penteli Athens, Greece.

References

1. Vandenesch F, Naimi T, Enright MC, Lina G, Nimmo GM, Heffernan H, et al. Community-acquired methicillin-resistant *Staphylococcus aureus* carrying Panton-Valentine Leukocidin genes: worldwide emergence. Emerg Infect Dis. 2003; 9:978-84.
2. Dufour P, Gilet Y, Bes M, Lina G, Vandenesch F, Floret D, et al. Community-acquired methicillin-resistant *Staphylococcus aureus* infections in France: emergence of a single clone that produces Panton-Valentine leukocidin. Clin Infect Dis. 2002; 35:819-24.
3. Naimi TS, Le Dell KH, Boxrud DJ, Groom AV, Steward CD, Johnson SK, et al. Epidemiology and clonality of community-acquired methicillin-resistant *Staphylococcus aureus* in Minnesota, 1996-1998. Clin Infect Dis. 2001; 33:990-6.
4. Wannet W. Virulent MRSA strains containing the Panton-Valentine leukocidin gene in the Netherlands. Eurosurveillance Weekly. 2003; 7. http://www.eurosurveillance.org/ew/2003/030306.asp
5. Salmenlinna S, Lyytikainen, Vuopio-Varkila J. Community acquired methicillin-resistant *Staphylococcus aureus*, Finland. Emerg Infect Dis. 2002; 8:602-7.
6. Okuma K, Iwakawa K, Turnidge JD, Grubb WB, Bell JM, O' Brien FG, et al. Dissemination of new methicillin-resistant *Staphylococcus aureus* clones in the community. J Clin Microbiol. 2002; 40:4289-94.
7. NCCLS. 2000. Performance standards for antimicrobial disk susceptibility tests. Approved standard, 7th ed. NCCLS document M2-A7. NCCLS, Wayne, Pa. 11.
8. Jarraud S, Mougel C, Thioulouse J, Lina G, Meugnier H, Forey F, et al. Relationships between *Staphylococcus aureus* genetic background, virulence factors, agr groups (alleles), and human disease. Infection and Immunity. 2002; 70:631-41.
9. Murchan S, Kaufmann ME, Deplano A, de Ryck R, Struelens M, Elsberg Zinn C, et al. Harmonization of Pulsed-Field Gel Electrophoresis protocols for epidemiological typing of strains of methicillin-resistant *Staphylococus aureus*: a single approach developed by consensus in 10 european laboratories and its application for tracing the spread of related strains. J Clin Microbiol. 2003; 41:1574-85.
10. Chen CJ, Huang YC, Chiu CH, Su LH, Lin TY. Clinical features and genotyping analysis of community-acquired methicillin-resistant *Staphylococcus aureus* infections in Taiwanese children. Pediatr Infect Dis J. 2005; 24:40-5.
11. Witte W, Cuny C, Strommenger B, Braulke C, Heuck D. Emergence of a new community acquired MRSA strain in Germany. Euro Surveill. 2004; 9:1-2.
12. Aires de Sousa M, Bartzavali C, Spiliopoulou I, Santos Sanches I, Crisostomo MI, de Lencastre H. Two international methicillin-resistant *Staphylococcus aureus* clones endemic in a university hospital in Patras, Greece. J. Clin Microbiol. 2003; 41:2027-32.
13. Tiemersma EW, Bronzwaer S, Lyytikäinen O, John E, Degener JE, Schrijnemakers P, Bruinsma N, Monen J, Witte W, Grundmann H. and European Antimicrobial Resistance Surveillance System Participants. Methicillin-resistant *Staphylococcus aureus* in Europe, 1999–2002 Emerg Inf Dis. 2004; 10:1627-1634.

ORIGINAL ARTICLES

Surveillance report

SURVEILLANCE OF ANTIMICROBIAL RESISTANCE IN BULGARIA - A SYNOPSIS FROM BULSTAR 2003

M Petrov, N Hadjieva, T Kantardjiev, TZ Velinov, A Bachvarova

We introduce Bulgarian Surveillance Tracking Antimicrobial Resistance (BulSTAR) and make the first report on surveillance data for 2003. This longitudinal surveillance programme monitors the isolation and antimicrobial susceptibility of all clinically significant microorganisms isolated from blood cultures, cerebrospinal fluid, upper and lower respiratory tract, urine and wound samples in the participating microbiology laboratories. Twenty eight public, 45 hospital and 6 private laboratories from all 28 counties of the Republic of Bulgaria participated in BulSTAR 2003. The total number of isolates from marked sources during the surveillance period was 98 929. Seven microorganisms represented 72% of all isolated bacteria in BulSTAR 2003: *Escherichia coli, Staphylococcus aureus*, Proteus-Providencia-Morganella group, Klebsiella spp., Pseudomonas spp, *Streptococcus pneumoniae* and *Streptococcus pyogenes*. Generally the resistance of clinically significant Gram positive and Gram negative bacteria in Bulgaria was estimated to be at a medium level when compared with many other surveillance sources worldwide. A unique 32-year experiment on the population by treating all severe infections with an ampicillin/gentamicin combination resulted in twofold higher levels of resistance to amynoglycosides compared with other countries worldwide. This is due to the extremely conservative treatment schemes used in the former socialist countries, based on national directives and cheap domestic production of gentamicin and ampicillin. The forthcoming introduction of a computer network and improvements in detecting mistakes are expected to increase the sensitivity and the significance of BulSTAR surveillance system – an indispensable tool in the combat against increasing worldwide antibiotic resistance.

Euro Surveill 2005; 10(6): 79-82 Published online June 2005

Key words: antimicrobial resistance, Bulgaria, BulSTAR, microbiology, surveillance

1. National Center of Infectious and Parasitic Diseases, Sofia, Bulgaria.
2. Queen Joanna University Hospital, Sofia, Bulgaria.

Introduction

Bulgaria is a small country situated in the north part of the Balkan Peninsula, near the geographical border between Europe and Asia. With a population of 7.9 million inhabitants, the Republic of Bulgaria is divided into 28 counties that are served by approximately 100 public microbiology laboratories of the national healthcare system. An increasing number of private microbiology laboratories are being established and are becoming part of the national healthcare surveillance system. The aims of this study are to introduce Bulgarian Surveillance Tracking Antimicrobial Resistance (BulSTAR), to make a synopsis on the surveillance data and to point out particular aspects of the resistance trends of some major pathogens in Bulgaria for 2003.

Methods

We introduce the Bulgarian Surveillance Tracking Antimicrobial Resistance (BulSTAR) and report summarised national data for year 2003. The surveillance programme was initiated in 1997 by the Department of Microbiology in the National Center of Infectious and Parasitic Diseases (NCIPD) in Sofia as a voluntary system for annual reporting of the isolation and antimicrobial susceptibility of all clinically significant microorganisms in 45 public microbiology laboratories from