This high cohesion level from 27 Mediterranean countries that belong to three WHO regions, underlines the need to strengthen public health information sharing in the area, a challenge that EpiSouth PLUS project is fulfilling in order to increase health security in the region.

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West Nile virus outbreak in the Mediterranean region, 2010-2011

C. Giese [1,*], F. Ait Belghiti [1], P. Barboza [1], F. EpiSouth network [2]

[1] *Institut de Veille Sanitaire (InVS), Saint Maurice, France*
[2] *27 Mediterranean and Balkan countries, Rome, Italy*

Background: In 2010, an unprecedented West Nile virus (WNV) outbreak occurred in the Mediterranean region. EpiSouth, the network of 27 Mediterranean and Balkan countries for the control of public health threats, reported WNV outbreaks (human or equine) in 11 EpiSouth countries during both 2010 and 2011 seasons.

Methods: Data regarding numbers of human and animal cases diagnosed in 2010 and 2011, types of WNV surveillance and laboratory capacities in those 27 countries were collected through questionnaires. Official reports issued by OIE and ministries of Health/Agriculture were also considered for cases counts.

Results: For 2010, 26 EpiSouth countries provided information: 485 human cases were reported by 9 countries (Albania, Greece, Israel, Italy, Palestine, Romania, Spain, Tunisia, Turkey), 54% of these cases were reported by Greece. For 2011, 24 EpiSouth countries answered the questionnaire: 230 human cases were reported in 8 countries. While the number of WNV cases was lower in 2011, a geographical extension was observed: an additional country was affected (Former Yugoslav Republic of Macedonia) as well as new regions within countries affected in 2010 (Italy, Greece, Romania and Tunisia). Since 2010, Bulgaria, Croatia, Serbia and the Former Yugoslav Republic of Macedonia have strengthened or implemented specific WN surveillance in their country.

Conclusion: Following the unprecedented 2010 WNV outbreak in the Mediterranean region, the close monitoring of the 2011 season was crucial to better appraise WNV circulation in the area. During both years, outbreaks were identified on all major birds' migratory routes crossing Mediterranean region and viral circulation was detected in a similar number of countries. It would be unlikely that these two outbreaks remain isolated: sustained transmission cannot be excluded in the coming year. Despite significant improvements since 2010, WNV surveillance systems and access to laboratory facilities still vary across EpiSouth countries. In this context early alerting and rapid information exchange is essential especially for countries with limited facilities. This highlights the importance of maintaining such a cross-border early warning network integrating a laboratory component in order to foster implementation of adequate and timely control measures across the region.

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Prevalence of *Bacillus cereus* strains associated with illness resembling cutaneous anthrax in South India

N. Ghosh [1], S. Alam [1], A.K. Goel [2,*]

[1] *Defence Research & Development Establishment, Gwalior, India*
[2] *Defence Research & Development Establsihment, Gwalior, India*

Background: *Bacillus anthracis*, the causative agent of anthrax is a Gram positive sporulating, non-motile, rod shaped, capsule forming bacterium. Cutaneous anthrax is an important disease of public health importance in several tropical countries including India. The virulence of *B. anthracisis* due to presence of two plasmids, pXO1 and pXO2 carrying the genes encoding a tripartite toxin and capsule, respectively. Recently, several close relatives of *B. anthracis* associated with diseases resembling anthrax have been identified. We report for the first time the isolation and characterization of *B. cereus* isolates from the patients having anthrax like infections in India.

Methods: The bacteria were isolated from the skin lesions on blood agar plates and subjected to biochemical, microbiological phenotypic characterization and 16S rRNA sequencing. Presence of protective antigen (PA) gene was confirmed by real-time PCR. Anthrax Biothreat alert kit (Tetracore, USA) was also used to confirm theB. anthracis. The exoproteome of the these isolates was compared with the B. *anthracis* Sterne and *B. cereus* exoproteome. A representative isolate was grown overnight and its exoproteiome analysis was done by 2-dimensional gel electrophoresis followed by identification of proteins by MALDI-TOF-TOF. Multilocus sequence typing (MLST) was performed based on partial nucleotide sequencing of 7 housekeeping genes.

Results: Contrary to *B. anthracis*, the isolates were haemolytic, motile, and resistant to penicillin. Other phenotypic, morphological, 16S rRNA gene sequencing and MLST confirmed the isolates belonging to *B. cereus* group. By real-time PCR, all the isolates were positive for PA gene, a characteristic marker of *B. anthracis*. Anthrax Biothreat alert kit also confirmed the bacteria as *B. anthracis*. MALDI-TOF-TOF analysis of proteins revealed the presence of many proteins which are absent in *B. cereus* strains but reported in *B. anthracis*. These proteins are reported to play important role in pathogenicity of *B. anthracis*

Conclusion: The present report described the involvement of *B. cereus* isolates in cutaneous anthrax like illness. The investigation corroborated the continuous emergence of new and novel pathogens in nature which can impose new challenges for diagnosis and prophylaxis of bacteria of public health importance.

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