# ISDS One Health Surveillance (OHS) Case Study

### CASE STUDY TITLE

First report on MRSA recovered from wild boars in the north of Portugal

### **PROJECT/ACTIVITY TITLE**

"Omic" tools to characterize methicillin-resistant Staphylococcus aureus (MRSA) recovered from wild animals: the labile epidemiology of virulence and drug resistance.

CONTACT INFORMATION			
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WHAT DOMAIN(S) DO YOU WORK IN?	Human health	x_Animal health	x_Environmental health
OHS AREA(S) OF FOCUS ADDRESSED BY CASE STUDY	Cross-Agency Communication and Collaboration	Training and Resources	Technologies and Methodologies
	Other: Antimicrobial resistance surveillance		

### **PROBLEM DESCRIPTION (150 word maximum)**

Summarize the problem/situation that was addressed with a OHS approach.

Antibiotic resistance is an emerging public health concern and the scientific community recognizes the need to evaluate its epidemiology. Staphylococcus aureus (MRSA) are a key to this problem. Often found in the natural flora of the skin, nose and mouth of humans and animals, these bacteria can cause both minor skin infections and serious diseases that can result in death. Apart from the hospital concern, this bacterium is becoming increasingly common in infections associated to both human and animal communities with high rates of antibiotic resistance. There is little information on the prevalence of MRSA in wild animals. For this reason, our research group aims to determine the prevalence of these bacteria in wild animals as well as to characterize the resistance genes and genetic lineages circulating in this ecosystem, supposedly free from antibiotic use.

### **ACTION TAKEN (500 word maximum)**

Describe how the problem was addressed and how the action taken was measured. Please include a description of the collaborators and the data sources used.

More than 47% of the portuguese hospital Staphylococcus aureus isolates are methicillin-resistant: the highest rate in Europe. However, its emergence is no longer a hospital exclusive phenomenon. MRSA are becoming prevalent in community-acquired infections, are found associated to companion animals, livestock animals, food- producing animals and in various foods. Nevertheless, wild animals are known as natural hosts of MRSA and other resistant bacteria. The convergence between habitats can lead to a frequent contact between wild animals, other animals and humans and this means an increased risk to human and animal health. The main objective of our study was to determine the prevalence of MRSA in wild animals, in Portugal. These results may add to our knowledge the occurrence of MRSA strains and the genetic lineages circulating in wild environments. Knowing which variants are associated with each focus of infection, each animal species and in a particular habitat may be important to carry a greater control over the dissemination of these zoonotic bacteria and better understand its transmissibility.

To acess MRSA from wild boars we recoved samples from the mouth and nose of 45 wild boars (Sus scrofa) during hunt activity from November 2012 to January 2013 in the North of Portugal with the help of the Forest Association of Trás-os-Montes and Alto Douro (AFTM), Vila Real, Portugal. Briefly, 30 S. aureus colonies from 30 different animals were isolated from Manitol Salt Agar and ORSAB agar plates (Oxoid) with oxacillin [2 mg/L] and identified by PCR and sequencing at the Centre of Studies in Animal and Veterinary Sciences (CECAV) and at the Functional Genomics and Proteomics' Unit, Department of Genetics and Biotechnology from the University of Trás-os-Montes and Alto Douro, Vila Real, Portugal. The susceptibility of the isolates was tested by disk-diffusion test against 18 antimicrobial agents and microdilution (MIC) was used to test oxacillin according to EUCAST guidelines. Also, the genetic lineages of S. aureus were characterized by agr-typing, spa-typing and MLST (multi- locus sequence typing) at the National Reference Laboratory of Antibiotic Resistances and Healthcare Associated Infections (NRL-AR-HAI), National Institute of Health Dr. Ricardo Jorge (NIH), Lisboa, Portugal.

18 S. aureus were susceptible to all antibiotics tested and 12 presented resistance various antimicrobials. We observed variable oxacillin MIC values ranging from 0.5 to 32mg/L. The MRSA CC398 (t899) isolate presented resistance to tetracycline, penicillin, ciprofloxacin, cefoxitin and oxacillin (harboring mecA gene, with MIC=32mg/L). It is a matter of concern when CC398 MRSA are taken as commensal habitants of the skin and nose of wild animals and are characterized with resistance to various antimicrobial agents in clinical use. MRSA are becoming frequent in veterinary clinics, in farms, livestock animals, and now there is the first report in wild boars that are frequently in contact with anthropogenic sources of those bacterial strains.

# FACILITATORS AND BARRIERS (100 words max each)

Please list and describe any factors that contributed positively to this project/activity.

The factors that contributed positively to this work were the collaborations between laboratories and associations, the previous knowledge of the area within our investigation group and the individual scholarships from the Portuguese Foundation for Science and Technology (FCT) that made it possible to our students get on the field and work at the laboratories.

# Please list and describe any factors that were a challenge or barrier to overcome.

The factors that were challenging were during the collection of the samples, during hunt activities, frequent accompanied with bad weather. The other factor that contributed negatively to this investigation was the poor investment that the Portuguese government made in the past years to scientific activities, due to the crisis we are facing, resulting in laboratories' tight budget.

# LESSONS LEARNED (250 word maximum)

# Please describe any lessons learned or best practices identified by this project/activity.

With these results we may say that, in Portugal, we are facing a serious problem regarding MRSA. We should monitorize MRSA antimicrobial gene flow throw the environment. More studies should take place to better understand this problem among wild animals frequently pointed as hosts of clinically important antimicrobial resistant bacteria.

### **ADDITIONAL COMMENTS (75 words max)**