

Session: OS199 One health perspective on MDR Gram-positives: VRE & MRSA

**Category: 3a. Resistance surveillance & epidemiology: MRSA, VRE & other Gram-positives**

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## Detection of MRSA-mecC-t843, MRSA-mecA-CC398 and *Staphylococcus delphini* in magpies and cinereous vultures in Spain

Laura Ruiz-Ripa<sup>1</sup>, Paula Gómez<sup>1</sup>, Mari Cruz Camacho<sup>2</sup>, Myriam Zarazaga<sup>1</sup>, Javier De la Puente<sup>3</sup>, Ursula Höfle<sup>2</sup>, Carmen Torres<sup>\*4</sup>

<sup>1</sup>*University of La Rioja; Area of Biochemistry and Molecular Biology*

<sup>2</sup>*Grupo Sabio Instituto de Investigación En Recursos Cinegéticos Irec (Csic-Uclm-Jccm)*

<sup>3</sup>*Grupo Ornitológico Seo-Monticola, Unidad de Zoología, Universidad Complutense de Madrid*

<sup>4</sup>*University of La Rioja; Biochemistry and Molecular Biology*

**Background:** Different genetic lineages of animal associated methicillin-resistant *Staphylococcus aureus* (MRSA) are gaining interest because of their implication in Public Health. This includes lineage MRSA-CC398, associated mainly with pigs, and lineage MRSA-CC130 with *mecC* gene, both of them also detected in human infections. The role of wildlife as source of *S. aureus* (especially MRSA) and of other coagulase-positive-staphylococci (CoPS) is unknown, especially for wild birds. **The objective** was to analyze the carriage of CoPS in nasotraqueal samples of different wild bird species and to characterize detected isolates.

**Material/methods:** 315 nasotraqueal samples of wild birds, obtained in 2015-2016 in different Spanish regions, were analyzed for CoPS detection [130 magpies, 109 cinereous vultures, 38 red kites, 27 bald ibises, and 11 bearded vultures]. Samples were inoculated on Mannitol-Salt-Agar and Oxacilline-Resistance-Screening-Agar-Base plates (supplemented with 2mg/L oxacillin) for CoPS and methicillin-resistant SCoP recovery, respectively. A maximum of two CoPS colonies per plate were recovered and identified by specific *nuc* gene or MALDI-TOF. CoPS isolates showing different phenotypes of antimicrobial resistance from each species and sample were further studied. Susceptibility testing for 13 antimicrobials was performed by disk-diffusion-method and antimicrobial

resistance genes by PCR. Molecular typing of *S. aureus* isolates was performed by *spa*-typing and the presence of the Immune Evasion Cluster (IEC) genes was checked by PCR.

**Results:** CoPS isolates were detected in 8.3% of tested samples. *S. aureus* was identified from 7 of 130 magpies (5.4%) and from 8 of 109 of cinereous vultures (7.3%); *S. delphini* was detected in 11 of 109 cinereous vultures (10.1%) and in 1 of 38 red kites (2.6%). No SCoP was isolated from ibises or bearded vultures. Positive magpies came from a single sampling location and were detected both in 2015 and 2016. Most of the *S. aureus* obtained were MRSA (13 of 15) and 12 of them harbored the *mecC*-gene and the remaining one the *mecA*-gene. The *mecC*-positive isolates were typed as *spa*-type t843 (n=12) and t1535 (n=1), associated to CC130, and were susceptible for all non-beta-lactams tested. The *mecA*-positive isolate was t011, was ascribed to CC398, and showed resistance for erythromycin/clindamycin/tetracycline (carried *tetM* and *tetK* genes). The 12 *S. delphini* isolates were methicillin-susceptible and 11 of them were tetracycline-resistant (with *tetK* gene). Among MRSA-*mecC*-t843, *scn*-positive and *scn*-negative isolates were identified.

**Conclusions:** Magpies and cinereous vultures could act as reservoir of CoPS playing a role in the epidemiology and the evolution of these staphylococcal species when exposed to it. All *S. aureus* isolates from magpie belonged to the lineage MRSA-*mecC*-CC130. This is the first detection of *S. delphini* in wild birds. The heterogeneous detection of the *scn* gene (marker of the human IEC system) among MRSA-*mecC* isolates suggest different evolutive clades in this lineage.