

27th
ECCMID

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

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Puente, Ursula Höfle, Carmen Torres



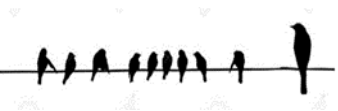
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Transparency Declaration

- Research grants from:
 - State Agency of Research (Ministry Economy and Competitiveness), Spain
 - Spanish Agency of International Cooperation (AECID), Spain



Background

- Coagulase-positive staphylococci (CoPS):

S. aureus



SIG Group:

S. pseudintermedius (dogs)

S. intermedius

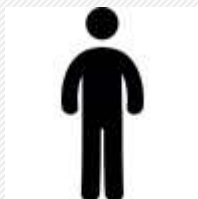
S. delphini (horses, donkeys, *Mustelidae* family)

Opportunistic pathogens of humans and animals

- **MRSA:** *mecA* and the recently described *mecC* gene

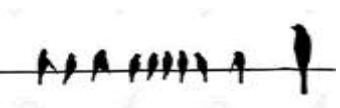
- **Animal-related-MRSA:**

CC398 (*mecA*) - mainly livestock



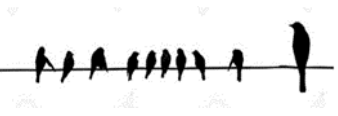
CC130/CC425 and others (*mecC*) - mainly wildlife





Objectives

- Determine the prevalence and diversity of CoPS species in nasotracheal samples of wild birds
- Carry out the molecular characterization of the recovered isolates:
 - Molecular typing
 - Antimicrobial resistance genes
 - Virulence genes



Material and methods

315 animals (2015-2016)



130 Magpies



109 Cinereous vultures



38 Red kites

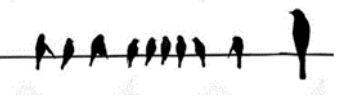


27 Ibises



11 Bearded vultures





Material and methods

315 animals (2015-2016)



130 Magpies



109 Cinereous vultures



38 Red kites



27 Ibises



11 Bearded vultures



Isolation and identification

BHI broth (6.5% NaCl)

MSA

ORSAB (2 mg/L oxacillin)

MALDI-TOF

PCR/RFLP-*pta* gene

PCR/seq *sodA*



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315 animals (2015-2016)



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MALDI-TOF

PCR/RFLP-*pta* gene
PCR/seq *sodA*

Antimicrobial susceptibility testing (EUCAST, 2016)

Antimicrobial resistance genes by PCR/seq

Molecular typing

S. aureus:
spa, MLST

S. delphini
group A or B
PCR/seq-*nuc*



Material and methods

315 animals (2015-2016)



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Antimicrobial susceptibility testing (EUCAST, 2016)

Antimicrobial resistance genes by PCR/seq

Molecular typing

S. aureus:
spa, MLST

S. delphini
group A or B
PCR/seq-*nuc*

Virulence factors

Immune Evasion Cluster (IEC)

S. aureus:
tst, *eta*, *etb*,
lukF/lukS-PV

S. delphini:
lukS/F-I
expA, *expB*, *siet*,
se-int, *sec_{canine}*



Results

Animal specie	N° of samples	% Samples with:		
		CoPS	<i>S. aureus</i>	<i>S. delphini</i>
Magpie (<i>Pica pica</i>)	130	5.4	5.4	-
Cinereous vulture (<i>Aegypius monachus</i>)	109	17.4	7.3	10.1
Red kite (<i>Milvus milvus</i>)	38	2.6	-	2.6
Ibis (<i>Geronticus eremita</i>)	27	-	-	-
Bearded vulture (<i>Gypaetus barbatus</i>)	11	-	-	-
Total	315	8.6	4.7	3.8



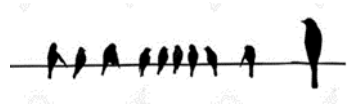
Results

Animal specie	N° of samples	S. aureus		
		CoPS		<i>delphini</i>
Magpie	130	5.4	5.4%	-
Cinereous vulture	109	17.4	7.3%	10.1
Red kite (<i>Milvus milvus</i>)	38	2.6	-	2.6
Ibis (<i>Geronticus eremita</i>)	27	-	-	-
Bearded vulture (<i>Gypaetus barbatus</i>)	11	-	-	-
Total	315	8.6%	4.7%	3.8



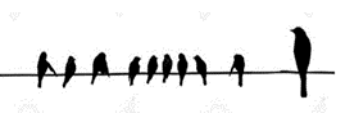
Results

Animal specie	N° of samples	% samples with		
		CoPS	<i>S. aureus</i>	<i>S. delphini</i>
Magpie (<i>Pica pica</i>)	130	5.4	5.4	-
Cinereous vulture	109	17.4	7.3	10.1%
Red kite	38	2.6	-	2.6%
Ibis (<i>Geronticus eremita</i>)	27	-	-	-
Bearded vulture (<i>Gypaetus barbatus</i>)	11	-	-	-
Total	315	8.6%	4.7	3.8%



Results

Animal specie	N° of samples	% samples with:		
		CoPS	<i>S. aureus</i>	<i>S. delphini</i>
Magpie (<i>Pica pica</i>)	130	5.4	5.4	-
Cinereous vulture (<i>Aegypius monachus</i>)	109	17.4	7.3	8.5
Red kite (<i>Milvus milvus</i>)	38	2.6	-	2.6
Ibis	27	No CoPS		
Bearded vultures	11			
Total	315	8.6	4.7	3.8



15 *S. aureus*



Cinereous vulture

6 MRSA

5 *mecC* -CC130

ST1945-ST1571-t843

ST1945-t1535

1 *mecA* CC398

ST398-t011

2 IEC type E

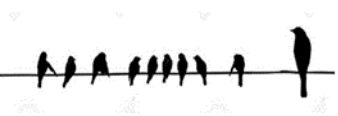
3 IEC -

Multiresistant
Tet-Ery-Cli

IEC -

Susceptible non beta-lactams

blaZ, *tet(K)*, *tet(M)*,
erm(C), *vga(A)*



15 *S. aureus*



Cinereous vulture

6 MRSA

2 MSSA

5 *mecC* -CC130

ST1945-ST1571-t843

ST1945-t1535

1 *mecA* CC398

ST398-t011

ST97-CC97-t267

ST425-CC425-t5998

2 IEC type E

3 IEC -

Multiresistant
Tet-Ery-Cli

IEC -

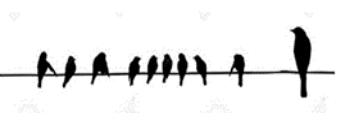
ST97
IEC type E

ST425
IEC -

Susceptible non beta-lactams

blaZ, *tet(K)*, *tet(M)*,
erm(C), *vga(A)*

Susceptible Ab



15 *S. aureus*



Cinereous vulture



Magpie

6 MRSA

2 MSSA

7 MRSA

5 *mecC* -CC130

ST1945-ST1571-t843
ST1945-t1535

1 *mecA* CC398

ST398-t011

ST97-CC97-t267

ST425-CC425-t5998

mecC -CC130

ST1583, ST1945, ST1581-t843

2 IEC type E

3 IEC -

Multiresistant
Tet-Ery-Cli

IEC -

ST97
IEC type E

ST425
IEC -

2 IEC type E

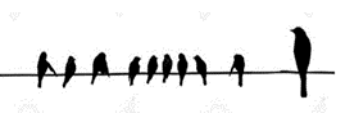
5 IEC -

Susceptible non beta-lactams

blaZ, *tet(K)*, *tet(M)*,
erm(C), *vga(A)*

Susceptible Ab

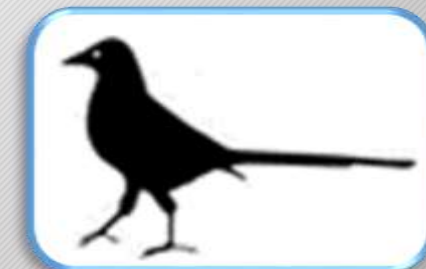
Susceptible non beta-lactams



15 *S. aureus*



Cinereous vulture



Magpie

6 MRSA

2 MSSA

7 MRSA

5 *mecC* -CC130

ST1945-ST1571-t843
ST1945-t1535

1 *mecA* CC398

ST398-t011

ST97-CC97-t267

ST425-CC425-t5998

7 *mecC* -CC130

ST1583, ST1945, ST1581-t843

2 IEC type E

3 IEC -

Multiresistant
Tet-Ery-Cli

IEC -

ST97

IEC type E

ST425

IEC -

33%

2 IEC type E

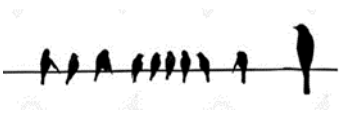
5 IEC -

Susceptible non beta-lactams

blaZ, *tet(K)*, *tet(M)*,
erm(C), *vga(A)*

Susceptible Ab

Susceptible non beta-lactams



12 *S. delphini*



Cinereous vulture

11 *S. delphini*

Group B (n=10)
Group A (n=1)



Red kite

1 *S. delphini*

Group B (n=1)

All methicillin susceptible

11 Tet^R

7 Pen^R

5 Cli^R

1 Clo^R, Str^R

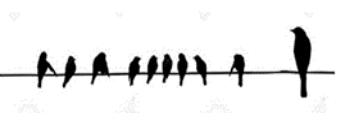
Resistance genes:

tet(K), *blaZ*, *str*, [*lnu\(A\)*](#), [*fexA*](#)

Virulence genes

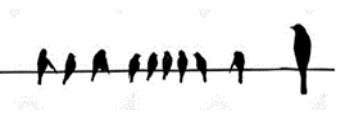
lukS-I, *siet*, *se-int* (n=12)

lukF-I (n=2)



Conclusions

- Magpies and cinereous vultures could act as reservoir of CoPS and MRSA (CC130-*mecC* and CC398-*mecA*)
- The heterogeneous detection of the IEC system among MRSA-*mecC*-CC130 suggests different evolutive clades in this lineage
- *S. delphini*, mostly of group B, is detected in birds of prey
- Wild birds could be a reservoir of CoPS with unusual antimicrobial resistance genes



Conclusions

- Magpies and cinereous vultures could act as potential reservoir of CoPS and MRSA (CC130-*mecC* and CC398-*mecA*)
- The heterogeneous detection of the IEC system among MRSA-*mecC*-CC130 suggests different evolutive clades in this lineage
- *S. delphini*, mostly of group B, is detected in wild birds
- Wild birds could be a reservoir of CoPS with unusual antimicrobial resistance genes

Wildlife is an important element in the evolution of CoPS that and should be closely monitored

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Thanks for your attention

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