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## ANTIBIOTIC RESISTANCE PROFILES OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* (MRSA) FROM PIG PRODUCTION CHAIN IN NORTHERN ITALY

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### Introduction

Pig herds are an important reservoir for Methicillin-Resistant *Staphylococcus aureus* (MRSA), one of the most commonly identified antimicrobial-resistant pathogens worldwide.

The aim of this survey was to evaluate antimicrobial resistance (AMR) profiles of MRSA isolated from finisher pigs in relationship with antimicrobial usage (AMU).

### Materials and Methods

A total of 400 samples were collected from 50 fattening herds, located in Lombardy (Italy). Three environmental samples were collected from each farm. Cutaneous swabs were also collected, from five pigs per farm, at slaughterhouse. MRSA identification was carried out by phenotypic and a quadruplex-PCR. AMR was evaluated by disk diffusion test, following the Clinical Laboratory Standard Institute recommendations. Fifteen prototype molecules, belonging to 12 different drug classes, were tested.

AMU was estimated, as days of treatments per bred pig (days/pig), using defined daily dose animal for Italy (DDDAit) and a standard weight at treatment of 100 kg. DDDAit were established according to Italian summaries of product characteristics. Data were collected retrospectively regarding AMU and pig population of 2016.

### Results

37 MRSA strains were isolated from 21 out of 50 finishing pig herds. 37/37 (100%), 30/37 (81.1%) and 8/37 (21.6%) isolates were resistant to at least one, four and eight classes of antimicrobials, respectively. Medians of AMU were 22.8, 19.5, and 18.3 days/pig in farms where isolates were resistant to 8 or more, 4-7, and 3 or less classes of antimicrobials, respectively. AMU was not significantly different among the three different groups of farms.

### Discussion & Conclusion

Multidrug resistance in MRSA was frequently observed in this survey. Nevertheless, AMR patterns seem not related to AMU, which may be due to a sampling limited in numbers and farms type (finishers only). Further studies are needed to confirm these preliminary findings, which should encompass a larger sample and MRSA molecular characterization.