51st World Congress on

Microbiology

13th International Conference on

Food Technology and Processing

May 24, 2022

WEBINAR

DJONKOUH YAMDEU TCHOUKOUAHA Willy, et al., J Food Ind Microbiol 2022, Volume 08

Epidemiology of nasal carriage of Methicillin-Resistant *Staphylococcus aureus* in pig farmers and their surroundings in the West region of Cameroon

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Objective: The spread of Methicillin Resistant *Staphylococcus aureus* is a major public health problem in hospitals and communities worldwide, in Africa in particular. We carried out a cross-sectional and analytical study to evaluate the epidemiology of nasal carriage of *Staphylococcus aureus* in pig breeders and their neighborhood.

Methodology: Our research was done over a period of 4 months (From 1st January to 15th March then from 1st June to 4th July 2020). A nasal swab was collected from 100 pig breeders, 77 family breeders, 292 pigs and 98 non breeders inhabitants from the Haut-Nkam, Haut- Plateaux, Nkoung-Khi, Mifi and NDE regions in the West region of Cameroon. Samples were cultured for microbial, biochemical, and susceptibility assays according to AC-FSM (2019).

Results: The prevalences of MRSA were 25%, 12.59%, 10.62% and 4.08% in breeders, family, pigs and non-breeders respectively. Our findings on risk factors showed that pig- breeder promiscuity (OR=1207,35; P=0.01), pig carriage of MRSA (OR=20.17; P=0.00), non- breeders living near the farm (OR=10.7; P=0.02), pigs from Koung-Khi (OR=6.3; P=0.0031) and antibiotics consumption (OR=1.34; P=0.0001) were statistically significant and associated to MRSA carriage. Interestingly, wearing protective clothing (OR=0.37; P=0.00), boots (OR= 0.36; P=0.006), gloves (OR= 0.34; P=0.0001) or nose patch (OR= 0.33; P=0.00) was a statistically significant protective factor against MRSA carriage. Our findings also showed that fusidic acid was more resistant to MRSA strains from pigs and non-breeders (51.5%; 75% respectively), and ofloxacin was the most potent antibiotic against MRSA strains in breeders and their family (18.5%; 20% respectively).

Conclusion: Our study showed a high prevalence of MRSA within West regions and the existence of MRSA transmission dynamic amongst pigs, breeders and their neighborhood. Further genetic and molecular study are required to elucidate the diversity in MRSA strains and mechanisms of spread.

Biography

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Received: April 11, 2022; Accepted: April 13, 2022; Published: May 24, 2022