

IntestiPhage, and staphylococcal bacteriophage) and laboratory phages were used for susceptibility testing.

Results: The best results were demonstrated for *S. aureus* strains with 96–98% of isolates being susceptible to the staphylococcal phage preparation. Commercial phages revealed high activity against *Acinetobacter* strains (~94%), *Enterococcus* spp. (~84%), *E. coli* (~87%), and *Klebsiella* spp. (~90%) clinical isolates. The clinical strains, resistant to commercial phages were tested against laboratory phages. The laboratory phages reveal 97–100% lytic activity against the isolates.

Conclusion: The growing problem of antibiotic-resistance in combination with the environmental burden caused by the unrestricted use of antibiotics, provides sufficient motivation for developing alternative solutions to bacterial infections. Bacteriophage treatment of various bacterial infections, including those that are caused by antibiotic-resistant bacteria, is considered a reliable and effective treatment approach. Selection and preparation of specific phages, active against multidrug resistant pathogens is an effective tool to eradicate and treat infections, caused by those pathogens. Use of phages can also decrease the distribution and spread of antibiotic-resistance in medical settings and various environments.

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Exotoxin-profiling and typing of clinical Panton-Valentine Leukocidin positive MSSA versus MRSA



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Purpose: *Staphylococcus aureus* (SA) is one of the most important human pathogens worldwide. SA is causing infections ranging from mild to severe, especially Panton-Valentine leukocidin (PVL) came into focus for the severity of clinical symptoms. Within the last 20 years community acquired PVL positive MRSA stains spread globally and proved to be a public health burden. PVL seems to be highly associated with CA-MRSA but its role in pathogenesis is still controversial and in MSSA neglected.

Methods & Materials: We investigated 79 PVL positive SA (18 MSSA and 61 MRSA) from Austria for SCCmec type, spa-type and 30 exotoxin-genes (sea-see, tst-1, seg-ser, seu, eta, etb, ahl, bhl, ghlabc, ghivar, dhl, lukDE).

Results: The most common agr-type was agr III (51%) followed by agr I (24%). The MRSA strains carried mainly SCCmec IV or V (93%). Analysis of spa-types revealed a diverse genetic background for MSSA and a narrower one for MRSA. The exotoxin-genes seb, seg, sei, sem, sen, seo, seu, ahl, bhl, and ghlabc were detected significantly more often ($p < 0,05$) in MSSA compared to MRSA. 50% of MSSA carried 11 or more (min. 5 - max. 15; average 10) exotoxin-genes whereas 50% of MRSA carried only 6 or more (min. 1 - max. 12; average 7) exotoxin-genes.

Conclusion: The PVL positive MRSA carried significantly less toxin-genes than PVL positive MSSA isolates. This finding supports

the theory that the methicillin resistance together with to many toxin-genes would be too much of a cost of fitness or because of the benefit of methicillin resistance less toxin-genes are more sufficient.

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Prevalence and antimicrobial-resistance features of *Staphylococcus* spp. from pets



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Purpose: *Staphylococci* have been developing, in the last decades, high resistance to beta-lactam antimicrobials, first to penicillin, then to methicillin. In recent years, the number of methicillin-resistant *staphylococci* due to the presence of *mecA* gene contained in the SCCmec, isolated from pets, has been raising. The *mecA* gene confers resistance to the semi-synthetic penicillins and increases the risk of developing multidrug-resistance. The aim of this study was to characterize the antimicrobial-resistance traits of potentially zoonotic *Staphylococcus* spp. strains isolated from dogs and cats with infection.

Methods & Materials: One hundred ninety-nine samples from 160 dogs and 39 cats referred to the Veterinary Teaching Hospital of Padua University were cultured using bacteriological standard techniques. The identification of *staphylococci* at the species level was assessed by biochemical determination and by multiplex-PCR assays for *Staphylococcus Intermedius Group* and *S. aureus*. Antimicrobial susceptibility to the main antimicrobial classes was determined by disk diffusion method based on CLSI guidelines. The presence of *mecA* genes, conferring resistance to beta-lactam antimicrobials, was detected by PCR and was correlated to phenotypic multidrug-resistance profile.

Results: Forty-six *Staphylococcus* spp., 36 from dogs and 10 from cats, were isolated. 76% were *S. pseudintermedius* while the remaining 24%, were represented by other species including *S. aureus*, *S. epidermidis* and *S. hyicus*.

The prevalence of *mecA* gene was 35%. Almost all *mecA*-positive strains were also multidrug-resistant, but the diffusion of multidrug-resistant strains was higher, with a prevalence of 47,8%.

The prevalence rates of *mecA* gene and of multidrug-resistance were similar between *S. pseudintermedius* and the other *Staphylococcus* species.

Conclusion: *S. pseudintermedius* was the most frequently detected species. Indeed this species often occurs as saprophyte on mucocutaneous surfaces and as opportunistic pathogen of pets. In addition to this species, other zoonotic *Staphylococcus* spp. were isolated with similar resistance features.

Our results confirm that multidrug-resistance is associated with the presence of *mecA* gene, although it is also a common feature of potentially pathogen *mecA*-negative strains that should be monitored.

The presence of some strains resistant to almost all drugs tested raises concern because they could spread in veterinary hospitals and to humans, seriously compromising patient outcomes.

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