Evolving landscape of methicillin-resistant *Staphylococcus pseudintermedius*

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1. Introduction

Staphylococcus pseudintermedius is a major opportunistic pathogen in companion animals, particularly dogs. Over the past two decades, methicillin-resistant *S. pseudintermedius* (MRSP) has emerged as a significant clinical concern, not only due to its resistance to β-lactams but also because of its frequent multidrug resistance and capacity for clonal dissemination. Unlike *S. aureus*, MRSP does not pose a major risk to humans, but its impact on veterinary medicine is profound, complicating treatment of both superficial and invasive infections. Several dominant MRSP clones have emerged across different regions, suggesting clonal expansion and replacement events driven by antimicrobial use and host or ecological factors. This lecture will present the global picture of MRSP epidemiology and antimicrobial resistance (AMR), based on an unpublished meta-analysis of 2,654 isolates from 46 studies.

2. Spatial variation

2.1. Differences in clonal distribution

Isolates from Europe, Asia and North America collectively accounted for more than 85.0% of the isolates included in our meta-analysis, followed by Oceania and South America, each contributing with less than 10% of total isolates. Eight CCs (CC45, CC68, CC71, CC196, CC277, CC309, CC551, and CC566) were detected in all five continents. Notably, no CC was confined to a single continent. All 18 CCs were identified in North America, with CC68 (20.1%) and CC757 (12.5%) being the most prevalent. CC71 (53%) and CC258 (17%) were predominant in Europe, while CC45 (35%), CC121 (17%), and CC566 (12%) were the most abundant in Asia. In Oceania, 13 CCs were detected, with CC121 (33%) and CC71 (250%) being the most common. Finally, eight CCs were identified in South America, where CC71 dominated (59%).

2.2. Differences by sample type

CC distribution varies notably by sample type, suggesting niche specialization or differing selection pressures. CC71 is the most commonly isolated clone from skin and ear swabs, comprising 40–50% of isolates from superficial infections—likely reflecting its association with canine pyoderma and otitis externa. In contrast, CC258 and CC496 are more frequently found in deep tissue or invasive infections, such as surgical site infections and wound swabs, where they represent 20–30% of isolates. Their lower prevalence in superficial samples may indicate differences in colonization versus invasion potential. Although urine isolates were less frequently typed, they showed a notable presence of CC45 and CC68, suggesting these lineages may be adapted to urogenital colonization or infection. Other CCs, such as CC232 and CC149, were overrepresented in nasal or perineal carriage studies, possibly indicating a

preference for asymptomatic colonization. These distribution patterns highlight distinct ecological niches and may reflect variations in tissue tropism, host immune response, or antimicrobial exposure across infection types.

3. Temporal variation

3.1. Differences in clonal distribution

Temporal trends across the dataset highlighted dynamic changes in MRSP epidemiology over the last two decades. A decline in the prevalence of historically dominant lineages, such as CC71 in Europe, CC68 in North America, and CC45 in Asia, coincided with the global emergence of CC551, as well as CC556 and CC1431 in North America, and CC363 and CC1631 in Asia. CC258 and CC496 emerged around 2010 and have become increasingly prevalent, particularly in Europe and Oceania. The overall number of distinct CCs reported has increased over time, suggesting greater diversification. These patterns are consistent with the concept of clonal replacement, where emerging lineages with competitive advantages, such as lower fitness costs or higher transmissibility, displace older clones.

3.2. Differences in AMR profiles

Over the last decade, resistance to non-β-lactams increased in North America, particularly for chloramphenicol (6% to 59%), remained largely stable in Europe except for tetracycline, and decreased in Asia. Temporal analysis revealed a general trend toward decreasing resistance in recently emerging clones. Newer lineages such as CC258 and CC496 display narrower resistance profiles, particularly reduced resistance to fluoroquinolones, clindamycin, and chloramphenicol. Resistance to trimethoprim-sulfamethoxazole has remained relatively stable across time and clones. This evolution toward clones with lower resistance could reflect selective pressures imposed by antimicrobial stewardship or natural fitness advantages of less resistant strains.

4. Conclusions

Our meta-analysis underscores the emergence of diverse MRSP lineages such as CC551 and CC309, alongside a marked decline in CC71 and the near disappearance of CC68. These shifts mirror patterns observed in human MRSA and likely reflect selective pressures and regional patterns of antimicrobial use. They also underscore the capacity of dominant clones to rapidly expand and be replaced by more competitive lineages. The ongoing evolution of MRSP highlights the critical need for continued surveillance of clonal diversity and AMR trends, particularly given the limited treatment options for MRSP infections in small animal practice.