Objectives: Infections due to multidrug-resistant *Stenotrophomonas maltophilia* (*SM*) has emerged globally as important nosocomial infections. The role of this bacterium in animal diseases is still less investigated. *SM* was considered to be the cause of fleece rot in sheep and it has been isolated from fish, lizards, frogs, rabbit feces, captive snakes, and African crocodiles, but it was never specifically associated with disease in these species. *SM* DNA was also detected in dogs with knee arthritis/degenerative anterior cruciate ligament rupture, in squirrel feces, in porcine semen, in bovine and ovine milk, and from the gastrointestinal tract of laboratory animals. In veterinary medicine, trimethoprim-sulphamethoxazole resistant *SM* strains have been observed from horses, dogs and cats with chronic respiratory disease and urinary tract infections. The purposes of the present retrospective observational study were: - to establish the frequency of occurrence of *SM* infections in animals by body site of infection; - to evaluate the antibiotic susceptibility of *SM* isolates; - to assess the antibiotic resistance trends in animal *SM* strains from 2008 to 2013.

Methods: Over 6-yrs period, 77 *SM* clinical isolates from dog/cat (n=46), horse/cattle (n=27), and snake/turtle/parrot (n=4) were identified by biochemical tests (Remel, Oxoid, Italy) and were subsequently tested by Kirby Bauer disk diffusion method using single veterinary and human antibiotics. Chi squared test (STATA software version 9.1) was used for data analysis. *P*<0.05 was considered statistically significant.

Results: *SM* strains were cultured from tracheal/bronchial alveolar lavages (38%), nasal/pharyngeal/tonsilar- (31%), uterine- (10%), cutaneous- (9%), ear-swabs (7%) and synovial fluid/abscess/fecal samples (5%). The multi-resistance percentages observed are listed in the Table. No significant differences (*P*>0.05) were recorded in relation to the source of specimens and between animal species both for Veterinary and human drugs. In the 6-yrs study period about two/thirds of *SM* isolates were resistant to trimethoprim-sulfamethoxazole and cefadroxil. From 2008 to 2013, an increasing, but not significant, resistance trends was observed for trimethoprim-sulphamethoxazole (*P*=0.9381), ciprofloxacin (*P*=0.8632) and enrofloxacin (*P*=0.9605), while a significant decrease was recorded for cefadroxil (*P*=0.030), amikacin (*P*=0.0152), and amoxicillin and clavulanic acid (*P*=0.033). A decrease trends were observed for cefquinome, gentamicin, and imipenem (*P*>0.05).

Conclusion: Trimethoprim-sulphamethoxazole is often considered the drug of choice in the treatment of *SM* infections; however, this study reveals that *SM* strains cultured from different animal species are highly resistant to this drug and to other human and veterinary antimicrobials. Thus, because of the emerging complex resistance patterns found in *SM* strains, surveillance programs should be increased for monitoring the spread of antibiotic-resistant *SM* strains in animals, and for analyzing the risk for the public health.