Antimicrobial resistance: a touchy interface between human and veterinary medicine

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The increasing challenge due to antimicrobial resistance of pathogenic bacteria in human-, and veterinary medicine prompted the general fear that several classes of antimicrobials are becoming more or less useless due to their prophylactic and/or therapeutic use for animals. In light of new knowledge on genomic flexibility and on clonal spreading of pathogens and/or commensal bacteria we aim to re-visit potential links of antimicrobial resistance between animals and man. Data about possible ways of evolution of resistances against the most critical antimicrobials (third generation cephalosporins, fluoroquinolones and aminoglycosides) show that foodborne enteric pathogens like Salmonella and Campylobacter seem to be trafficking frequently from animals to man, with the occasional opportunity to transfer critical resistance determinants. In contrast to enteric pathogens, the dominant clones of non-enteritis causing antibiotic resistant bacteria - methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus faecium, multiresistant Pseudomonas aeruginosa - usually differ substantially in the human healthcare setting from those occurring in animals. Adaption of distinct clones of bacteria to various species of animals or to humans may have contributed to the observed clonal diversity. The use of fluoroquinolone type antibiotics could also emerge as an enhancer of major international clones of MRSA and of some additional multiresistant pathogens. Thus, evolution and spread of resistant enteric isolates is frequently driven by the development of some major clones originating and spreading from/within human clinical settings, while the resistant clones of animal/food origin seem to be more diverse with a partial human overlap. Therefore, the differences in spreading antimicrobial resistance within and between differing epidemiological compartments of animals and humans should be considered more analytically.