SESSIONE 2 LA RESISTENZA AGLI ANTIBIOTICI NEGLI ENTEROCOCCHI: SIAMO PRONTI PER AFFRONTARE L'EMERGENZA?

MOLECULAR MECHANISMS OF ANTIBIOTIC RESISTANCE IN ENTEROCOCCI: A MODEL OF ADAPTABILITY AND VERSATILITY

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Over the past three decades there has been a dramatic increase in the rates of enterococcal infections, particular those associated with the healthcare system. Two species cause the majority of enterococcal infections: Enterococcus faecalis and Enterococcus faecium, and have developed resistance to virtually all antimicrobials currently used in clinical practice using a diverse number of genetic strategies. Both species are intrinsically resistant to many commonly used antimicrobial agents, such as cephalosporins, aminoglycosides, clindamycin, and trimethoprim-sulfamethoxazole.

All enterococci may harbor different degrees of β-lactam resistance: decreased susceptibility to penicillin and ampicillin, as well as high-level resistance to most cephalosporins and all semi-synthetic penicillin, due to the over-production of intrinsic low-affinity penicillin-binding proteins. E. faecalis strains resistant to penicillin and ampicillin have been associated with increases in quantities of low-affinity PBP4 (occasionally designated PBP5) or with amino acid substitutions in PBP4. Moreover, they have also acquired resistance by the ability to produce enzymes such as β-lactamases, even if this resistance mechanism has been rarely observed. For many strains, their level of resistance to ampicillin does not preclude the clinical use of this agent. In fact, ampicillin remains the treatment of choice for enterococcal infections that lack other mechanisms for high-level resistance.

Moreover, their plastic genomes allow enterococci to readily recruit antibiotic resistance determinants to further antibiotics by mutations or acquisition of genetic elements by horizontal transfer, conferring high-level aminoglycoside resistance, high-level ampicillin resistance, and vancomycin resistance.

Multidrug-resistant (MDR) enterococci display a wide repertory of antibiotic resistance mechanisms such as drug-target modifications, enzymatic inactivation, efflux pump overexpression and a complex cell envelope adaptive response that promotes survival in the human host and the nosocomial environment.

A thorough understanding of the mechanisms underlying antibiotic resistance in enterococci is the first step for devising strategies to control the spread of these organisms and potentially establish novel therapeutic approaches.

An in-depth understanding of the mechanisms underlying antibiotic resistance is crucial in inventing strategies to monitor spread of MRD enterococci and potentially design new therapeutic approaches.