

Title Direct detection of antibiotic resistance genes in specimens of chicken and pork meat

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Abstract

Antibiotic resistance (AR) in bacteria, a major threat to human health, has emerged in the last few decades as a consequence of the selective pressure exerted by the widespread use of antibiotics in medicine, agriculture and veterinary practice and as growth promoters in animal husbandry.

The frequency of 11 genes [*tet(M)*, *tet(O)*, *tet(K)*, *erm(A)*, *erm(B)*, *erm(C)*, *vanA*, *vanB*, *aac* (δ')-*Ie aph* ($2''$)-*Ia*, *mecA*, *blaZ*] encoding resistance to some antibiotics widely used in clinical practice was analysed in raw pork and chicken meat and in fermented sausages as well as in faecal samples from the relevant farm animals using a molecular approach based on PCR amplification of bacterial DNA directly extracted from specimens.

Some of the 11 AR genes were highly prevalent, the largest number being detected in chicken meat and pig faeces. The genes found most frequently in meat were *tet(K)* and *erm(B)*; *vanB* and *mecA* were the least represented. All 11 determinants were detected in faecal samples except *mecA*, which was found only in chicken faeces. *erm(B)* and *erm(C)* were detected in all faecal samples. The frequency of AR genes was not appreciably different in meat compared to faecal specimens of the relevant animal except for *vanB*, which was more prevalent in faeces.

Our findings suggest that AR genes are highly prevalent in food-associated bacteria and that AR contamination is likely related to breeding rather than processing techniques.

Finally, the cultivation-independent molecular method used in this work to determine the prevalence of AR genes in foods proved to be a rapid and reliable alternative to traditional tools.