Comment on: An assessment of the risks associated with the use of antibiotic resistance genes in genetically modified plants: report of the Working Party of the British Society for Antimicrobial Chemotherapy

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Keywords: antibiotic resistance, veterinary antibiotic use, zoonosis, food animals

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Sir,

In the recent assessment of the risks associated with the use of antibiotic resistance genes in genetically modified (GM) plants by Bennett et al.,1 the authors considered whether occasional transfers of antibiotic-resistance genes \([\text{bla}\text{TEM, }\text{aph}(3')\text{, }\text{aadA1}]\) from GM plants into bacteria would pose a threat to public health. The authors pointed to the fact that these antibiotic resistance genes are common in many bacteria and that each is found on mobile genetic elements that have moved extensively between DNA molecules and bacterial cells. They concluded that this gene mobility has already severely compromised clinical use of antibiotics to which resistance is conferred and that the argument that occasional transfer of these particular resistance genes from GM plants to bacteria would pose an unacceptable risk to human or animal health has little substance. We would like to comment on some of the issues raised, specifically in relation to the animal health and veterinary context.

In the veterinary field in the UK (and in many other countries), a significant number of species of veterinary bacteria remain fully susceptible to β-lactam compounds, such as ampicillin, despite continued therapeutic use of these compounds for decades. Considered against this background of extremely low or no detected resistance in certain bacterial species of veterinary origin, any occasional transfer of resistance genes to these organisms would be a very significant event and we do not feel that the potential hazard to animal health should be characterized as slight in such circumstances. We agree with the authors’ statement that the three resistance genes in question are already widespread in Enterobacteriaceae and that this constitutes a major potential source for transfer of resistance genes to organisms that are currently susceptible, but over recent decades this does not appear to have resulted in transfer to some important bacterial genera in the veterinary field, which remain susceptible.

The authors have stated that the drugs to which the resistance genes \([\text{bla}\text{TEM, }\text{aph}(3')\text{, }\text{aadA1}])\) confer resistance, with the exception of ampicillin/penicillin, are now used infrequently, and rarely as first choice therapy. With regard to animal health, we would like to confirm that this comment does not apply to the UK veterinary situation, where neomycin and spectinomycin are important antimicrobials for first-line treatment of certain conditions, particularly in pigs and poultry. Again with specific regard to the veterinary situation in the UK and because neomycin and spectinomycin still have an important therapeutic role, we do not agree that these particular resistance genes should be considered as ‘old’ resistance genes whose spread has already severely compromised use of the corresponding antibiotic in most, if not all, cases where their use was appropriate in the past.

Regarding the potential transfer of these antimicrobial resistance genes into veterinary bacteria, the argument that there are potent alternative antimicrobials that can be, and are, used in place of the ones that could be compromised of course holds true. However, if it became necessary to use much more potent antimicrobials in the animal health field, then there could be significant consequences for the consumer through the food chain, because increased use of such potent antimicrobials would be likely to provide greater selective pressure for the emergence of resistance to such compounds in bacteria in animals.

Acknowledgements

All DARC Group members are thanked for their contribution to this letter. The DARC Group members are: Dr Kay Goodyear [Veterinary Medicines Directorate (VMD)], Mr John FitzGerald (VMD), Mr Phil Davies (VMD), Miss Jane Gregory (VMD), Dr Jack Kay (VMD), Dr Nick Renn [Veterinary Research Division (VRD)], Professor John Threlfall [Health Protection Agency (HPA)], Mr Chris Teale [Veterinary Laboratories Agency (VLA)], Ms Sally Wellsteed [Department of Health (DH)], Mr Paul Gayford (Defra), Ms Judy Johnson (Defra), Dr Bill Parish (Defra), Dr Marion Rawlins (Defra), Dr Paul Cook [Food Standards Agency (FSA)], Mr Tony Edwards [State Veterinary Service (SVS) Wales], Mr Stanley McDowell [Department of Agriculture and Rural Development in Northern Ireland (DARD)], Mrs Sheila Voas [Scottish Executive Environment and Rural Affairs Department (SEERAD)] and Dr Steven Hill [Chemicals and Genetic Modification (CGM) Policy].

References