An assessment of the impact of antibiotic resistance in different bacterial species and of the contribution of animal sources to resistance in human infections

Robin J. Bywater* and Mark W. Casewell

"Bywater Consultancy, 4 Waterlow Road, Reigate, Surrey RH2 7EX; "King’s College School of Medicine, London SE5 9PJ, UK

*Corresponding author. Tel: +44-1737-211-680; Fax: +44-1737-244-150.

Sir,

Individual bacterial species vary in prevalence and the extent of multiple antibiotic resistance. Little attempt has been made to quantify this variation, or to assess the contribution from animal sources to the overall antibiotic resistance problem in humans. We have therefore attempted to do so by a questionnaire directed to recognized experts in the UK and elsewhere. These were chosen on the basis of their experience and wide knowledge of clinical microbiology, and not on prior knowledge of their attitudes to the topics in question.

The questions posed were based in part on those used by the Public Health Laboratory Service (PHLS) in setting their priorities.1 We added a further criterion to assess the extent to which animal sources may contribute to antibiotic resistance in human infection. The bacteria listed for assessment were those where resistance presents a problem in therapy and were identified in an authoritative report from the Scientific Steering Committee of the European Union Directorate General XXIV.2 A continuous scale was used to assign scores for increasing degrees of importance for each criterion for each bacterial species or subgroup.

The criteria scored for each organism were: (i) the burden of ill-health, assessed according to the prevalence and severity of infection (mortality, post-infection sequelae, treatment cost, etc.). This was scored from 1 (negligible burden) to 5 (major burden of ill health). (ii) The extent to which, for each organism, antibiotic resistance restricts treatment choice. This was scored from 1 (resistance to usual treatments is rare or antibiotic treatment is seldom required) to 5 (resistance is common and can leave few or no treatment options). (iii) The extent to which, for each bacterial species, an animal source may contribute to resistance in human infection. This was scored from 0 (not a source of resistance in human infection) to 5 (the main source of resistance in human infection).

The mean result for each score was treated as follows. For each bacterial species, multiplied (giving the ‘resistance impacts’ of that species) and the resistance impacts of all the species were added to give (i) the mean scores from questions and (ii) the ‘total impact of resistance’. This was then normalized as 100% and the species impact scores for each organism were expressed as a percentage of the total impact of resistance. Finally, the contribution (%) of the resistance in human infections considered to be derived from animal sources was assigned to each organism from the mean score allocated to question (iii) using the following arbitrary criteria (interpolated arithmetically where the mean figure lay between the points listed): ‘not a source’ = 0%; ‘an unlikely source’ = 1%; ‘may be a rare source’ = 5%; ‘is a source’ = 20%; ‘is a significant source’ = 50%; ‘is the main source’ = 80%.

Of 31 questionnaires, 22 were returned (71%), of which two were not completed since these respondents felt unable to respond adequately to the questions. For those completed, there was reasonable agreement between the scores allocated, although in some cases (such as enterococci) more variation in response was seen. Mean results are shown in the Figure. The participants clearly considered that, of all the organisms, the greatest impact of resistance was due to methicillin-resistant Staphylococcus aureus (MRSA) (11.08% overall), both in terms of ill-health and the extent to which resistance restricts treatment.

The perceived contribution of animal sources to the overall impact of resistance was estimated to be very low. Of the 20 species in the questionnaire, the mean score for 12 was less than 1, i.e. that animal sources were not or unlikely to be a source of resistance in human infection. The highest mean scores for animal sources were for non-typhoid salmonellae (3.44) and campylobacter (3.38), both recognized zoonoses. There was some disagreement about the contribution of animals to human infection with vancomycin-resistant enterococci, with scores varying from 0 to 4. The animal contribution to the overall human resistance problem in the species listed, expressed as percentages, are shown in the Figure. Overall, the mean scores indicate that animal sources might account for 3.88% of the human antibiotic resistance problem.

Despite the statistical limitations, we have found this survey helpful to clarify semi-quantitatively the contribution, as perceived by those with experience and expertise in
human infections, of the various bacterial species to the overall antibiotic resistance problem. Most importantly, the survey indicates that the role played by animal use of antibiotics as a source of resistance is perceived to be relatively minor and shows the organisms that need to be targeted for research and control efforts.

Acknowledgement

R. J. B. is a consultant to Pfizer Animal Health, Ltd.

Figure. Perceived contribution (%) of individual bacterial species (□), and of possible animal sources (■), to antibiotic resistance in humans.

References

