



Antibiotic resistance in *Salmonella*: animals may not be major source

Contrary to some established views, the local animal population is unlikely to be the major source of resistance diversity for *Salmonella* Typhimurium DT104 in humans in Scotland, according to a study. The researchers suggest that a broader approach to fighting antibiotic resistance is needed, which goes beyond focusing solely on curbing the use of antibiotics in domestic animal populations.

The emergence of bacteria that are resistant to certain antibiotics is of concern because it means that these antibiotics may no longer work, and that diseases considered treatable may again pose a greater threat. It is thought that many antibiotic-resistant bacteria originate from animals, with resistance driven by the routine use of antibiotics to prevent disease or its spread in livestock animals. However, although there is evidence that contact with animals is associated with infection, it is not clear whether or not animals are the main source of the diversity of resistance observed in human pathogens.

The new study suggests that for one subtype of *Salmonella* bacteria, at least, animal populations may not be the main source of resistance diversity. The researchers based their study on isolates of *Salmonella* Typhimurium DT104 submitted to veterinary and medical diagnostic laboratories in Scotland, UK, between 1990 and 2004. Most animal samples came from cattle.

The study, which received some funding through the EU FMD-DISCONVAC project¹, characterised resistance profiles, i.e., the spectrum of resistance to 13 different antibiotics exhibited by the bacterium. Without considering genetics, the resistance profiles of over five thousand different bacterial isolates were analysed. The researchers also considered whether resistance was first observed in animal or human populations. There were fewer similarities between the resistance profiles of DT104 in human and animal populations than would have been expected if all were regularly mixing together. Of the 65 distinct resistance profiles identified by the researchers, 22 were common to both populations, which left 30 unique to humans and 13 unique to animals.

There was no clear pattern to where resistance to individual drugs was first observed. However, 11 of the 22 profiles shared by both animals and humans were first identified in humans. A further six appeared simultaneously in both, while only five were identified first in animals.

The researchers also looked for the closest relatives (based again on resistance profiles) of each resistance profile to provide an idea of whether they might have originated in animals or humans. They identified more close relatives in the human population, which suggested that the predominant direction of transmission of resistance diversity was not animal-to-human. In addition, resistance profiles in animals were less diverse than in humans. If the animal population was the major source of resistance diversity, the researchers say they would have expected it to be more diverse.

The contributions of other sources of resistance, such as imported food, the environment and exchange of genes between bacteria, could not be investigated due to lack of relevant data, but which may be significant contributors of resistance diversity for the human population. However, the conclusions of this study apply only to the Scottish animal populations, which are unlikely to be the major source of resistance diversity for DT104 in humans, whereas the broader issue requires consideration of other organisms in other settings. The researchers say that appropriate and measured policy to address antibiotic resistance must be developed through a complete understanding of the ecology of resistance.

1. FMD-DISCONVAC (Development, enhancement and complementation of animal-sparing, foot-and-mouth disease vaccine-based control strategies for free and endemic regions) is supported by the European Commission under the Seventh Framework Programme. See: <http://fmdconvac.net/>

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