ANTIBIOTIC RESISTANCE ANALYSIS AS A MEANS OF DETECTING THE ORIGIN OF FAECAL POLLUTION IN WATER

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Introduction

The microbiological quality of mountain water is occasionally endangered by faecal bacteria.

In mountain watersheds, nonpoint sources of microbial pollution can be linked to the presence of domestic herbivores, of wild animals or of man himself.

The possibility of pinpointing the different possible sources of faecal pollution of water would be important for the attribution of **responsibility**, the **prevention** and the **restoration** of water quality.

An interesting approach for the classification of pollution sources is based on the comparison of the **antibiotic resistance** of faecal streptococci.

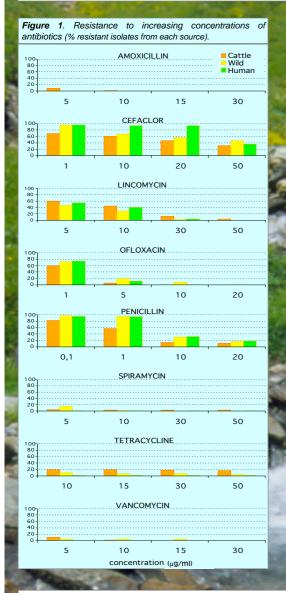
Materials and methods

From June 2004 to April 2005, in Valle d'Aosta, **24 samples** of mixed wastes were collected: 12 from dairy and beef **cattle**, 6 from **wildlife** (chamois, ibex, deer, fox) and 6 from **human** wastes.

The strains of faecal streptococci isolated from these samples were submitted to each of 4 concentrations of 8 antibiotics.

The following active principles were used: amoxicillin (AMO), cefaclor (CEF), lincomycin (LIN), ofloxacin (OFL), penicillin G (PEN), spiramycin (SPI), tetracycline (TET) and vancomycin (VAN).

Data on the growth of isolates in the presence of each concentration of each antibiotic (32 variables per isolate) were treated with the **discriminant analysis** of the SPSS programme.



Results

A total of **3,256** isolates were obtained and their patterns of antibiotic resistance were determined and analysed (*Figure 1*).

The overall resistance levels were **lower** than the values reported in bibliography: that could be explained by a relatively moderate utilisation of antibiotics, particularly in veterinary medicine, in Valle d'Aosta.

A relatively high resistance to PEN, CEF and, to a lesser extent, to OFL was recorded for isolates of all three sources but especially for wild and human ones. On the other hand, these isolates were very sensitive to AMO, even at the lowest concentrations. Human isolates were also the least resistant to SPI, TET and VAN and cattle ones were generally the most resistant to LIN and TET.

In wild samples, the relatively high resistance was mainly due to isolates from faeces of **foxes** and **ibexes** living close to human settlements.

The discriminant analysis correctly classified 85.5%, 82.2% and 72.5%, respectively, cattle, human and wild isolates (*Table 1*).

Cattle isolates were quite accurately classified, while a certain confusion was observed regarding wild and human isolates: more than 10% of human

1.056

Human

Isolates were classified as wild, the opposite occurred for nearly 20% of wild ones.

The overall average rate of correct classification (ARCC), calculated as the ratio of correctly classified data to the total number of isolates, was 80.5%.

If all the isolates were grouped in only two categories (i.e. cattle vs. wild+human), the ARCC improved to 89.8% (Table 2).

Table 1.	. Cross-validate	ed discriminar	nt analysis	of antibiotic
resistance	e profiles of fac	ecal streptoco	cci isolated	from various
sources.				
	no. of	Isolates	(%) class	sified as:
Source	isolates	Cattle	Wild	Human
Cattle	1,208	85.5	8.4	6.0
Wild	992	8.0	72.5	19.6

Table 2. Cross-validated discriminant analysis of antibiotic resistance profiles of faecal streptococci isolated from cattle and non-cattle sources.

6.8

11.0

82.2

	no. or	isolates (%) classified as:	
Source	isolates	Cattle	Wild + Human	
Cattle	1,208	86.3	13.7	
Wild + Human	2,048	8.1	91.9	

This **pooling** may be useful when it is necessary to determine if the source of the pollution is an agricultural one (grazing animals, manuring) or not.

Conclusions

The discriminant analysis of multiple antibiotic resistance **confirmed its effectiveness** in distinguishing the sources of faecal streptococci and could be a useful tool for pinpointing, to a suitable level of precision, the source of unknown faecal pollutions in natural waters in Valle d'Aosta.

Acknowledgments

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