

Antibiotic resistance racing downriver

A river that runs through Colorado's plains carries two different genes that protect microbes from antibiotics.

Naomi Lubick

17 October 2012



Philip Nealey/Getty

The pristine Platte river picks up microbial genes for antibiotic resistance as it flows past human settlements.

The South Platte River system begins in pristine Rocky Mountain streams and flows east through the Coloradan plateau dotted with cattle ranches, sheep pastures, dairy farms — and human wastewater-treatment plants. In the first quantitative survey of a whole landscape, researchers have mapped how human activities affect the concentrations of antibiotic-resistance genes in the watershed¹.

Amy Pruden of Virginia Tech in Blacksburg and her colleagues tracked two integrons — genetic elements that can be traded by microbes or persist on their own in the environment — called *su1* and *tet(W)*, which confer resistance to sulphonamide and tetracycline antibiotics, respectively. Both classes of drugs are used in animals and humans.

Over the course of a year, the researchers sampled ten sites in the watershed, including both the relatively pristine upstream areas and those downstream of human activity. The team characterized 89 water-treatment plants and 100 animal-feeding operations that feed into the river. The South Platte receives treated waste effluent from places such as Denver, and in February, the driest time of the year, its flow can be dominated by effluent.

Pruden says that *su1* antibiotic-resistance genes were 1,000–10,000 times higher in human-affected sites than in the 'natural background' of more pristine areas of the watershed. There was also a linear correlation between *su1* concentrations and the number and location of wastewater-treatment plants and animals upstream.

But there was no clear correlation between *tet(W)* and human activity, nor did *tet(W)* concentrations match previous measurements of tetracycline antibiotics in river sediments that might have led to the development of local pockets of resistance in microbial communities.

The team speculates that *su1* genes are more "promiscuous", or more readily taken up by bacteria in the environment and spread around, whereas *tet(W)* is more limited. Mechanical means of transportation might dominate its movement in the environment, such as being attached to sediments.

Background resistance

Resistance genes occur naturally in the environment; prehistoric ice samples show TetM alongside mammoth DNA in 30,000-year-old Alaskan permafrost². That background makes it important to characterize "both the natural occurrence of the antibiotic-resistance genes and the anthropogenic load, and where those genes come from, and it's good to do it in a quantitative way," as Pruden's team did for the South Platte, says Joakim Larsson of the University of Gothenburg, Sweden, who has tracked antibiotics and resistance

genes in India and Sweden³.

Dana Kolpin of the US Geological Survey in Iowa City says that the findings highlight the complex issue of antibiotic-resistance genes, which will continue to be of concern as treated effluent becomes more widely used in regions that have scarce water resources. But he cautions that although Pruden's model is helpful in understanding the South Platte system, "you cannot extrapolate to all basins, as all will be unique".

Pruden and other researchers may have a chance to track these risks soon: she and her colleagues recently completed an unpublished study of wastewater effluent from Flagstaff, Arizona, showing that microbes that might carry antibiotic resistance survive the treatment plant's relatively thorough methods, and thrive in the pipes that carry the treated effluent to be used elsewhere. The scientists have also detected resistance genes for sulphonamides and another antibiotic in the treated wastewater — which will be turned into snow at a nearby ski resort, in a relatively pristine part of a river basin, later this year.

Nature | doi:10.1038/nature.2012.11612

References

1. Pruden, A., Arabi, M. & Storteboom, H. *Environ. Sci. Technol.* <http://dx.doi.org/10.1021/es302657r> (2012).
2. D'Costa, V. M. *et al. Nature* **477**, 457–461 (2011).
3. Kristiansson, E. *et al. PLoS ONE* **6**, e17038 (2011).