

Antibiotic resistant bacteria in the environment - we have a problem

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Imagine you were sick, let's say, you had a bacterial infection. What would you do? Of course you'd go to the doctor! And he'd give you antibiotics, simple as that. You would make sure that you take all your medicine and by the end of next week, you'd feel happy and healthy again. Now imagine your antibiotics wouldn't work anymore. Wouldn't that be scary? It is startling, but what sounds like a future dystopian scenario is already happening right now. Bacteria (among which also those that can cause severe infections in humans) are growing more and more resistant to the antibiotics that are widely used by today's medicine and livestock industry. Because we handle antibiotics – probably the most powerful weapon of today's health care - on an inflationary basis, bacteria get the chance to adapt to them. They do this by mutation or acquisition of resistance genes. When this happens, antibiotics lose their power and simple bacterial infections that we cured easily yesterday using antibiotics, might today become life-threatening again. The prevalence of antibiotic resistance in the environment is shown to correlate with antibiotic usage, meaning that countries, that have a high antibiotic consume, are dealing with alarming cases of antibiotic resistant bacteria. Especially in Southern Europe, the situation is worrisome. At the same time, Northern Europe is reported to have little prevalence of antibiotic resistant microorganisms, most likely due to a conservative antibiotic usage. Once the resistant bacteria have reached the environment, they can disperse to virtually everywhere: Through extensive human usage they can be found in human waste (for example leftovers from poultry farms, where antibiotics are widely used to promote health and growth of animals). Wild birds that scavenge from this waste then acquire the bacteria via feeding. They are very mobile and can reach even remote natural environments through migration. This way, they shed out the resistant bacteria into for example lakes, ponds or rivers where they get in touch with other bacteria for exchanging genetic material.

In the present study, we examined *Escherichia coli* isolates, a common bacterium found in the intestines of mammals. We took fecal samples from wild birds from Portugal, Spain and Sweden to compare antibiotic resistance patterns between countries with high (Portugal and Spain) and low (Sweden) antibiotic pressures in the environment. We also analyzed how the isolates were related to each other, hypothesizing that we might find specific lineages in all three countries, and that they would all share similar genetic resistance profiles. Although the diversity of *E. coli* from all countries was very high, we could identify isolate relatedness based on geographic regions. This means that all isolates from Northern Europe were more closely related to each other than to the isolates from Southern Europe. However, those isolates that were related to each other, did not share the same resistance profiles to tested antibiotics. Also, they did not share the same genetic resistance patterns, leading us to the conclusion that other factors that were not considered in this study might influence resistance development. These factors might for example be isolation date and location, isolation method and host species, as we took isolates from various species. Study results nevertheless underline the need for us to take action in this very threatening environmental pollution.

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