



S4.3 Intermediate concentrations of synthetic antibiotics drive drastic changes in aquatic bacterial communities

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The spread of resistances to commonly used synthetic antibiotics (AB) in natural environments is one of the major threats to human health. A large number of publications investigated the relations between different human pathogens and the spread of AB resistances, but a comparably low number of studies targeted the ecological effect of the presence of synthetic AB on non-pathogenic bacteria in waters. We tested the long-term impact of a cocktail of synthetic antibiotics of commercial use (Imipenem, Levofloxacin, and Tetracycline) on artificial bacterial communities miming a very simplified natural freshwater community. The experimental setup consisted in a 24 days-long continuous culture system where the bacterial communities were exposed to three different AB concentrations: no AB (control), sub-lethal AB concentration (comparable to anthropized European lakes), and in AB concentration 10 folds higher (comparable to heavily contaminated water treatment plants). Bacterial number and morphological distribution were daily monitored (epifluorescence microscopy), while community composition (CARD-FISH) and antibiotic resistance were assessed bi-weekly. Bacterial production, and thus abundance, dropped by 75% in the presence of AB, independently by their concentration, while bacterial community composition resulted highly affected by intermediate AB concentration, with reversal in the proportion of the dominant groups (*A. hydrophila* and *Brevundimonas* sp.). These results, for the first time focussing on the ecological consequences of AB on a experimental bacterial community, highlight the potential risk posed by low AB concentrations in waters. Their effect is not only limited to the spread of potentially pathogenic strains, but it extends to modification of interspecific ecological interactions, weakening the natural resistance of the aquatic communities to the success of allochthonous, and potentially dangerous, strains.

S4.4 Ecology and genetic diversity of *Escherichia coli* associated with macroalgae

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Interactions between epiphytic bacteria and macroalgae have been described in aquatic ecosystems. Like other eukaryotic organisms, seaweeds harbour a wide diversity of associated microorganisms with functions related to host health and defense. However, the occurrence of *Escherichia coli* and other potential human pathogens associated with macroalgae has been little investigated. From February to May 2013, we collected macroalgal samples (*Ulva* spp., *Undaria* spp. and *Sargassum* spp.) in the Venice lagoon, at three sites along a gradient of microbiological contamination. About 400 *E. coli* isolates were screened to confirm their identification as *E. coli*, to assign them to the phylogenetic group (A, B1, B2, C, D, E and F), to determine the presence of toxins and virulence factors genes, and to study their genetic diversity. All macroalgae hosted high abundance of *E. coli* (up to 103 cfu/g) belonging to all known phylogroups. Only few strains belonged to cryptic clades, and were prevalently isolated from seawater. No toxins or intimin genes were detected. Macroalgae-associated *E. coli* showed wide temporal variability, lack of correlations with populations in the overlying seawater, and ability to grow on macroalgal extracts as only source of carbon. We suggest the existence of an environmental reservoir of *E. coli* genotypes, which possibly includes “naturalized” genotypes adapted to the macroalgal habitat, with implications from either the public health and ecological perspectives.