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## Understanding regulatory networks of *Escherichia coli* ST131: a novel approach to combat multiresistant infectious microorganisms

Eight years ago, a hitherto unknown *E. coli* clonal group, sequence type 131 (ST131) was simultaneously identified in three continents. Nowadays ST131 is the *E. coli* lineage that predominates around the world among the pathogenic *E. coli* isolates that cause extraintestinal infections. These clones exhibit antibiotic multiresistance and cause severe infections (i.e., meningitis, urinary tract infections). The reasons for the epidemiological success of this clonal type remain unknown.

A recent work of the research group (Prieto et al., 2016. *Scientific Reports* 6:25793) has shown that a novel variant of the Hha global modulator (Hha2) is widespread among pathogenic *E. coli* isolates, specifically among ST131 clones. The objectives of the project are to determine the targets of Hha and Hha2 modulators in these isolates, and compare them with those existing in other pathotypes. Identifying specific ST131 genes modulated by Hha/Hha2 may shed light into the mechanisms underlying their epidemiological success, and hence offer new approaches to combat ST131 infections.