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Diverse fitness associated with resistance to fluoroquinolones influenced the clonal dynamics of various multiresistant pathogens

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Fitness cost associated with resistance to fluoroquinolones was recently shown to vary across clones of methicillin-resistant *Staphylococcus aureus* (MRSA) and extended-spectrum β-lactamase (ESBL)-producing *Klebsiella pneumoniae*. The resulting dissimilar fitness should have influenced the clonal dynamics and thereby the rates of resistance for these pathogens. Moreover, a similar mechanism was recently proposed for the emergence of the H30 and H30R lineages of ESBL-producing E. coli and the major international clone (ribotype 027) of *Clostridium difficile*. The overwhelming part of the available epidemiological data supports the connection. An ability to develop favorable mutations in the gyrase and topoisomerase IV genes seems to be a prerequisite for pathogens to retain fitness while showing high-level resistance to fluoroquinolones. Moreover, the mechanism was observed to select for the CTX-M-15 type ESBL in *K. pneumoniae* that may account for the widespread dissemination of this enzyme. The findings suggest that the use of fluoroquinolones as a function of clonal distribution could ameliorate the state of antibiotic resistance. When the proportions of multiresistant clones influenced by fluoroquinolones are low the use of these antibiotics remains highly beneficial. However when their proportion increases the consumption of fluoroquinolones should transiently be reduced.

Biography

Miklos Fuzi has completed his PhD in 2001 and has been engaged in the investigation of clonality and antibiotic resistance during the last 15 years. He has published 38 papers in reputed journals. He is an Associate Professor at Semmelweis University, Budapest, Hungary.

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