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Paper Poster Session

Microbial pathogenesis and virulence

Epidemiological characterization and phylogenetic analysis of the emerging *Salmonella enterica* serovar Napoli: the first cause of invasive nontyphoidal salmonellosis in Lombardy, northern Italy

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Background: *Salmonella enterica* serovar Napoli is a nontyphoidal serotype that is currently emerging in Europe, mainly affecting Switzerland, France and Italy. In the latter, *S. Napoli* incidence has increased by 28.2% during the period 2000-2011, most cases occurring in Lombardy region. Furthermore, a recently large outbreak occurred in Milan, Italy, associated to elevated rates of hospitalization and bacteraemia, has evidenced that *S. Napoli* infections may become invasive. By considering the elevated invasive rate observed for that recent outbreak and the knowledge gaps, we aimed to investigate the role of *S. Napoli* in invasive salmonellosis in Lombardy during the period 2010-2014, and infer the phylogeny of this emerging serotype.

Material/methods: Data of human salmonellosis cases in Lombardy during the period 2010-2014 (10,858 records) were obtained from IT-ENTER-NET, a network of diagnostic laboratories. Comparative genomics analysis based on sequence data for 93 core genome loci, as described by den Bakker *et al.*, was performed to define phylogenetic relationships of 14 *Salmonella enterica subsp. enterica* serotypes, including *S. Napoli* outbreak strain, and one *S. enterica subsp. arizonae* strain.

Results: *S. Napoli* incidence in Lombardy continued to increase during the period 2010-2014. Moreover, this serotype was the first cause of invasive nontyphoidal salmonellosis during 2010-2014 (35 invasive cases out of 691, invasive rate of 5.1%). Phylogenetic analysis revealed that *S. Napoli* belongs to the Typhi subclade of clade A, and the most related serotype was found to be Paratyphi A. Additionally, *S. Napoli* genome carries the invasive determinant gene *cdtB* and the pathogenicity island SPI-18.

Conclusions: *S. Napoli* is an emerging public health concern in Italy. Nevertheless, the role of nontyphoidal serotypes in invasive disease is yet poorly studied. A combination of SPI-18 island and *cdtB* gene was previously reported only in *S. Typhi*, *S. Paratyphi A* and clade B serotypes, all of them associated to elevated rates of invasive disease. Thus, to the best of our knowledge, this is the first time that a clade A nontyphoidal serotype presents the same virulence-genes pattern of *S. Typhi* and *S. Paratyphi A*. Our work suggests that *S. Napoli* potential virulence deserves attention and highlights a need to discuss its classification in nontyphoidal group.