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.