ES18: Prevalence of feline bartonellosis and multilocus sequence typing of *Bartonella henselae* isolates in urban stray cats living in Milan, Italy

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Cat scratch disease is a worldwide zoonosis caused predominately by Bartonella henselae and, to a lesser extent, by B. clarridgeiae. Cats are the natural reservoir and vectors for B. henselae and B. clarridgeiae infections in humans. Genetic heterogeneity of B. henselae strains has been reported and multiple sequence types (STs) have been identified by the use of multilocus sequence typing (MLST). Particular sequence types have been more frequently associated with zoonosis than others. The aim of this study was to evaluate the prevalence of B. henselae and B. clarridgeiae infection in stray cats from Milan, Italy, and to explore the genotypes of the B. henselae population for the evaluation of the potential risk of transmission to humans. Whole blood samples collected from 89 stray cats were cultured and analysed by PCR. Sequence types of the feline B. henselae isolates were delineated using MLST. Bartonella henselae was detected in four (4.5%) cats and B. clarridgeiae was detected in one (1.1%) cat by PCR on blood samples. Co-infection by B. henselae type I and type II was identified in one cat. Four B. henselae isolates were cultured and were characterised as ST1 (2/4), ST5 (1/4) and ST8 (1/4), which are more commonly regarded as human associated or zoonosis associated STs. Typical feline associated B. henselae STs were not observed. Despite the low prevalence of B. henselae infection in stray cats from Milan, further investigations are needed to assess the risk for human health.

ES19*: Unifying the epidemiological and population dynamics of the monophasic *Salmonella* infections using whole genome sequencing

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S. enterica serovar Typhimurium is defined by somatic antigens O 4,[5],12) and H i:1,2 that are determined by the long chain polysaccharide (LPS) and flagella antigens, respectively. However, since 1990 there has been increasing incidence in many locations worldwide of human and animal infection with Salmonella with antigenic formula 4,[5],12:i:- and 4,12,:i:- (monophasic *Salmonella*). In the European Union these isolates are generally of phage type DT120 or DT193 and appear to be replacing DT104 as the dominant phage type associated with multi-drug resistance (MDR). Using next-generation sequencing (NGS) technology we have used whole genome sequence variation to determine the phylogenetic relationship of 127 monophasic Typhimurium isolates from animals in the UK from 1995-2010 and from human clinical cases of disease from 2007-2010 and compare these with the genomic sequence of 29 commonly isolated human and animal biphasic S. Typhimurium (4,[5],12:i:1,2) isolates. These data indicate a clonal expansion of a clade of S. Typhimurium beginning in about the year 2000, that are phylogenetically distinct from the epidemic DT104 clade and monophasic isolates prior to the year 2000. Comparative genomics identified two novel genetic islands and a region encoding multiple antibiotic resistance genes. The monophasic phenotype was due to multiple deletion events that occurred during the epidemic.

This study provided a scientific basis for the phylogenetic classification of monophasic *Salmonella* as S. Typhimurium and not another separate emerging multidrug resistant serovar as well as an insight into the development of Salmonella epidemics that can inform future control programmes.

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