Is the Evolution of Salmonella enterica subsp. enterica Linked to Restriction-Modification Systems?

Salmonella enterica subsp. enterica bacteria are highly diverse foodborne pathogens that are subdivided into more than 1,500 serovars. The diversity is believed to result from mutational evolution, as well as intra- and interspecies recombination that potentially could be influenced by restriction-modification (RM) systems. The aim of this study was to investigate whether RM systems were linked to the evolution of Salmonella enterica subsp. enterica. The study included 221 Salmonella enterica genomes, of which 68 were de novo sequenced and 153 were public available genomes from ENA. The data set covered 97 different serovars of Salmonella enterica subsp. enterica and an additional five genomes from four other Salmonella subspecies as an outgroup for constructing the phylogenetic trees. The phylogenetic trees were constructed based on multiple alignment of core genes, as well as the presence or absence of pangenomes. The topology of the trees was compared to the presence of RM systems, antimicrobial resistance (AMR) genes, Salmonella pathogenicity islands (SPIs), and plasmid replicons. We did not observe any correlation between evolution and the RM systems in S. enterica subsp. enterica. However, sublineage correlations and serovar-specific patterns were observed. Additionally, we conclude that plasmid replicons, SPIs, and AMR were all better correlated to serovars than to RM systems. This study suggests a limited influence of RM systems on the evolution of Salmonella enterica subsp. enterica, which could be due to the conjugal mode of horizontal gene transfer in Salmonella. Thus, we conclude that other factors must be involved in shaping the evolution of bacteria.

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