The Genetic Diversity of Salmonella and Listeria Isolates from Food Facilities

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Food production-related facilities (farms, packing houses, shipping warehouses, etc.) are monitored for foodborne pathogens, and data from these facilities can provide a rich source of information about the population structure and genetic diversity of Salmonella and Listeria. This information is of both academic interest for understanding the evolutionary forces acting on these organisms, and of practical interest to those responsible for controlling pathogens in facilities and to those analyzing data from facilities in the context of public health decision making. We have collected information about all positive isolates from facility inspections performed by the FDA for which whole-genome sequencing (WGS) data is available. The within- and between-facility genetic diversity of isolates was computed and related to the common origin of isolates. Our results show that if the genetic distance between two isolates is low, then more likely than not they are from the same facility or have some overlap in their supply chain (for example, if the genetic distance is no more than 20 SNPs, then the probability that they come from the same facility is .66 for Salmonella and .70 for Listeria). However, if two isolates come from different facilities, their genetic distance ($D$) is likely large (for Salmonella, $P(D>20\text{ SNPs})=.9998$; for Listeria, $P(D>20\text{ SNPs})=.9995$); even if two isolates come from the same facility, their genetic distance is also very likely large (for Salmonella, $P(D>20\text{ SNPs})=0.79$; for Listeria, $P(D>20\text{ SNPs})=0.69$). These results provide insight into what SNP thresholds might be appropriate when determining whether two isolates are from the same facility and, thus, be of interest to those investigating foodborne outbreaks and conducting traceback investigations.