Listeria monocytogenes is a ubiquitous bacterium that may cause the foodborne illness listeriosis. Only a small amount of data about the population genetic structure of strains isolated from food is available. This study aimed to provide an accurate view of the L. monocytogenes food strain population in France. From 1999 to 2014, 1,894 L. monocytogenes strains were isolated from food at the French National Reference Laboratory for L. monocytogenes and classified according to the five risk food matrices defined by the European Food Safety Authority (EFSA). A total of 396 strains were selected on the basis of different pulsed-field gel electrophoresis (PFGE) clusters, serotypes, and strain origins and typed by multilocus sequence typing (MLST), and the MLST results were supplemented with MLST data available from Institut Pasteur, representing human and additional food strains from France. The distribution of sequence types (STs) was compared between food and clinical strains on a panel of 675 strains. High congruence between PFGE and MLST was found. Out of 73 PFGE clusters, the two most prevalent corresponded to ST9 and ST121. Using original statistical analysis, we demonstrated that (i) there was not a clear association between ST9 and ST121 and the food matrices, (ii) serotype IIc, ST8, and ST4 were associated with meat products, and (iii) ST13 was associated with dairy products. Of the two major STs, ST121 was the ST that included the fewest clinical strains, which might indicate lower virulence. This observation may be directly relevant for refining risk analysis models for the better management of food safety. This study showed a very useful backward compatibility between PFGE and MLST for surveillance. The results enabled better understanding of the population structure of L. monocytogenes strains isolated from food and management of the health risks associated with L. monocytogenes food strains. Moreover, this work provided an accurate view of L. monocytogenes strain populations associated with specific food matrices. We clearly showed that some STs were associated with food matrices, such as meat, meat products, and dairy products. We opened the way to source attribution modeling in order to quantify the relative importance of the main food matrices.