The contamination routes of Listeria monocytogenes in cold-smoked salmon processing plants were investigated by analyzing 3,585 samples from products (produced in 1995, 1996, 1998, and 1999) and processing environments (samples obtained in 1998 and 1999) of two Danish smokehouses. The level of product contamination in plant I varied from 31 to 85%, and no L. monocytogenes was found on raw fish (30 fish were sampled). In plant II, the levels of both raw fish and product contamination varied from 0 to 25% (16 of 185 raw fish samples and 59 of 1,000 product samples were positive for L. monocytogenes). A total of 429 strains of L. monocytogenes were subsequently compared by random amplified polymorphic DNA (RAPD) profiling, and 55 different RAPD types were found. The RAPD types detected on the products were identical to types found on the processing equipment and in the processing environment, suggesting that contamination of the final product (cold-smoked salmon) in both plants (but primarily in plant I) was due to contamination during processing rather than to contamination from raw fish. However, the possibility that raw fish was an important source of contamination of the processing equipment and environment could not be excluded. Contamination of the product occurred in specific areas (the brining and slicing areas). In plant I, the same RAPD type (RAPD type 12) was found over a 4-year period, indicating that an established in-house flora persisted and was not eliminated by routine hygienic procedures. In plant II, where the prevalence of L. monocytogenes was much lower, no RAPD type persisted over long periods of time, and several different L. monocytogenes RAPD types were isolated. This indicates that persistent strains may be avoided by rigorous cleaning and sanitation; however, due to the ubiquitous nature of the organism, sporadic contamination occurred. A subset of strains was also typed by using pulsed-field gel electrophoresis and amplified fragment length polymorphism profiling, and these methods confirmed the type division obtained by RAPD profiling.