Flavobacterium psychrophilum is the causative agent of bacterial cold water disease (BCWD), which affects a variety of freshwater-reared salmonid species. A large-scale study was performed to investigate the genetic diversity of F. psychrophilum in the four Nordic countries: Denmark, Finland, Norway, and Sweden. Multilocus sequence typing of 560 geographically and temporally disparate F. psychrophilum isolates collected from various sources between 1983 and 2012 revealed 81 different sequence types (STs) belonging to 12 clonal complexes (CCs) and 30 singleton STs. The largest CC, CC-ST10, which represented almost exclusively isolates from rainbow trout and included the most predominant genotype, ST2, comprised 65% of all isolates examined. In Norway, with a shorter history (<10 years) of BCWD in rainbow trout, ST2 was the only isolated CC-ST10 genotype, suggesting a recent introduction of an epidemic clone. The study identified five additional CCs shared between countries and five country-specific CCs, some with apparent host specificity. Almost 80% of the singleton STs were isolated from non-rainbow trout species or the environment. The present study reveals a simultaneous presence of genetically distinct CCs in the Nordic countries and points out specific F. psychrophilum STs posing a threat to the salmonid production. The study provides a significant contribution toward mapping the genetic diversity of F. psychrophilum globally and support for the existence of an epidemic population structure where recombination is a significant driver in F. psychrophilum evolution. Evidence indicating dissemination of a putatively virulent clonal complex (CC-ST10) with commercial movement of fish or fish products is strengthened.