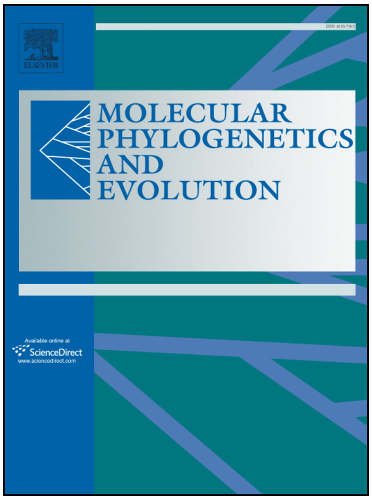

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Abstract

At present, the genus *Edwardsiella* compiles five species: *E. tarda*, *E. hoshinae*, *E. ictaluri*, *E. piscicida* and *E. anguillarum*. Some species of this genus such us *E. ictaluri* and *E. piscicida* are important pathogens of numerous fish species. With the description of the two latter species, the phylogeny of *Edwardsiella* became more complicated. With the aim to clarify the relationships among all species in the genus, a multilocus sequence typing (MLST) approach was developed and applied to characterize 56 isolates and 6 reference strains belonging to the five *Edwardsiella* species. Moreover, several analyses based on the MLST scheme were performed to investigate the evolution within the genus, as well as the influence of recombination and mutation in the speciation. *Edwardsiella* isolates presented a high genetic variability reflected in the fourteen sequence types (ST) represented by a single isolates out of eighteen total ST. Mutation events were considerably more frequent than recombination, although both approximately equal influenced the genetic diversification. However, the speciation among species occurred mostly by recombination. *Edwardsiella* genus displays a non-clonal population structure with some degree of geographical isolation followed by a population expansion of *E. piscicida*. A database from this study was created and hosted on pubmlst.org (http://pubmlst.org/edwardsiella/).

1. Introduction

The genus *Edwardsiella* was described in 1965 by Ewing *et al.* to define a distinct taxon within the family *Enterobacteriaceae* (Abbott and Janda, 2006). The species belonging to this genus can be found in many different environmental niches and associated to a high variety of animals including fish, reptiles, amphibians, chickens and other warm-blooded animals (Abbott and Janda, 2006; Mohanty and Sahoo, 2007). *Edwardsiella* is also responsible for some infections of humans causing gastroenteritis presented as acute watery diarrhea (Leung et al., 2012). The most common cause for this zoonosis is the exposition to the causal agent during the fishing or working offshore (Diaz, 2014) since water environment is a common niche of members of *Edwardsiella* (Du, 2007). At present, the genus compiles 5 species: *Edwardsiella tarda*, *Edwardsiella hoshinae*, *Edwardsiella ictaluri*, *Edwardsiella piscicida* and *Edwardsiella anguillarum*. *E. tarda* (Ewing et al., 1965), the best studied taxon in this genus, exhibits a broad geographical distribution and host range. *E. hoshinae* (Grimon et al., 1980) was associated to birds