

## **Geographical distribution and molecular characterization of Integrative Conjugative Elements in environmental *Vibrio cholerae*.**

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Lateral gene transfer is universally recognized as a major contributor in bacterial evolution. Integrative conjugative elements (ICEs) are one of the three principal classes of self-transmissible mobile elements that mediate horizontal gene transfer in bacteria. ICEs can transfer via conjugation and integrate into and replicate with the host chromosome. Members of this class of mobile elements have been isolated from several species of gram-negative bacteria of clinical importance, demonstrating them to be important vectors of drug resistance and virulence dissemination. However, the isolation of ICEs from a broad range of environmental isolates suggested that the natural environment represents a reservoir for these elements, where they play an important role as genetic vectors modulating ecological adaptation. Since 1992, the SXT/R391 family of ICEs have been found to be widely distributed among *Vibrio cholerae* clinical and environmental isolates. To date, ICEs in *V. cholerae* have been found in Asian and African isolates, with a single exception of an SXT-related ICE isolated in the western hemisphere. However, ICEs in other species have been found in many geographical areas, suggesting a broader distribution of these elements, especially in organisms of environmental origin. In this study we focused on the geographical distribution of this class of genetic elements in a large collection of *V. cholerae* strains isolated from different geographical areas and at different chronological times, where the presence of ICEs has not yet been reported, namely North and South America, the Republic of Georgia and Iceland. Molecular characterization and genomic comparison with those elements that have been documented to date were done, using ICEs from our culture collection.

Results support the hypothesis that the SXT/R391 family of ICEs is widely distributed in environmental *V. cholerae* populations. All elements share a common

backbone which works as genetic machinery for capturing and disseminating a diversity of information. This variable genetic content contributes to genomic evolution responsible for adaptation of the bacterial host to new ecological niches.