What integrase phylogeny tells us about *Vibrio* evolution

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Pathogenicity Islands (PAIs) encompass a functionally diverse but distinct group of mobile and integrative genetic elements (MIGEs) that encode genes that enhance the virulence of their host bacterium. Among Gram-negative bacteria, PAIs mostly integrate into the bacterial genome at tRNA sites using site specific recombination and are stably maintained within the chromosome. We determined the evolutionary history of pathogenicity islands from *Vibrio cholerae*, specifically the 57 kb *Vibrio* pathogenicity Island-1(VPI-1) and the non-homologous 40 kb VPI-2 region. By using the VPI-encoded tyrosine recombinase integrase IntV1 (VC1758) as a seed, we identified 383 homologues of this protein (cut off >35% protein identity) in the genome database. These homologues were identified in predominantly *Gamma-Proteobacteria* but also in *Beta-Proteobacteria*, *Alpha-Proteobacteria*, *Delta-Proteobacteria*, with single representatives from phyla *Synergistetes, Chlorobi, and Planctomycetes*. We determined in detail the distribution of IntV2 and IntV1 (VC0847) among all sequenced *Vibrionaceae* and uncovered 78 PAI-encoded integrases. IntV1 and IntV2 did not share a common evolutionary history each branching within divergent lineages. However, we identified two novel recombination directionality factor (RDF) encoded by *vefA* (VC1785) and *vefB* (VC1809) within VPI-2, which are absent from VPI-1. We found that VefA is essential for VPI-2 excision but also induces excision of VPI-1 suggesting cross-talk between the islands.